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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 18.8788 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-2_COPY_36_478

Perfect score: 2369

Sequence: 1 GLTONKALPENVKYGVILDA.....TNMIPAEQPLSTPLSHSTYV 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2369	100.0	502	4	US-09-557-800C-55
2	2369	100.0	502	4	US-09-370-625A-38
3	2369	100.0	510	3	US-08-930-921-1
4	2369	100.0	510	4	US-09-781-796C-1
5	911	38.5	529	3	US-09-240-639-4
6	911	38.5	529	4	US-09-908-510A-4
7	911	38.5	529	4	US-09-905-744B-4
8	911	38.5	529	4	US-10-107-660-4
9	911	38.5	529	4	US-10-107-576-4
10	911	38.5	529	4	US-09-905-732B-4
11	911	38.5	529	4	US-09-923-304-4
12	911	38.5	529	4	US-09-949-016-6049
13	911	38.5	529	4	US-09-905-743B-4
14	911	38.5	556	4	US-09-949-016-11328
15	868.5	36.7	282	4	US-09-949-016-7977
16	865	36.5	479	4	US-09-949-016-11559
17	803	33.9	153	3	US-09-240-639-13
18	803	33.9	153	4	US-09-908-510A-13
19	803	33.9	153	4	US-09-905-744B-13
20	803	33.9	153	4	US-10-107-660-13
21	803	33.9	153	4	US-10-107-576-13
22	803	33.9	153	4	US-09-905-732B-13
23	803	33.9	153	4	US-09-905-743B-13
24	604	25.5	154	3	US-09-240-639-14
25	604	25.5	154	4	US-09-908-510A-14
26	604	25.5	154	4	US-09-905-744B-14
27	604	25.5	154	4	US-10-107-660-14

28	604	25.5	154	4	US-10-107-576-14
29	604	25.5	154	4	US-09-905-732B-14
30	604	25.5	154	4	US-09-905-743B-14
31	442.5	18.7	153	3	US-09-240-639-15
32	442.5	18.7	153	4	US-09-908-510A-15
33	442.5	18.7	153	4	US-09-905-744B-15
34	442.5	18.7	153	4	US-10-107-660-15
35	442.5	18.7	153	4	US-10-107-576-15
36	442.5	18.7	153	4	US-09-905-732B-15
37	442.5	18.7	153	4	US-09-905-743B-15
38	427	18.0	462	4	US-09-129-112-2
39	421.5	17.8	462	4	US-09-129-112-15
40	417.5	17.6	150	3	US-09-240-639-16
41	417.5	17.6	150	4	US-09-908-510A-16
42	417.5	17.6	150	4	US-09-905-744B-16
43	417.5	17.6	150	4	US-10-107-660-16
44	417.5	17.6	150	4	US-10-107-576-16
45	417.5	17.6	150	4	US-09-905-732B-16

ALIGNMENTS

RESULT 1
US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent NO. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 100.0%; Score 2369; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.5e-244;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GLTONKALPENVKYGIVLDAGSSHTSYLYIKWPAEKENDTG	VVHVQVSECRVKGPGISKFV	60
Db	36	GLTONKALPENVKYGIVLDAGSSHTSYLYIKWPAEKENDTG	VVHVQVSECRVKGPGISKFV	95
Qy	61	QKNEIGIYLTDCHMERAREVIPSQHQETPVYLGATAGMRLLRMESEBELAD	RVLDDVVVERS	120
Db	96	QKNEIGIYLTDCHMERAREVIPSQHQETPVYLGATAGMRLLRMESEBELAD	RVLDDVVVERS	155
Qy	121	LSNYPDFQGARIIITGOEGAYGWIITINYLKGFSQKTRWFSIVPYETNNQETFGALD	ILG	180

Db	156	LSNTPDFQGARIIITGQEGAGYITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG	215
Qy	181	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	240
Db	216	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	275
Qy	241	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	300
Db	276	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	335
Qy	301	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	360
Db	336	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	455
Qy	421	LNLTNMIPAEQPLSTPLSHSTYV	443
Db	456	LNLTNMIPAEQPLSTPLSHSTYV	478
RESULT 2			
US-09-370-625A-38			
; Sequence 38, Application US/09370625A			
; Patent No. 6600032			
; GENERAL INFORMATION:			
; APPLICANT: Mulero, Julio			
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES			
; FILE REFERENCE: 28110735908			
; CURRENT APPLICATION NUMBER: US/09/370,625A			
; PRIOR FILING DATE: 1999-08-09			
; PRIOR FILING DATE: 1999-07-16			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR FILING DATE: 1999-03-19			
; NUMBER OF SEQ ID NOS: 39			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 38			
; LENGTH: 502			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-370-625A-38			
Query Match 100.0%; Score 2369; DB 4; Length 502;			
Best Local Similarity 100.0%; Pred. No. 4.5e-244;			
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHVEECRVKPGISKFV	60
Db	36	GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHVEECRVKPGISKFV	95
Qy	61	QKVEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGWRLLRMESEELADRLVDVVERS	120
Db	96	QKVEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGWRLLRMESEELADRLVDVVERS	155
Qy	121	LSNYPDFQGARIIITGQEGAGYITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG	180
Db	156	LSNYPDFQGARIIITGQEGAGYITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG	215
Qy	181	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	240
Db	216	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	275
Qy	241	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	300
Db	276	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	335
Qy	301	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	360
Db	336	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	455
Qy	421	LNLTNMIPAEQPLSTPLSHSTYV	443
Db	456	LNLTNMIPAEQPLSTPLSHSTYV	478
RESULT 3			
US-08-930-921-1			
; Sequence 1, Application US/08930921B			
; Patent No. 6287837			
; GENERAL INFORMATION:			
; APPLICANT: BEAUDOIN, Adrien R.			
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION			
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT			
; TITLE OF INVENTION: TECHNOLOGY			
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEADUOIN			
; CURRENT APPLICATION NUMBER: US/08/930,921B			
; EARLIER FILING DATE: 1998-01-02			
; EARLIER FILING DATE: 1996-04-10			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 510			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: Description of Unknown Organism: unknown			
US-08-930-921-1			
Query Match 100.0%; Score 2369; DB 3; Length 510;			
Best Local Similarity 100.0%; Pred. No. 4.6e-244;			
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHVEECRVKPGISKFV	60
Db	36	GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHVEECRVKPGISKFV	95
Qy	61	QKVEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGWRLLRMESEELADRLVDVVERS	120
Db	96	QKVEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGWRLLRMESEELADRLVDVVERS	155
Qy	121	LSNYPDFQGARIIITGQEGAGYITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG	180
Db	156	LSNYPDFQGARIIITGQEGAGYITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG	215
Qy	181	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	240
Db	216	GASTQVTFVFNQNTIESPDNALQRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN	275
Qy	241	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	300
Db	276	EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFT	335
Qy	301	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	360
Db	336	SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYM	455
Qy	421	LNLTNMIPAEQPLSTPLSHSTYV	443
Db	456	LNLTNMIPAEQPLSTPLSHSTYV	478

RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 100.0%; Score 2369; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.6e-244;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLTNKALPENVKIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHQBECRVKGGISKFV 60
Db 36 GLTNKALPENVKIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHQBECRVKGGISKFV 95
Qy 61 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDADRVLDVVERS 120
Db 96 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDADRVLDVVERS 155
Qy 121 LSNYPDFQGARIIITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 180
Db 156 LSNYPDFQGARIIITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 215
Qy 181 GASTQVTFVFPQNTIESPDNALQFRLYGKDYNYVTHSFCLYQKQALWQKLAKDIQVASN 240
Db 216 GASTQVTFVFPQNTIESPDNALQFRLYGKDYNYVTHSFCLYQKQALWQKLAKDIQVASN 275
Qy 241 EILRDCPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFQOFEIQGIGNYQOCHQSILELFT 300
Db 276 EILRDCPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFQOFEIQGIGNYQOCHQSILELFT 335
Qy 301 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPQW 360
Db 336 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPQW 395
Qy 361 EIKTSYAGVKBYLSEYCFSGTYSILSLQYHFTADSWEHIFIGIKQSDAGWTLYG 420
Db 396 EIKTSYAGVKBYLSEYCFSGTYSILSLQYHFTADSWEHIFIGIKQSDAGWTLYG 455
Qy 421 LNLNMTIPAEQPLSTPLSHSYV 443
Db 456 LNLNMTIPAEQPLSTPLSHSYV 478

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4
Query Match 38.5%; Score 911; DB 3; Length 529;
Best Local Similarity 40.9%; Pred. No. 3.5e-88;
Matches 182; Conservative 81; Mismatches 174; Indels 8; Gaps 6;
Qy 4 QNKALPENVKIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHQBECRVKGGISKFVQKV 63
Db 47 QKQVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVSQTEKCSVKSGISSYGNP 106
Qy 64 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDADRVLDVVERSLSN 123
Db 107 QDVPAFECCQKVKGVQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166
Qy 124 YPDFQGARIIITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGAS 183
Db 167 QPDFRGAQIIISQEGEGYGVWITANLYLNGFLEKNLWMMV--HPHGVETTGALDLGAS 224
Qy 184 TQVTFVFPQNTIESPDNALQFRLYGKDYNYVTHSFCLYQKQALWQKLAKDIQVA-SNEI 242
Db 225 TQISFVAGERMDLNTSDIMQVSLYGVYVTLVTHSFQCVGRNEAEKKFLAMLQNSPTKH 284
Qy 243 LRDCPCHPGYKVKVNVSDLYKTPCT--KRFEMTLPPFOQFEIQGIGNYQOCHQSILELFT 300
Db 285 LTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDVITPEGTGDPSELCKEKVASI 344
Qy 301 SYC-PYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPQW 359
Db 345 KACHDQETCSFDGVYQKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWFCSQNW 403
Qy 360 EEIKTSYAGVKBYLSEYCFSGTYSILSLQYHFTADSWEHIFIGIKQSDAGWTLYG 419
Db 404 SOLPLLLPKFDEVYVARSYCFSSANYIYHLFVNGYKFTETWQIHFKEVGVNSSIATSLGY 463
Qy 420 LNLNMTIPAEQPL-STPLSHSYV 443
Db 464 MSLTNQIPAESPLIRLPIEPVFEV 488

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/361208
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

Qy 360 EEIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGKIQSDAGWTGLY 419
 Db 404 SOLPLLPKPFDEVYARSYCFGSANYIYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 463
 Qy 420 MLNLTNMIPAEQPL-STPLSHSTYV 443
 Db 464 MSLTNOIPAESPLIRLPIEPVVFV 488

RESULT 9
 US-10-107-576-4
 ; Sequence 4, Application US/10107576
 ; Patent No. 6783959
 ; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
 ; FILE REFERENCE: 28110/36120H
 ; CURRENT APPLICATION NUMBER: US/10/107,576
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: 09/240,639
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-107-576-4

Query Match 38.5%; Score 911; DB 4; Length 529;
 Best Local Similarity 40.9%; Pred. No. 3.5e-88;
 Matches 182; Conservative 81; Mismatches 174; Indels 8; Gaps 6;
 Qy 4 QNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGGISGFVKQV 63
 Db 47 KOEVLPPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVSQTFCVKSGSGISSYGNP 106
 Qy 64 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEBELADRVLDVVERSLN 123
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 Qy 124 YPFDFOGARIITGOEAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 183
 Db 167 QPFPFRAQIISGQEGYGVGHITANYLMGNFLEKXLMHWMV--HPHGVETTTGALDLGGAS 224
 Qy 184 TQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKQDQALWQKLAKDIQVA-SNEI 242
 Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
 Qy 243 LRDFCFHPGKVVNVSDLYKTPTCT--KRPEMTLPFOQFEIQGIGNYQOCHSILELPT 300
 Db 285 LTNPFCYPRDYSISFTMGHVFSLCTVDQRPESYNPNVDITFEGTGDPSLCKEKVASIFDF 344
 Qy 301 SYC-PYSQCAFNGIFLPPLODGFAGSAPYFVMKFLNLTSEKVSQEKVTEMMKFCQAPW 359
 Db 345 KACHDOETCSFDGVYQPKIGPFAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
 Qy 360 EEIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGKIQSDAGWTGLY 419
 Db 404 SOLPLLPKPFDEVYARSYCFGSANYIYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 463
 Qy 420 MLNLTNMIPAEQPL-STPLSHSTYV 443
 Db 464 MSLTNOIPAESPLIRLPIEPVVFV 488

RESULT 10
 US-09-905-732B-4
 ; Sequence 4, Application US/09905732B
 ; Patent No. 6787328

; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; APPLICANT: Frischaut, Anna Maria
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
 ; FILE REFERENCE: 28110/36120B
 ; CURRENT APPLICATION NUMBER: US/09/905,732B
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 09/240,639
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-905-732B-4

Query Match 38.5%; Score 911; DB 4; Length 529;
 Best Local Similarity 40.9%; Pred. No. 3.5e-88;
 Matches 182; Conservative 81; Mismatches 174; Indels 8; Gaps 6;
 Qy 4 QNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGGISGFVKQV 63
 Db 47 KOEVLPPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVSQTFCVKSGSGISSYGNP 106
 Qy 64 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEBELADRVLDVVERSLN 123
 Db 107 QDVPRAECEMOKVKGQVPSHLHGSTPIHLGATAGMELLRQLQNETAANEVLESISQYFKS 166
 Qy 124 YPFDFOGARIITGOEAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 183
 Db 167 QPFPFRAQIISGQEGYGVGHITANYLMGNFLEKXLMHWMV--HPHGVETTTGALDLGGAS 224
 Qy 184 TQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKQDQALWQKLAKDIQVA-SNEI 242
 Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
 Qy 243 LRDFCFHPGKVVNVSDLYKTPTCT--KRPEMTLPFOQFEIQGIGNYQOCHSILELPT 300
 Db 285 LTNPFCYPRDYSISFTMGHVFSLCTVDQRPESYNPNVDITFEGTGDPSLCKEKVASIFDF 344
 Qy 301 SYC-PYSQCAFNGIFLPPLODGFAGSAPYFVMKFLNLTSEKVSQEKVTEMMKFCQAPW 359
 Db 345 KACHDOETCSFDGVYQPKIGPFAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
 Qy 360 EEIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGKIQSDAGWTGLY 419
 Db 404 SOLPLLPKPFDEVYARSYCFGSANYIYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 463
 Qy 420 MLNLTNMIPAEQPL-STPLSHSTYV 443
 Db 464 MSLTNOIPAESPLIRLPIEPVVFV 488

RESULT 11
 US-09-923-304-4
 ; Sequence 4, Application US/09923304
 ; Patent No. 6797471
 ; GENERAL INFORMATION:
 ; APPLICANT: KATZ, RUTH
 ; APPLICANT: JIANG, FENG
 ; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
 ; FILE REFERENCE: UTSC:658US
 ; CURRENT APPLICATION NUMBER: US/09/923,304
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-923-304-4


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Db 345 KACHDQETCSGDYVQPKIKGFFVAFAGFYTASALNL-SGSFSLDTFNSWTNFCQNW 403
Qy 360 BEIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWHEHIFIGKIQGSDAGWTLYG 419
Db 404 SOLPLLPKPKDEVVARSYCFSANVYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 463
Qy 420 MLNLTNMPAEQPL-STPLSHSTYV 443
Db 464 MSLTNQIPAESPLIRLPPIEPVVF 488

RESULT 14
US-09-949-016-11328
; Sequence 11328: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 38.5%; Score 911; DB 4; Length 556;
Best Local Similarity 40.9%; Pred. No. 3.8e-88;
Matches 182; Conservative 81; Mismatches 174; Indels 8; Gaps 6;

Qy 4 QNKLALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQQVEECRVKGGISKFQKV 63
Db 74 KQVLPPLKGLKGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQQVEECRVKGGISGNNP 133
Qy 64 NEIGYLTDCMERAREVIPSQHOETPVYLCATAGMRLLRMESEELADRVLDVVERSLSN 123
Db 134 QDVPRAEFCQKVGQVPSHLRGSPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 193
Qy 124 YPFDFOGARIITGOEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGAS 183
Db 194 QPFDGCAQIIISGOEGYGVGWTANYLGNFLEKNLHMWV--HPHGVTETGALDLGAS 251
Qy 184 TQVTFVQNTIESPDNALQRLYKGDYVNYVTHSFLCYGKQDQALWQKLAKDQIQA-SNEI 242
Db 252 TQISFVAGEKMDLNTSDIMQVSLYGYVYVYTHSFCYGRNEAKKFLAMLLQNSPTQW 311
Qy 243 LRDCPFHPGYKKVNVSDLYKTPCT--KRFTMTLPPQOFEIQGIGNYQOCHQSILELNT 300
Db 312 LTNPCYPRDISISFTMGHVFSLCTVDQRPESYNPNVDITPEGTGDPDLCKEKEVASIPDF 371
Qy 301 SYC-PYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 359
Db 372 KACHDQETCSGDYVQPKIKGFFVAFAGFYTASALNL-SGSFSLDTFNSWTNFCQNW 430
Qy 360 BEIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWHEHIFIGKIQGSDAGWTLYG 419
Db 431 SOLPLLPKPKDEVVARSYCFSANVYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 490
Qy 420 MLNLTNMPAEQPL-STPLSHSTYV 443
Db 491 MSLTNQIPAESPLIRLPPIEPVVF 515
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RESULT 15

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US-09-949-016-7977
; Sequence 7977: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7977
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7977

Query Match 36.7%; Score 868.5; DB 4; Length 282;
Best Local Similarity 43.3%; Pred. No. 4.4e-84;
Matches 192; Conservative 0; Mismatches 0; Indels 251; Gaps 1;

Qy 1 GLTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQQVEECRVKGGISKFV 60
Db 59 GLTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQQVEECRVKGGISKFV 118
Qy 61 QKNEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLLRMESEELADRVLDVVERS 120
Db 119 QKNEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLLRMESEELADRVLDVVERS 178
Qy 121 LSNYPFDFQAGARIITGOEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLG 180
Db 179 LSNYPFDFQAGARIITGOEGAYGWITINYLIGKFSQ----- 214
Qy 181 GASTQVTFVQNTIESPDNALQRLYKGDYVNYVTHSFLCYGKQDQALWQKLAKDQIQA-SN 240
Db 215 ----- 214
Qy 241 EILRDCPFHPGYKKVNVSDLYKTPCTKRFTMTLPPQOFEIQGIGNYQOCHQSILELNT 300
Db 215 ----- 214
Qy 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 360
Db 215 ----- 214
Qy 361 EIKTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWHEHIFIGKIQGSDAGWTLYG 420
Db 215 -----IQGSDAGWTLYG 227
Qy 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db 228 LNLTNMIPAEQPLSTPLSHSTYV 250
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Search completed: March 7, 2005, 13:27:50
Job time : 20.8788 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 13.5165 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147A-2_COPY_39_476
Perfect score: 2343
Sequence: 1 QNKALPENVKYGIIVLDAGSS.....NLTNMPAEQPLSTPLSHST 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2343	100.0	510	2 I56242	lymphoid cell acti
2	505	21.6	483	2 D86276	hypothetical prote
3	469.5	20.0	405	2 E86276	hypothetical prote
4	453	19.3	630	2 S50463	hypothetical prote
5	416	17.8	572	2 T40856	probable nucleotid
6	406.5	17.3	516	2 G84442	probable nucleosid
7	402.5	17.2	485	2 T34147	hypothetical prote
8	394.5	16.8	508	2 C86276	7A19.33 protein -
9	383.5	16.4	557	2 T16696	hypothetical prote
10	381.5	16.3	556	2 T39109	probable guanosine
11	374	16.0	455	2 S48859	nucleoside triphos
12	334	14.3	454	2 J4616	aprase (EC 3.6.1.
13	332	14.2	1052	2 T04339	hypothetical prote
14	328.5	14.0	479	2 T23508	hypothetical prote
15	320.5	13.7	518	2 A40732	guanosine-diphosph
16	167	7.1	628	2 A55421	nucleoside-triphos
17	103	4.4	369	2 S77299	C4-dicarboxylase-b
18	101.5	4.3	716	2 T21516	hypothetical prote
19	100	4.3	307	2 T27332	hypothetical prote
20	99	4.2	1951	2 B43963	RNA viral polymera
21	98.5	4.2	590	2 A81411	autolysin, N-acety
22	98.5	4.2	797	2 D86247	hypothetical prote
23	98.5	4.2	989	2 B84532	hypothetical prote
24	98.5	4.2	1509	2 B89985	hypothetical prote
25	98	4.2	371	2 T05213	hypothetical prote
26	98	4.2	665	2 T18979	hypothetical prote
27	98	4.2	3848	2 T17414	TpC protein - sli
28	97.5	4.2	392	2 A36738	hypothetical prote
29	97	4.1	494	2 T03774	probable histidine

30	96	4.1	883	2 B85725	probable fimbrial
31	96	4.1	1028	2 I51173	myosin I beta - bu
32	96	4.1	1415	2 A72369	(R)-2-hydroxygluta
33	95.5	4.1	591	2 F89770	hypothetical prote
34	95.5	4.1	1900	2 AC2391	seine/threonine k
35	95	4.1	288	1 B48583	spore germination
36	95	4.1	451	2 G59859	Mg2+ transporter h
37	95	4.1	564	2 S15962	lactacin 481/lacto
38	95	4.1	927	2 T43110	probable permease
39	94.5	4.0	461	2 G91228	probable permease
40	94.5	4.0	461	2 F86075	hypothetical prote
41	92.5	3.9	404	2 T21251	hypothetical 51.7
42	92.5	3.9	468	2 H65192	probable dnaK-type
43	92.5	3.9	556	2 A30715	probable dnaK-type
44	92.5	3.9	556	2 H64799	fibroblast growth
45	92.5	3.9	806	1 TVHUF3	

ALIGNMENTS

RESULT 1

I56242
lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56242
R:Maliszewski, C.R.; Deleseppe, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A:Reference number: I56242; MUID:95015846; PMID:7930580
A:Accession: I56242
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: UNIPROT:P49961; GB:S73813; NID:g765255; PIDN:AAB32152.1; PID:g765255
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	100.0%;	Score	2343;	DB 2;	Length	510;			
Best Local Similarity	100.0%;	Pred. No.	6.8e-183;						
Matches	438;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	QNKALPENVKYGIIVLDAGSSHTSLYIIKWPAEKENDTG	VVHQV	EECRV	KPGIS	KFPVQ	KV	60	
Db	39	QNKALPENVKYGIIVLDAGSSHTSLYIIKWPAEKENDTG	VVHQV	EECRV	KPGIS	KFPVQ	KV	98	
Qy	61	NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLR	MESEELADRV	LDV	VER	SLN	120		
Db	99	NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLR	MESEELADRV	LDV	VER	SLN	158		
Qy	121	YPFDFQGARIIITGQEEGAYGWITINLLGKFSQKTRWFS	IVPYETNNQET	FGALD	LGAS	180			
Db	159	YPFDFQGARIIITGQEEGAYGWITINLLGKFSQKTRWFS	IVPYETNNQET	FGALD	LGAS	218			
Qy	181	TQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCY	GKDQALWQKLAKDI	QVASNEIL	240				
Db	219	TQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCY	GKDQALWQKLAKDI	QVASNEIL	278				
Qy	241	RDPCFHFPGYKKVNVSDLYKTPCTKRFEMTLPFOQFEI	TGQIGNYQQCHQSILEL	FNTSYC	300				
Db	279	RDPCFHFPGYKKVNVSDLYKTPCTKRFEMTLPFOQFEI	TGQIGNYQQCHQSILEL	FNTSYC	338				
Qy	301	PYSQCAFNGIFLPPLOQDFGAFSAFYFVWKFLNLTSEK	VSQEKVTEMMKKKCAQ	PWEEK	360				
Db	339	PYSQCAFNGIFLPPLOQDFGAFSAFYFVWKFLNLTSEK	VSQEKVTEMMKKKCAQ	PWEEK	398				
Qy	361	TSYAGVKEKYLSEYCFSGTGYILSLLQGYHFTADSWEH	IFIGIKIQGSDAGWTL	GYMLNL	420				
Db	399	TSYAGVKEKYLSEYCFSGTGYILSLLQGYHFTADSWEH	IFIGIKIQGSDAGWTL	GYMLNL	458				
Qy	421	TNMTIPAEQPLSTPLSHST	438						
Db	459	TNMTIPAEQPLSTPLSHST	476						

[illegible]

C;Cross-references: A;Gene: At2g02970 A;Map position: 2 C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.3%; Score 406.5; DB 2; Length 516;
Best Local Similarity 27.5%; Pred. No. 4.2e-25;
Matches 117; Conservative 68; Mismatches 187; Indels 53; Gaps 13;

Qy 8 NVKYGIVLDAGSHTSLIYIKWPAEKENDTGVVHVQVECEYK-GPGISKEVQKVEIGIY 66
Db SLRYSVVDGGSTGTRIHFVGYRIESGKPVFEPRGANYASLKLHPLGSFADDPDGASVS 124
Qy 17 LDCMERAREVIPSQHOETPVVLGATAGNRLRMSEELADRLVDVVERSL--SNYPFD 124
Db LTELVEFAKGRVPKGMWIEVELMATAGNRLLELPVQE---KILGVARRVLKSSGFLFR 181
Qy 125 FQGIARIITQOEGAGWITINYLGRKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVT 184
Db 182 DEWASVISGSDEGVYAWVANFALGSLG-----GDPLKTTGIVELGGASAQVT 229
Qy 185 FVPQNTQIESPDNALQRLYKGDYNYVTISFLCYGKDQA---LW-QKLAKD-----IQVAS 236
Db 230 FVSSEPM--PPEFSRTISFGNVTNYLSHSLFHFGQNAADKLWGSLLSRDHNSAVEPTR 287
Qy 237 NEILRDPCHPGYKVVVNSDLVKTCTKRFEMTLPQOPEIQIGIGNYQOCHOSILEFN 296
Db 288 EKIFTDPCAPKGYNDANTQKHLGSLLABESRLDSF-----QAGGNYSQCRSAALTILQ 342
Qy 297 TSYCPYSQCAFNGIFLPLQDGFAPSAFYVNMKFLNLTSEKVSQEKVEMMKFKCAQPV 356
Db 343 DG-----NQRILIIITAG-----FSFLFFGI-----GEKAWLSNMISAGERFCGEDW 383
Qy 357 EEIKTSYAGYKEKYLSEYCFSGTYIILSLQLQGYHFTADSWEHIFHTKIQGSDAGMTLGY 416
Db 384 SKLRVKDPSLHEEDLLRYCFSSAYIVSLDHTLIGIPLDD-ERIGYANQAGDIPLDWALGA 442
Qy 417 MLNLT 421
Db 443 FIQOT 447

Mon Mar 7 13:29:10 2005

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <STO>
A:Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN
C:Genetics:
C:Map position: 1
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.8%; Score 394.5; DB 2; Length 508;
Best Local Similarity 28.2%; Pred. No. 3.9e-24;
Matches 123; Conservative 71; Mismatches 171; Indels 71; Gaps 20;
Qy 8 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGV---VHQVEECRVK-GPGISKFKVQKNEI 63
Db 63 SLHYSVIIDGSSGTRVHVFGYRIESGKPVDFGGENYASLKLSPGLSAYADNPEGVSES 122
Qy 67 LTDCMERAREVTPRSQHQETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPFDFQ 126
Db 123 VTELVEFAKRVHKGKLSKDIRLMATAGRLLELPQB---QILDVTRVLRSSGDFP- 178
Qy 127 GARIITQBEQAYGMITINYLKFKSQKTRWFSIVPYETNN-QETFGALDLG-----GA 179
Db 179 -----RDWASVISEILENFQDLMKVYMLGILLIMRSV 211
Qy 180 STQVTVFQNTQIESPDNALQFRLYK-DYNYTHSFYCYGKQALWOKLAKDI-QVASN 237
Db 212 RLEVTTFV---STELVPSEFSRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
Qy 238 E-----ILRDCPHPGYKVVNV-SLYKTPCTK-RPEMTLPFOQFBIQIGNYQQCHSI 291
Db 268 STQEGIVPDCIPKGIILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
Qy 292 LELF---NTSYCPYSCAFNGIFLPPIQDGFAPSAFYFVKFNLNLTSEKVSQKVTMM- 348
Db 321 FAMLQBEKGTCTYKRCISGIFTNQLGSLATENFHTSKFFGL-GEK---EMLSEMIL 376
Qy 349 --KKFCAQPEEIKTSYAGVKEKVLSEYCFSGVYVILSLILQGVHFTADSWEHITFGIKI 406
Db 377 AKRFGCEESKLVKYPFTKDENLRLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
Qy 407 GSD--AGWTILG-YMLN 419
Db 436 EEDIPLDWALQAFILN 451

Query Match 17.2%; Score 402.5; DB 2; Length 485;
Best Local Similarity 26.7%; Pred. No. 8.2e-25;
Matches 116; Conservative 69; Mismatches 187; Indels 63; Gaps 15;
Qy 8 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGV---VHQVEECRVK-GPGISKFKVQKNEI 63
Db 22 NIKYGVICDAGSSGTRFVYTLKPLSGGLTNTDILIHSEPVWKKVTPGLSSFGDKPEQV 81
Qy 64 GYLTDCEMERAREVTPRSQHQETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPF 123
Db 82 VEYLTPLRFABEHIPEYQLQGETDLIFATAGMRLLRPEAQDAIKNLQGLKSVTALRV 141
Qy 124 DFQGAIRITQBEQAYGMITINYLKFKSQKTRWFSIVPYETNNQETFGALDLGASTQV 183
Db 142 SDSNRIIDGAWEGYIYIAVNYILGRDKE-----NDSKVGIMDGGASVQI 189
Qy 184 TFPVQNTQIESPD--NALQFRLYKGD-----YNYTHSFYCYGKQALWOKLAKDIOVA 235
Db 190 APELANEK-ESYNGNGVVEINLSTETNEDYKIYITFLYGANEGL-KKYENSLVKS 247
Qy 236 SNEILRDCPHPGYKVVNVSDLYKTPCTKREMTLPFOQFBIQIGNYQQCHSIILF 295
Db 248 GNS--NDSCSPRGLNRLIG-----EFTVNGTGEWDVCLAQVSLI 285
Qy 296 NTS---YCPYSQCAFNGIFLPLQ---GDFGAFSAFYFVKFNLNLTSEKVSQKVTMMK 349
Db 286 GDAQPSQCNPTCFLENNVAPSVNLSTVQLYGFSEVYVYTSNFGSGGE-YHYQKFTDEV 344
Qy 350 KFCAPQWBEI-----KTSYAGVKEKVLSEYCFSGVYVILSLILQGVHFTADSWEHITFG 403
Db 345 KYCQKDWNDIQGFKRNEFPNADIERLGTNCPCFAAWVTSLVHDG--FNVDTKHLFQSVL 402
Qy 404 KICSSDAGWTGLVML 418
Db 403 KIAGEEMQWALGAML 417

RESULT 7
T34147
hypothetical protein C33H5.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34147
R:Bradshaw, H.; Steliyes, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C33H5.
A:Reference number: 221482
A:Accession: T34147
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-485 <BRA>
A:Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C33H5.14
A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C:Superfamily: nucleoside triphosphatase chromatin-associated

RESULT 8
C86276
7A19.33 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Query Match 16.4%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.5e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
Qy 8 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGV---VHQVEECRVK-GPGISKFKVQKNEI 66
Db 63 SLHYSVIIDGSSGTRVHVFGYRIESGKPVDFGGENYASLKLSPGLSAYADNPEGVSES 122
Qy 67 LTDCMERAREVTPRSQHQETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPFDFQ 126
Db 123 VTELVEFAKRVHKGKLSKDIRLMATAGRLLELPQB---QILDVTRVLRSSGDFP- 178
Qy 127 GARIITQBEQAYGMITINYLKFKSQKTRWFSIVPYETNN-QETFGALDLG-----GA 179
Db 179 -----RDWASVISEILENFQDLMKVYMLGILLIMRSV 211
Qy 180 STQVTVFQNTQIESPDNALQFRLYK-DYNYTHSFYCYGKQALWOKLAKDI-QVASN 237
Db 212 RLEVTTFV---STELVPSEFSRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
Qy 238 E-----ILRDCPHPGYKVVNV-SLYKTPCTK-RPEMTLPFOQFBIQIGNYQQCHSI 291
Db 268 STQEGIVPDCIPKGIILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
Qy 292 LELF---NTSYCPYSCAFNGIFLPPIQDGFAPSAFYFVKFNLNLTSEKVSQKVTMM- 348
Db 321 FAMLQBEKGTCTYKRCISGIFTNQLGSLATENFHTSKFFGL-GEK---EMLSEMIL 376
Qy 349 --KKFCAQPEEIKTSYAGVKEKVLSEYCFSGVYVILSLILQGVHFTADSWEHITFGIKI 406
Db 377 AKRFGCEESKLVKYPFTKDENLRLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
Qy 407 GSD--AGWTILG-YMLN 419
Db 436 EEDIPLDWALQAFILN 451

RESULT 9
T16696
hypothetical protein R07E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16696
R:Miller, N.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid R07E4.
A:Reference number: 218561
A:Accession: T16696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-557 <MIL>
A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R07E4.4
A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match 16.4%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.5e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
Qy 8 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGV---VHQVEECRVK-GPGISKFKVQKNEI 66
Db 63 SLHYSVIIDGSSGTRVHVFGYRIESGKPVDFGGENYASLKLSPGLSAYADNPEGVSES 122
Qy 67 LTDCMERAREVTPRSQHQETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPFDFQ 126
Db 123 VTELVEFAKRVHKGKLSKDIRLMATAGRLLELPQB---QILDVTRVLRSSGDFP- 178
Qy 127 GARIITQBEQAYGMITINYLKFKSQKTRWFSIVPYETNN-QETFGALDLG-----GA 179
Db 179 -----RDWASVISEILENFQDLMKVYMLGILLIMRSV 211
Qy 180 STQVTVFQNTQIESPDNALQFRLYK-DYNYTHSFYCYGKQALWOKLAKDI-QVASN 237
Db 212 RLEVTTFV---STELVPSEFSRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
Qy 238 E-----ILRDCPHPGYKVVNV-SLYKTPCTK-RPEMTLPFOQFBIQIGNYQQCHSI 291
Db 268 STQEGIVPDCIPKGIILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
Qy 292 LELF---NTSYCPYSCAFNGIFLPPIQDGFAPSAFYFVKFNLNLTSEKVSQKVTMM- 348
Db 321 FAMLQBEKGTCTYKRCISGIFTNQLGSLATENFHTSKFFGL-GEK---EMLSEMIL 376
Qy 349 --KKFCAQPEEIKTSYAGVKEKVLSEYCFSGVYVILSLILQGVHFTADSWEHITFGIKI 406
Db 377 AKRFGCEESKLVKYPFTKDENLRLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
Qy 407 GSD--AGWTILG-YMLN 419
Db 436 EEDIPLDWALQAFILN 451

Query Match	16.3%	Score 381.5	DB 2	Length 556		
Best Local Similarity	27.1%	Pred. No. 5.1e-23				
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Gaps	17					
QY	10	KYGVLDAGSHTSLXYTKYPAEKENDGTGVVHVEE--CRVKGPGISKVFQVKVNI	GI	VL 67		
DB	133	QYVLMIDAGTSGSRVHYQF-----NNCNPSPKLEEEFFKMEPLGSLSPAGD	PE	GAASL 187		
QY	68	TDCMERAREVTPRSQHQETPVYLGATGMRLLRMESELA	DR	VL 125		
DB	188	DPLLDYAMENVPPEYRRCSPIAVATAG--LRLTGESEAKAILKSVRQHL	ENDY	PPFIV 244		
QY	126	-QGARIITQDEGAGVGTITINVLGKPSQKTRWPSIVPVTNNQSTFGAL	DGGAS	TQV 184		
DB	245	KDGVSLIEGSMEGYAMITINVLGTLGCKA-----TSTVA	MDLGGAS	TQV 293		
QY	185	FVPO-----NQTI	SPDNALQRLY	GKDYNVYTHSFLCYGKQOALWQKLAK	DIQV	ASNEIL 240
DB	294	FEPRFASDGSLSVDCDGHKVLVDYNGEQLYQSHLGYCLKEA--RKL	THK	FVLNNASAL 351		

Query Match	16.0%; Score 374; DB 2; Length 455;
Best Local Similarity	25.6%; Pred. No. 1.6e-22;
Matches	Conservative 80; Mismatches 169; Indels 88; Gaps 18;

Qy	11	YGIVLDAGSSHSLYIKWPAEKENDTGVVH---QVEECRVKGGISKFVKQVNEIGIYL	67
Db	44	YAVVFAGSTGSRHHYHF-----NQNLDDLHLHGKVGEYYNKKITPGLSSSYANNPEQAAKSL	99
Qy	68	TDCMERAREVIPRSQHQTTPVVLGATAGMRLLMSEELADRDVLDDVVERSLSN--YPPDFQ	126
Db	100	IPLLEQAEADVPPDLPQKTFVRLGATAGLRLNGDASE---KILQSVRDMLSNRSTFNVQ	156
Qy	127	--GARIIITQBEGAGWITINILLKPSQKTRWFISIVPYETNNQHTFGALDLGGASTQVT	184
Db	157	PDAVISIIDGTQSGYLLWTVNYALGNLKGK-----YTKTVGVIDLGGGSVQMA	204
Qy	185	FVPQNQTIESPNAL-----QFLYKGDVNVTYTHSELFCYKDQALWQKLAKDIQVAS	236
Db	205	YAVSKKTAKNAPKVADGDDPYIKKKVVLKGIPLYLVHSHLHFR-----EASR	252
Qy	237	NEILR-----DPCFHFGYKVVNVSDLYKTPCTKRFEMLTPQQFIEQGIGNYQQCHOS	290
Db	253	AETLKLTSPSPNCLLAGFNIGITYSG-----EEFKAT-----AYTSGANFNKCNT	299
Qy	291	ILELFNTSY-CPVSQCAFNGIFLPPLOGDFG-----AFSAFYVMKFLNLITSEK----	338
Db	300	IRKALKLNTPCPYQNCTFGGIW----NGGGNGQKNLFASSSFYPILPEDTGMDASTPNF	355
Qy	339	-VSQEKVTEMMKFCQAPHEEIKTSYAGVKEKYLSY-CFSGYIISLLIQGHVFTADSW	396
Db	356	ILRPVDIETKAEACALNFEDAKSTYFFIDKKRVASYCMDLIIYQVLLVDG--FGLDPL	413
Qy	397	EHIHFITGKIQGSd-----AGWTLLGYMLNLTNMIP	425
Db	414	OKITSKEIEYQDAIVEAAWPLGNAVEAISALP	446

RESULT 12
 JC4616


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A:Map position: 5L
C:Function:
A:Description: nucleoside triphosphatase chromatin-associated
C:Superfamily: nucleoside triphosphatase; hydrolase; transmembrane protein
C:Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F:10-24/Domain: transmembrane #status predicted <TMM>
F:41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      13.7%; Score 320.5; DB 2; Length 518;
Best Local Similarity 26.8%; Pred. No. 4.3e-18;
Matches 121; Conservative 70; Mismatches 188; Indels 73; Gaps 20;

QY      7  ENVKYGI VLDAGSSHTSLVIYKPKAEKENDGTGVHQQVECRVKPGGIGSKFVKQKVEIGI- 65
DB      89  EEHKYVIMIDAGSTGRVHIYFDVCTSPPTLL---DEKFDMLPEGLSSF--DTDSVGAA 143

QY      66  -YLTDCMERAREVIPRSQHOETFPVYLGATAGMRLLL-RMSEBELADRLVDVVERSLSNYPF 123
DB     144  NSLDPLLLKVMANVVPPIKARSCTPVAVKATAGRLLLGDAAKSKILSAVRDHLK--DYDF 200

QY     124  ---DFOGARIITCGEBAGVMTINVLGKFKSQKTFWFSIVPYETNNQE--TFGALDGLG 178
DB     201  PVVEGDSVIMGDEEGVFAWITNTYLLGNIG-----ANGPKLPTAAVFDLGG 248

QY     179  ASTQVTFVPQ---NOTIESPDNALOPRLYKGDYNNVYTHSFLCVG-----KDQALWQKL 228
DB     249  GSTQIVFETFPINERKWDGHEKFDLKFCDENYTLYQFSLHGLGKEGRKNYSVLVENA 308

QY     229  AKDIQVASNE-----ILRDPCHPHGGYKVVNVSDLYKTCTKRFEMTLFPQGFEOGIG- 282
DB     309  LKDGKTLKGDNTKTHQLSSPCFLPP-----KVNATNEKVTLESK-----ETYTIDFIGP 356

QY     283  ---NYQQCHQSILELFN-TSYCPYSOCAPNGIFLPLP-----QGDGFAGSAFYFMVKFL 332
DB     357  DEPSGNAQCFLTDEILNKDAQCOQSPCSFNGVHQPSLVTTFKESNDIYIYFSFYDTRPL 416

QY     333  NLTSEKVSQEKVTMMKKFC--AQPWEETIKTSVAGVKEKYLSE--YCPFGTYILSLLLQG 388
DB     417  GMPLSPFTLNE-LNDLARIYCKGEETWNSVFSGIAGSLDELSDSHFCLDSLFSQVSLHTG 475

QY     389  YHFTADSWEHIFIGIKIQGSDAGTWLTGYMLNL 420
DB     476  YDIPLQ--RELRTGKKIANKEIGWCLGASLPL 505

Search completed: March 7, 2005, 13:24:52
Job time : 14.5165 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 21.734 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-2
Perfect score: 2698
Sequence: 1 MEDTKSNVTKFCSKNILAI.....VAITGLLIHFHKPSYFWKDMV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	3	US-08-930-921-1
2	2698	100.0	510	4	US-09-781-786C-1
3	2650	98.2	502	4	US-09-557-800C-55
4	2650	98.2	502	4	US-09-370-625A-38
5	1171.5	43.4	282	4	US-09-949-016-7977
6	942.5	34.9	529	3	US-09-240-639-4
7	942.5	34.9	529	4	US-09-908-510A-4
8	942.5	34.9	529	4	US-09-905-744B-4
9	942.5	34.9	529	4	US-10-107-660-4
10	942.5	34.9	529	4	US-10-107-576-4
11	942.5	34.9	529	4	US-09-905-732B-4
12	942.5	34.9	529	4	US-09-923-304-4
13	942.5	34.9	529	4	US-09-949-016-6049
14	942.5	34.9	529	4	US-09-905-743B-4
15	938.5	34.8	556	4	US-09-949-016-11328
16	897	33.2	479	4	US-09-949-016-11559
17	803	29.8	153	3	US-09-240-639-13
18	803	29.8	153	4	US-09-510A-13
19	803	29.8	153	4	US-09-905-744B-13
20	803	29.8	153	4	US-10-107-660-13
21	803	29.8	153	4	US-10-107-576-13
22	803	29.8	153	4	US-09-905-732B-13
23	803	29.8	153	4	US-09-905-743B-13
24	604	22.4	154	3	US-09-240-639-14
25	604	22.4	154	4	US-09-908-510A-14
26	604	22.4	154	4	US-09-905-744B-14
27	604	22.4	154	4	US-10-107-660-14

28	604	22.4	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	22.4	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	22.4	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	16.4	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	16.4	153	4	US-09-908-510A-15	Sequence 15, Appl
33	442.5	16.4	153	4	US-09-905-744B-15	Sequence 15, Appl
34	442.5	16.4	153	4	US-10-107-660-15	Sequence 15, Appl
35	442.5	16.4	153	4	US-09-905-732B-15	Sequence 15, Appl
36	442.5	16.4	153	4	US-09-905-743B-15	Sequence 15, Appl
37	442.5	16.4	153	4	US-09-905-743B-15	Sequence 15, Appl
38	427	15.8	94	4	US-09-513-999C-4273	Sequence 4273, Ap
39	427	15.8	462	4	US-09-129-112-2	Sequence 2, Appli
40	421.5	15.6	462	4	US-09-129-112-15	Sequence 15, Appl
41	417.5	15.5	150	3	US-09-240-639-16	Sequence 16, Appl
42	417.5	15.5	150	4	US-09-908-510A-16	Sequence 16, Appl
43	417.5	15.5	150	4	US-09-905-744B-16	Sequence 16, Appl
44	417.5	15.5	150	4	US-10-107-660-16	Sequence 16, Appl
45	417.5	15.5	150	4	US-10-107-576-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVICNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE REFERENCE: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; CURRENT FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1

Query Match	100.0%	Score	2698	DB	3	Length	510
Best Local Similarity	100.0%	Pred. No.	5.8e-277				
Matches	510	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MEDTKSNVTKFCSKNILAILGESSITAVTALLAVGLTQNKALPENVKYGIIVLDAGSSHT	60				
Db	1	MEDTKSNVTKFCSKNILAILGESSITAVTALLAVGLTQNKALPENVKYGIIVLDAGSSHT	60				
Qy	61	SLYIKKPAEKENDTGVVHVEECRVKPGISKEVQKNEIGIYLTDCMERAREVIPSQ	120				
Db	61	SLYIKKPAEKENDTGVVHVEECRVKPGISKEVQKNEIGIYLTDCMERAREVIPSQ	120				
Qy	121	HQETPVYLGATAGNRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQEEGAYGWI	180				
Db	121	HQETPVYLGATAGNRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQEEGAYGWI	180				
Qy	181	TINYLLKFKSQKRWFSIVPYETNNQETFGALDGGASTQVTFVQNTTIESPNALQFR	240				
Db	181	TINYLLKFKSQKRWFSIVPYETNNQETFGALDGGASTQVTFVQNTTIESPNALQFR	240				
Qy	241	LYGKDYNYTHSFUCYCKDQALWQKAKDIQVASNEILRDPCHFGYKVVVNSDLYKTP	300				
Db	241	LYGKDYNYTHSFUCYCKDQALWQKAKDIQVASNEILRDPCHFGYKVVVNSDLYKTP	300				
Qy	301	CTKRFEMLFPQFPIQIGNYQQCHOSILEFNTSCPYSCQAFNGIFLPLQDGFAG	360				

Db 301 CTKREFMTLPQQFEIQGIGNYQCHQSILELFTNTSYCPYSQCAFNGIFLPLPQDGFAG 360
Qy 361 SAFYFVWKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVWKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFGKIQGSAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTVFL 480
Db 421 SLLQGYHFTADSWEHIFGKIQGSAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 2

US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHODIOLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781.796C
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 100.0%; Score 2698; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.8e-277;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTONKALPENVKYGLVDAGSSHT 60
Db 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTONKALPENVKYGLVDAGSSHT 60
Qy 61 SLIYIKYKPAEKENDTGTVHQQVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYIKYKPAEKENDTGTVHQQVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
Qy 121 HOETPVYLGATAGMELLRMESEELADRLVDVVERSLNYPDFQAGRIITQEGEGAYGI 180
Db 121 HOETPVYLGATAGMELLRMESEELADRLVDVVERSLNYPDFQAGRIITQEGEGAYGI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQOTIESPDNALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQOTIESPDNALQFR 240
Qy 241 LYGKDYNNVTHSFLCYGKQDALWQKLAKDIQVANSNEILRDPCHFPGYKVVVNSDLYKTP 300
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Db 301 CTKREFMTLPQQFEIQGIGNYQCHQSILELFTNTSYCPYSQCAFNGIFLPLPQDGFAG 360

Qy 361 SAFYFVWKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVWKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFGKIQGSAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTVFL 480
Db 421 SLLQGYHFTADSWEHIFGKIQGSAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 3

US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 98.2%; Score 2650; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 7e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTONKALPENVKYGLVDAGSSHT 60
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Db 61 SLIYIKYKPAEKENDTGTVHQQVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
Qy 121 HOETPVYLGATAGMELLRMESEELADRLVDVVERSLNYPDFQAGRIITQEGEGAYGI 180
Db 121 HOETPVYLGATAGMELLRMESEELADRLVDVVERSLNYPDFQAGRIITQEGEGAYGI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQOTIESPDNALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQOTIESPDNALQFR 240
Qy 241 LYGKDYNNVTHSFLCYGKQDALWQKLAKDIQVANSNEILRDPCHFPGYKVVVNSDLYKTP 300
Db 241 LYGKDYNNVTHSFLCYGKQDALWQKLAKDIQVANSNEILRDPCHFPGYKVVVNSDLYKTP 300

Qy 301 CTKEFMTLPQOEIIOGNYQOCHOSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Db 301 CTKEFMTLPQOEIIOGNYQOCHOSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Qy 361 SAFYFVVKFNLTLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVVKFNLTLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLSLVLFTVAIIGLLIFHKP 502
Db 481 MVLSLVLFTVAIIGLLIFHKP 502
RESULT 4
US-09-370-625A-38
; Sequence 38, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Fodd, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-38
Query Match 98.2%; Score 2650; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 7e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT 60
Db 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT 60
Qy 61 SLIYKWPAAKENDTGWHQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYKWPAAKENDTGWHQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 120
Qy 121 HOETPVILGATAGMRLLRMESEELADRLDVVERSLSNYPDFQGARIIITGOEAGYGI 180
Db 121 HOETPVILGATAGMRLLRMESEELADRLDVVERSLSNYPDFQGARIIITGOEAGYGI 180
Qy 181 TINYLKGFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQTIESPDNALQFR 240
Db 181 TINYLKGFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQTIESPDNALQFR 240
Qy 241 LYGKDYNYTHSFLCYGKQDALWQKLAKDIQVASNEILRDRPCFHPGKVVNVSLEYKTP 300
Db 241 LYGKDYNYTHSFLCYGKQDALWQKLAKDIQVASNEILRDRPCFHPGKVVNVSLEYKTP 300
Qy 301 CTKEFMTLPQOEIIOGNYQOCHOSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Db 301 CTKEFMTLPQOEIIOGNYQOCHOSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Qy 361 SAFYFVVKFNLTLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

Db 361 SAFYFVVKFNLTLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLSLVLFTVAIIGLLIFHKP 502
Db 481 MVLSLVLFTVAIIGLLIFHKP 502
RESULT 5
US-09-949-016-7977
; Sequence 7977, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7977
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7977
Query Match 43.4%; Score 1171.5; DB 4; Length 282;
Best Local Similarity 50.3%; Pred. No. 1.9e-115;
Matches 254; Conservative 0; Mismatches 0; Indels 251; Gaps 1;
Qy 6 ESNVKTFCCKNLAAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHTSLIY 65
Db 29 ESNVKTFCCKNLAAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHTSLIY 88
Qy 66 KWPAEKENDTGWHQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQHOETP 125
Db 89 KWPAEKENDTGWHQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQHOETP 148
Qy 126 VYLGATAGMRLLRMESEELADRLDVVERSLSNYPDFQGARIIITGOEAGYGITINYL 185
Db 149 VYLGATAGMRLLRMESEELADRLDVVERSLSNYPDFQGARIIITGOEAGYGITINYL 208
Qy 186 LGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQTIESPDNALQFLYKCD 245
Db 209 LGKFSQ----- 214
Qy 246 YNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDRPCFHPGKVVNVSLEYKTPCKTRF 305
Db 215 ----- 214
Qy 306 EMTLPFOQFEIQIGNYQOCHOSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAFAPYF 365
Db 215 ----- 214
Qy 366 VNKFLNLTLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLQ 425
Db 215 ----- 214
Qy 426 GYHFTADSWEHIFIGIKQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMWLFS 485
Db 215 -----IQSDAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMWLFS 257
Qy 486 LVLFVTAIIGLLIFHKPSYFWKDMV 510


```
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;
QY 25 SIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEEC 84
Db 33 SIVLVSTVIQIHQKQVLPGLKYGIVLDAGSSRTTVVYQWPAKENNTGVVSQTFKC 92
QY 85 RVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEL 144
Db 93 SVKSGISSYGNPNQDVPRAPEECQKVKGVPSHLHGSTPIHLGATAGMRLLRQNETA 152
QY 145 ADRLVDVVERSLSNYPDFOGARIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETN 204
Db 153 ANEVLESIQSYFKSQPFDFRGAQIIISGOEEGVGWITANYLMGNFLEKNLHMMV--HPH 210
QY 205 NOETFGALDLGGASTQVTFVQNOTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALWQ 264
Db 211 GVVTTGALDLGGASTQISFVAGEKMDLNTSDIMQVSLYGYVYTYLTHSFQCYGRNEAEKK 270
QY 265 KLAKDIQVA--SNEILRDPCHPGYKVVNVSDLYKTPTCT--KRFEMTLPPQOFEIQGIGN 321
Db 271 FLAMLLQNSPTKNHLTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGD 330
QY 322 YQOCHOSILELFTNTSYC--PYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQE 380
Db 331 PSLCKEKVASIFDFKACHDQETCSDFGVYQPKIGPFVAFAGFYTTASALNL--SGSFSLD 389
QY 381 KVTEMMKKFCAQPMEEIKTSVAGVKEKYLSEYCFSGTYLSLLQGYHFTADSEHIIHFI 440
Db 390 TFNSSTWNFCNSQNSQLPPLLKPFDEVYARSYCFSSANYIYHLFVNGYKFTETWPIHFE 449
QY 441 GKIQSDAGWTGLGYMLNTNMIAPAOPL--STPLSHSTVFLMVLPSLVLTVAIIGLLIF 499
Db 450 KEVGNSSIAWSLGLMSLTNQIPAESPLIRLPIEPFVF-----GTLAFTTVAALLCLAF 504

RESULT 14
US-09-905-743B-4
; Sequence 4, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-743B-4

Query Match 34.9%; Score 942.5; DB 4; Length 529;
Best Local Similarity 39.8%; Pred. No. 1.1e-90;
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;
QY 25 SIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEEC 84
Db 33 SIVLVSTVIQIHQKQVLPGLKYGIVLDAGSSRTTVVYQWPAKENNTGVVSQTFKC 92
QY 85 RVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEL 144
Db 93 SVKSGISSYGNPNQDVPRAPEECQKVKGVPSHLHGSTPIHLGATAGMRLLRQNETA 152
QY 145 ADRLVDVVERSLSNYPDFOGARIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETN 204
Db 153 ANEVLESIQSYFKSQPFDFRGAQIIISGOEEGVGWITANYLMGNFLEKNLHMMV--HPH 210
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QY 205 NOETFGALDLGGASTQVTFVQNOTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALWQ 264
Db 211 GVVTTGALDLGGASTQISFVAGEKMDLNTSDIMQVSLYGYVYTYLTHSFQCYGRNEAEKK 270
QY 265 KLAKDIQVA--SNEILRDPCHPGYKVVNVSDLYKTPTCT--KRFEMTLPPQOFEIQGIGN 321
Db 271 FLAMLLQNSPTKNHLTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGD 330
QY 322 YQOCHOSILELFTNTSYC--PYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQE 380
Db 331 PSLCKEKVASIFDFKACHDQETCSDFGVYQPKIGPFVAFAGFYTTASALNL--SGSFSLD 389
QY 381 KVTEMMKKFCAQPMEEIKTSVAGVKEKYLSEYCFSGTYLSLLQGYHFTADSEHIIHFI 440
Db 390 TFNSSTWNFCNSQNSQLPPLLKPFDEVYARSYCFSSANYIYHLFVNGYKFTETWPIHFE 449
QY 441 GKIQSDAGWTGLGYMLNTNMIAPAOPL--STPLSHSTVFLMVLPSLVLTVAIIGLLIF 499
Db 450 KEVGNSSIAWSLGLMSLTNQIPAESPLIRLPIEPFVF-----GTLAFTTVAALLCLAF 504

RESULT 15
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 34.8%; Score 938.5; DB 4; Length 556;
Best Local Similarity 39.6%; Pred. No. 3.2e-90;
Matches 190; Conservative 90; Mismatches 187; Indels 13; Gaps 7;
QY 25 SIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEEC 84
Db 60 SIVLVSTVIQIHQKQVLPGLKYGIVLDAGSSRTTVVYQWPAKENNTGVVSQTFKC 119
QY 85 RVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEL 144
Db 120 SVKSGISSYGNPNQDVPRAPEECQKVKGVPSHLHGSTPIHLGATAGMRLLRQNETA 179
QY 145 ADRLVDVVERSLSNYPDFOGARIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETN 204
Db 180 ANEVLESIQSYFKSQPFDFRGAQIIISGOEEGVGWITANYLMGNFLEKNLHMMV--HPH 237
QY 205 NOETFGALDLGGASTQVTFVQNOTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALWQ 264
Db 238 GVVTTGALDLGGASTQISFVAGEKMDLNTSDIMQVSLYGYVYTYLTHSFQCYGRNEAEKK 297
QY 265 KLAKDIQVA--SNEILRDPCHPGYKVVNVSDLYKTPTCT--KRFEMTLPPQOFEIQGIGN 321
Db 298 FLAMLLQNSPTKNHLTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGD 357
QY 322 YQOCHOSILELFTNTSYC--PYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQE 380
Db 358 PSLCKEKVASIFDFKACHDQETCSDFGVYQPKIGPFVAFAGFYTTASALNL--SGSFSLD 416
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 83.3137 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147A-2
Perfect score: 2698
Sequence: 1 MEDYKSNVTKFCSKNILAI.....VAIGLLIFPKPSYFVKDMV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2698	100.0	510	2 AAW04334	Human lym
2	2698	100.0	510	2 AAW04264	Human CD3
3	2698	100.0	510	3 AAY70910	Human sol
4	2698	100.0	510	3 AAY70887	Human sol
5	2698	100.0	510	4 AAB71917	Human CD3
6	2698	100.0	510	7 ADJ57262	Human CD3
7	2698	100.0	510	8 ADL24295	Human CD3
8	2698	100.0	510	8 ADQ99453	Human CD3
9	2698	100.0	510	8 ADQ99453	Human CD3
10	2698	100.0	510	8 ADQ99453	Human CD3
11	2698	100.0	510	8 ADQ99453	Human CD3
12	2698	100.0	510	8 ADQ99453	Human CD3
13	2698	100.0	510	8 ADQ99453	Human CD3
14	2698	100.0	511	8 ADK60421	Angiogene
15	2698	100.0	511	8 ADK60421	Angiogene
16	2698	100.0	511	8 ADK60421	Angiogene
17	2677	99.2	517	8 ADP73345	CD39 lym
18	2677	99.2	517	8 ADK60421	Angiogene
19	2677	99.2	517	8 ADK60421	Angiogene
20	2677	99.2	517	8 ADK60421	Angiogene
21	2677	99.1	522	8 ABO84672	Human can
22	2469	91.5	529	8 ABO84672	Human can
23	2358	87.4	464	3 AAY70922	Human sol
24	2358	87.4	464	3 AAY70922	Human sol
25	2348	87.0	439	4 AAB71918	Soluble h

26	2348	87.0	454	3 AAY70913	Human sol
27	2348	87.0	454	3 AAY70890	Protein e
28	2348	87.0	463	3 AAY70925	Human sol
29	2348	87.0	463	3 AAY70902	Protein e
30	2348	87.0	473	3 AAY70924	Human sol
31	2348	87.0	473	3 AAY70901	Protein e
32	2348	87.0	474	3 AAY70923	Human sol
33	2348	87.0	474	3 AAY70900	Protein e
34	2348	87.0	476	3 AAY70911	Human CD3
35	2348	87.0	476	3 AAY70888	Protein e
36	2348	87.0	478	3 AAY70914	Human sol
37	2348	87.0	478	3 AAY70891	Protein e
38	2348	87.0	487	3 AAY70921	Human sol
39	2348	87.0	487	3 AAY70898	Protein e
40	2311	85.7	503	8 ABM83377	Human dia
41	2297	85.1	476	3 AAY70912	Human CD3
42	2297	85.1	476	3 AAY70889	Protein e
43	2144	79.5	402	8 ABO84671	Human can
44	2016	74.7	377	7 ADI62735	Human apo
45	1293	47.9	311	8 ABO84673	Human can

ALIGNMENTS

RESULT 1
AAW04334
ID AAW04334 standard; protein; 510 AA.

AC AAW04334;

XX 29-DEC-1996 (first entry)

XX Human lymphoid cell activation antigen CD39.

XX ATP diphosphohydrolase; ATPase; bovine aorta; pig pancreas; apyrase;
XX CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;
XX thrombogenicity; anti-haemostatic.

XX Homo sapiens.

XX WO9632471-A2.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-CA000223.

XX 10-APR-1995; 95US-00419204.

XX (UYSH) UNIV SHERBROOKE.

XX Beaudoin AR, Sevigny J;

XX WPI; 1996-477122/47.

XX N-PSDB; AAT38516.

XX Isolated ATP di-phospho-hydrolase enzymes - have anti-haemostatic

XX activity, useful for reducing platelet aggregation and thrombogenicity.

XX Claim 17; Page 42-44; 60pp; English.

XX The bovine aorta (AAW04335 and AAW04338 and AAW04340) and porcine
XX pancreatic (AAW04339) ATPases have been partially sequenced. The
XX sequences have been found to be highly homologous to a human lymphoid
XX cell activation antigen designated CD39 (Maliszewski et al. (1994). J.
XX Immunol.: 3574-3583). The complete sequences of the ATPases types I and
XX II have not been obtained yet. Assuming that the CD39 gene product is an
XX ATPase type II, the use of CD39 in the reduction of platelet aggregation
XX and of thrombogenicity may be contemplated, as well as a process of
XX making ATPases using the CD39 sequence (AAT38516)

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTCCKNLAAILGFSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60
DB 1 MEDTKESNVKTCCKNLAAILGFSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60

QY 61 SLIYIKVPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLIYIKVPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

QY 121 HOETPVYLGAAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180
DB 121 HOETPVYLGAAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQTIESPNDALQFR 240
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQTIESPNDALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWOKLADIOVASNEILRDCPFHPGYKVVNSDLYKTP 300
DB 241 LYGDYNNVYTHSFLCYGKDQALWOKLADIOVASNEILRDCPFHPGYKVVNSDLYKTP 300

QY 301 CTKEFEMTLPFQOFEIQIGNYQQCHQSILELFTNSYCPYSQCAFNGIFLPLQDGFAG 360
DB 301 CTKEFEMTLPFQOFEIQIGNYQQCHQSILELFTNSYCPYSQCAFNGIFLPLQDGFAG 360

QY 361 SAFYFMKFLNLTSEKVSQEKVTEMMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFMKFLNLTSEKVSQEKVTEMMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL 480
DB 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL 480

QY 481 MVFLSLVLTVAIIIGLIFHKPSYFWKDMV 510
DB 481 MVFLSLVLTVAIIIGLIFHKPSYFWKDMV 510

RESULT 2
AAW04264
ID AAW04264 standard; protein; 510 AA.
AC AAW04264;
XX
DT 29-MAY-1997 (first entry)
DE Human CD39 protein.
XX
KW Human; lymphocyte activation marker; gene therapy;
KW ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;
KW transplantation; endothelial cell; prosthetic device;
KW platelet aggregation; inhibition; intravascular.
XX
OS Homo sapiens.
XX
PN WO9630532-A1.
PD 03-OCT-1996.
XX
PF 22-MAR-1996; 96WO-EP001270.
XX
PR 24-MAR-1995; 95US-00410371.
PR 12-FEB-1996; 96US-00600383.
XX
PA (SANO) SANDOZ LTD.
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Bach FH, Robson S;
XX
DR WPI; 1996-455377/45.

DR N-PSDB; AAT33966.
XX Gene therapy of inflammatory or immunological stimulation of platelet aggregation - using CD39 protein with ATP di:phosphohydrolase activity, useful for preventing or alleviating thrombotic condition in mammalian subject.
PT
PT
XX
PS Claim 3; Page 39; 65pp; English.
XX
CC Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence is that of the human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584
XX
SQ Sequence 510 AA;
Query Match 100.0%; Score 2698; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTCCKNLAAILGFSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60
DB 1 MEDTKESNVKTCCKNLAAILGFSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60

QY 61 SLIYIKVPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLIYIKVPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

QY 121 HOETPVYLGAAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180
DB 121 HOETPVYLGAAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQTIESPNDALQFR 240
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQTIESPNDALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWOKLADIOVASNEILRDCPFHPGYKVVNSDLYKTP 300
DB 241 LYGDYNNVYTHSFLCYGKDQALWOKLADIOVASNEILRDCPFHPGYKVVNSDLYKTP 300

QY 301 CTKEFEMTLPFQOFEIQIGNYQQCHQSILELFTNSYCPYSQCAFNGIFLPLQDGFAG 360
DB 301 CTKEFEMTLPFQOFEIQIGNYQQCHQSILELFTNSYCPYSQCAFNGIFLPLQDGFAG 360

QY 361 SAFYFMKFLNLTSEKVSQEKVTEMMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFMKFLNLTSEKVSQEKVTEMMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL 480
DB 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLNTNMIPAEQPLSTPLSHSTYVFL 480

QY 481 MVFLSLVLTVAIIIGLIFHKPSYFWKDMV 510
DB 481 MVFLSLVLTVAIIIGLIFHKPSYFWKDMV 510

RESULT 3
AAW70910
ID AAW70910 standard; protein; 510 AA.
XX
XX
AC AAW70910;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 protein.

XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiatic; vasotropic; thrombolytic.
 XX
 OS Homo sapiens.
 XX
 XX Location/Qualifiers
 FH 17..37
 FT Domain
 FT /label= Transmembrane domain
 FT /note= "N-terminal end"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT Domain
 FT /label= Transmembrane domain
 FT /note= "C-terminal end"
 XX
 XX WO200023459-A1.
 XX
 XX 27-APR-2000. 99WO-US022955.
 XX
 XX 13-OCT-1999; 99WO-US022955.
 XX
 XX 16-OCT-1998; 98US-0104585P.
 XX 06-NOV-1998; 98US-0107466P.
 XX 13-AUG-1999; 99US-0149010P.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX
 XX WPI: 2000-339644/29.
 XX N-PSDB; RAD00205.
 XX
 XX New soluble CD39 polypeptides having apyrase activity, useful for
 XX inhibiting angiogenesis and treating unstable angina, myocardial
 XX infarction, stroke, coronary artery disease or injury.
 XX
 XX Claim 1a; Fig 1; 122pp; English.
 XX
 XX The present sequence is the human soluble CD39 protein, a cell surface
 XX molecule, having apyrase activity. It is derived from a human B cell line
 XX cDNA library, referred to as MP-1. Soluble CD39 is constructed by
 XX removing the N- and C-terminal transmembrane domains. It retains the
 XX capacity to metabolise ATP and ADP at relevant concentrations and the
 XX ability to block and reverse ADP-induced platelet activation and
 XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
 XX are useful for inhibiting angiogenesis. It is useful for the treatment of
 XX unstable angina, myocardial infarction, stroke, coronary artery disease
 XX or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,
 XX embolism, platelet-associated ischaemic disorders including lung,
 XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
 XX peripheral and cerebral artery thrombosis, intracardiac and venous
 XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
 XX for preventing thrombus formation or reformation, occlusion, reocclusion,
 XX stenosis or restenosis of blood vessels or stroke
 XX

SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 3; Length 510;
 Best Local Similarity 100.0%; Pred. No. 5.2e-262;
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKSNVTKFCCKNLAIIIGFSSIIIAVALLAVGLTQNKALPENVKYIGVLDAGSSHT 60
 Db 1 MEDTKSNVTKFCCKNLAIIIGFSSIIIAVALLAVGLTQNKALPENVKYIGVLDAGSSHT 60
 Qy 61 SLIYKWPAPKENDTGVVHVECRVKGPGISKFQVKNIEIGIYLTDCMERAREVIPSQ 120
 Db 61 SLIYKWPAPKENDTGVVHVECRVKGPGISKFQVKNIEIGIYLTDCMERAREVIPSQ 120
 Qy 121 HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITQEEGAYGWI 180
 Db 121 HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITQEEGAYGWI 180
 Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDVGASTQVTFVQNTIESPDNALQFR 240
 Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDVGASTQVTFVQNTIESPDNALQFR 240
 Qy 241 LYGKDYNNVYTHSFLCYGKQDALWOKLAKDIQVNASNEILRDCFHPGKVVVNSDLYKTP 300
 Db 241 LYGKDYNNVYTHSFLCYGKQDALWOKLAKDIQVNASNEILRDCFHPGKVVVNSDLYKTP 300
 Qy 301 CTXRFEMTLFPQPEIQIGNYQQCHOSILELFNTSCYPSQCAFNGIFLPLQDGFAG 360
 Db 301 CTXRFEMTLFPQPEIQIGNYQQCHOSILELFNTSCYPSQCAFNGIFLPLQDGFAG 360
 Qy 361 SAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIYL 420
 Db 361 SAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIYL 420
 Qy 421 SLLQGYHFTADSWEHIFIKIGQSDAGTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
 Db 421 SLLQGYHFTADSWEHIFIKIGQSDAGTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
 Qy 481 MVLPSLVLFVTAIIGLLIFHKPSYFWKDMV 510
 Db 481 MVLPSLVLFVTAIIGLLIFHKPSYFWKDMV 510

RESULT 4

AAAY70887
 ID AAAY70887 standard; protein; 510 AA.

AC AAAY70887;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 protein.

KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiatic;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 17..37

FT /label= Transmembrane_domain

FT Modified-site 73..75

FT /note= "Asn is N-glycosylated"

FT Modified-site 227..229

FT Modified-site /note= "Asn is N-glycosylated" 292..294
 FT Modified-site /note= "Asn is N-glycosylated" 334..336
 FT Modified-site /note= "Asn is N-glycosylated" 371..373
 FT Modified-site /note= "Asn is N-glycosylated" 457..459
 FT Modified-site /note= "Asn is N-glycosylated" 477..499
 FT Domain /label= Transmembrane_domain
 FT W0200023094-A2.
 FT 27-APR-2000.
 XX 13-OCT-1999; 99WO-US023641.
 XX 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107456P.
 PR 13-AUG-1999; 99US-0149010P.
 XX (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 DR N-PSDB; AAD00200..
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 FT coronary artery disease or injury, comprises administering soluble CD39
 FT polypeptides.
 XX Claim 2; Fig 1; 118pp; English.
 XX The present sequence is soluble CD39 having apyrase activity. Soluble
 CC CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at
 CC physiologically relevant concentrations as well as the ability to block
 CC and reverse ADP-induced platelet activation and recruitment including
 CC platelet aggregation. This is used in the treatment of unstable angina,
 CC myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 XX restenosis of blood vessels or stroke
 SQ Sequence 510 AA;
 Query Match 100.0%; Score 2698; DB 3; Length 510;
 Best Local Similarity 100.0%; Pred. No. 5.2e-262;
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
 DB 1 MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
 QY 61 SLTYIKPAEKENDTGTVVHVEECRVKPGIGSKFQVKNVIGIYLTDCMERAREVPRSQ 120
 DB 61 SLTYIKPAEKENDTGTVVHVEECRVKPGIGSKFQVKNVIGIYLTDCMERAREVPRSQ 120
 QY 121 HQETPVYLGATAGWRLRMESEELADVLVDVVERSLSNYPDFOGARITTCQEGAYGWI 180
 DB 121 HQETPVYLGATAGWRLRMESEELADVLVDVVERSLSNYPDFOGARITTCQEGAYGWI 180
 QY 181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240

Db 181 TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPQNQTIESPDNALQFR 240
 QY 241 LYCKDYNNVYTHSLCYGKQOALWQKLAKDIOVASNEILRDPCHPHGKVKVNVSDLYKTP 300
 Db 241 LYCKDYNNVYTHSLCYGKQOALWQKLAKDIOVASNEILRDPCHPHGKVKVNVSDLYKTP 300
 QY 301 CTKRFEMTLFPQCFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAF 360
 Db 301 CTKRFEMTLFPQCFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAF 360
 QY 361 SAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
 Db 361 SAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
 QY 421 SLLLQGVHFTADSWEHIFIGKIQGSADAGWTLGMLNLTNMI PAEQPLSTPLSHSTVFL 480
 Db 421 SLLLQGVHFTADSWEHIFIGKIQGSADAGWTLGMLNLTNMI PAEQPLSTPLSHSTVFL 480
 QY 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
 Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
 RESULT 5
 AAB71917
 ID AAB71917 standard; protein; 510 AA.
 XX AAB71917;
 AC AAB71917;
 DT 09-MAY-2001 (first entry)
 XX Human CD39.
 DE Human CD39.
 XX Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
 KW stroke; thrombotic disorder; ischaemic disorder.
 XX Homo sapiens.
 OS Homo sapiens.
 XX W02000111949-A1.
 XX 22-FEB-2001.
 XX 11-AUG-2000; 2000WO-US022060.
 XX 13-AUG-1999; 99US-00374586.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX Pinsky DJ;
 XX WPI; 2001-202805/20.
 XX Treating stroke in a subject susceptible to intracranial hemorrhaging and
 PT an ischemic disorder, involves administering a CD39 polypeptide which
 FT inhibits ADP-mediated platelet aggregation or leukocyte accumulation.
 PT Claim 1; Page 14; 118pp; English.
 XX The present sequence is the human CD39 polypeptide. The present sequence
 CC or its active fragment may be administered to treat or prevent stroke in
 CC a subject susceptible to intracranial haemorrhaging or an ischaemic
 CC disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
 CC or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
 CC subject. It is useful for treating or preventing stroke, thrombotic
 CC disorders and ischaemic disorders such as peripheral vascular disorder,
 CC pulmonary embolus, venous thrombosis, myocardial infarction, transient
 CC ischaemic attack, unstable angina, reversible ischaemic neurological
 CC deficit and sickle cell anaemia. It is also useful for treating or
 CC preventing a stroke disorder in a subject undergoing heart surgery, lung
 CC surgery, spinal surgery, brain surgery, vascular surgery, abdominal
 CC surgery, or organ transplantation surgery
 XX Sequence 510 AA;

PD	28-AUG-2003.
XX	
PF	19-FEB-2003; 2003WO-US004845.
XX	
PR	20-FEB-2002; 2002US-0358303P.
XX	
PA	(GEHO) GEN HOSPITAL CORP.
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX	
PI	Elmaleh DR, Robson SC, Papisov MI;
XX	
DR	WPI; 2003-778966/73.
DR	N-PSDB; ADJ57261.
XX	
PT	New enzyme polymer conjugate used for treating abnormal levels of
PT	extracellular nucleotides or platelet aggregation, graft transplant,
PT	cardiovascular disease, cancer and sepsis.
XX	
PS	Claim 20; SEQ ID NO 2; 82pp; English.
XX	
CC	The invention relates to a conjugate (I) comprising an enzyme and a
CC	biodegradable polymer, where (i) enzymatic activity of the enzyme is
CC	higher relative to that of the enzyme in the absence of the biodegradable
CC	polymer, or (ii) the half life of the enzyme is longer than that of the
CC	enzyme in the absence of the polymer. The enzymatic activity (i) is at
CC	least 10 (preferably at least 100) times higher in the presence of the
CC	polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,
CC	preferably an apyrase, especially a soluble form of CD39 and catalyzes
CC	hydrolysis of nucleoside diphosphate. The conjugate can be used to treat
CC	diseases relating to abnormal levels of extracellular nucleotides or
CC	abnormal aggregation of platelets, particularly cardiovascular disease,
CC	cancer, sepsis or a disease related to graft transplant. (I) is also used
CC	for treating coronary artery disease or injury following myocardial
CC	infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,
CC	platelet associated ischaemic disorders including lung, coronary and
CC	cerebral ischaemia, reocclusion following thrombosis, thrombotic
CC	disorders, and thrombosis and coagulopathies associated with exposure to
CC	a foreign or injured tissue surface, in combination with angioplasty,
CC	carotid endarterectomy, anastomosis of vascular grafts and chronic
CC	cardiovascular devices. The present sequence represents a human CD39
CC	polypeptide.
XX	
SQ	Sequence 510 AA;

Query Match		100.0%;	Score 2698;	DB 7;	Length 510;
Best Local Similarity		100.0%;	Pred. No. 5.2e-262;		
Matches 510;		Conservative	0;	Mismatches	0;
Qy	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT	60		
Db	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT	60		
Qy	61	SLYIKKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ	120		
Db	61	SLYIKKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ	120		
Qy	121	HOETPVYLGATAGNRLRMESEBELADRLVDVVERSLSNYPDFQGARIIITQEEGAYGI	180		
Db	121	HOETPVYLGATAGNRLRMESEBELADRLVDVVERSLSNYPDFQGARIIITQEEGAYGI	180		
Qy	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQTVFPQNTIESPDNALQFR	240		
Db	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQTVFPQNTIESPDNALQFR	240		
Qy	241	LYGKDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDCPFHPGKVVNSDLYKTP	300		
Db	241	LYGKDYNNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDCPFHPGKVVNSDLYKTP	300		
Qy	301	CTKRFEMTLFPQOFEIQIGIGNYQOCHQSILELFTNTSYCPYSQCAFNGIFLPLQDGFAG	360		
Db	301	CTKRFEMTLFPQOFEIQIGIGNYQOCHQSILELFTNTSYCPYSQCAFNGIFLPLQDGFAG	360		
Qy	361	SAFYFVMKFLNLTSEKVSQEKVTMMKFCACQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL	420		
Db	361	SAFYFVMKFLNLTSEKVSQEKVTMMKFCACQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL	420		
Qy	421	SLLLOQYHFTADSWEHIFIGIKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL	480		
Db	421	SLLLOQYHFTADSWEHIFIGIKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL	480		
Qy	481	MVLSFLVLTVAIIGLILFHKPSYFWKDMV	510		
Db	481	MVLSFLVLTVAIIGLILFHKPSYFWKDMV	510		
RESULT 6					
ADJ57262					
ID	ADJ57262 standard; protein; 510 AA.				
XX					
AC	ADJ57262;				
XX					
DT	06-MAY-2004 (first entry)				
XX					
DE	Human CD39 polypeptide.				
XX					
KW	CD39; nucleoside diphosphate; thrombolytic; anticoagulant;				
KW	cardiovascular; cytosolic; antibacterial; immunosuppressive; vasotropic;				
KW	cardiant; antianginal; antiarteriosclerotic; gynaecological;				
KW	cerebroprotective; cancer; human; apyrase; enzyme.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Domain	55..61	/note = ACR1		
FT	Domain	125..135	/note = ACR2		
FT	Domain	171..183	/note = ACR3		
FT	Domain	213..220	/note = ACR4		
FT	Domain	447..454	/note = ACR5		
XX					
PN	W02003070823-A2.				
XX					

```
Db 361 SAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGGVHFTADSWEHIFHTGKIQQSDAGWTLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGGVHFTADSWEHIFHTGKIQQSDAGWTLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 7
ADL24295 standard; protein; 510 AA.
XX
AC ADL24295;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human CD39.
XX
KW cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;
KW antagonist.
XX
OS Homo sapiens.
XX
PN WO2004019866-A2.
XX
PD 11-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-US026354.
XX
PR 28-AUG-2002; 2002US-0406418P.
PR 12-AUG-2003; 2003US-0494457P.
XX
PA (IMMUNEX CORP.
XX
PI Burton PB, Deisher TA;
XX
DR WPI; 2004-239107/22.
DR N-PSDB; ADL24294.
XX
PT Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a
PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart
PT failure, aneurysm, angina, embolism, restenosis, ischemia or
PT thrombocytopenic purpura.
XX
PS Disclosure; Page 133-134; 135pp; English.
XX
CC The present invention relates to a method of treating cardiovascular
CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,
CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40
CC antagonists are useful for treating cardiovascular disorders, e.g.
CC (chronic immune) myocarditis, congestive heart failure, aneurysms,
CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The
CC present sequence is a polypeptide used in the exemplification of the
CC invention.
XX
SQ Sequence 510 AA;
Query Match 100.0%; Score 2698; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEDTKSNVKTFCCKNLAIIIGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Db 1 MEDTKSNVKTFCCKNLAIIIGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Qy 61 SLIYIKWPAEKENDTGVVHVEECRVKPGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYIKWPAEKENDTGVVHVEECRVKPGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
```

```
Qy 121 HOETPVYLGATAGMRLRMESEELADRVLDVVVERSLSNYPFDQFQARIITGQEGAYGWI 180
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVVERSLSNYPFDQFQARIITGQEGAYGWI 180
Qy 181 TINYLLGKSQKTRWFSIVPYETNNQETFGALDLGGASTQVTPVQNTTIESPDNALQFR 240
Db 181 TINYLLGKSQKTRWFSIVPYETNNQETFGALDLGGASTQVTPVQNTTIESPDNALQFR 240
Qy 241 LYCKDYNVYTHSLCYGKQOALWQKLAKDIOVASNEILRDPCHPHGKVKVNVVSDLYKTP 300
Db 241 LYCKDYNVYTHSLCYGKQOALWQKLAKDIOVASNEILRDPCHPHGKVKVNVVSDLYKTP 300
Qy 301 CTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPLQGGDFGAF 360
Db 301 CTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTSYCPYSQCAFNGIFLPLQGGDFGAF 360
Qy 361 SAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGGVHFTADSWEHIFHTGKIQQSDAGWTLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGGVHFTADSWEHIFHTGKIQQSDAGWTLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 8
ADQ99453 standard; protein; 510 AA.
XX
AC ADQ99453;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human CD39 protein.
XX
KW CD39-like protein; gene mapping; molecular weight marker;
KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW NTPase; human; enzyme.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 47..68
FT /note= "Apyrase region (ACR) I"
FT Region 124..142
FT /note= "Apyrase region (ACR) II"
FT Region 169..191
FT /note= "Apyrase region (ACR) III"
FT Region 207..228
FT /note= "Apyrase region (ACR) IV"
XX
PN US6759214-B1.
XX
PD 06-JUL-2004.
XX
PF 13-JUL-2001; 2001US-00908510.
XX
PR 29-JAN-1999; 99US-00240639.
XX
PA (NUVE-) NUVELO INC.
XX
PI Chadwick BP, Frischauf A;
XX WPI; 2004-515395/49.
XX
PT New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT gene mapping, as molecular weight markers, as food supplements, or as
PT anti-thrombotic or anti-tissue graft rejection agents.
```


XX Example; Fig 8; 104pp; English.

XX The invention relates to novel CD39-like polypeptides (CD39-like

CC nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding

CC such polypeptides. CD39-like polynucleotides may be used as hybridisation

CC probes, PCR primers and in chromosome and gene mapping. Polypeptides of

CC the invention may be used as molecular weight markers, as food

CC supplements, in generating an antibody that specifically binds the

CC polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or

CC for regulating ATP neurotransmission in smooth muscle, peripheral ganglia

CC or brain. Sequences of the invention are useful in modulating ecto-ATPase

CC activity and for identifying compounds that modulate ecto-ATPase

CC activity. The present sequence is human CD39 protein, a member of the

CC CD39-like protein family. Note: This sequence is stated to be the same as

CC that shown as SEQ ID NO:13 in the sequence listing of the specification.

CC However this sequence has additional residues at its ends.

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;

Best Local Similarity 100.0%; Pred. No. 5.2e-262;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

Qy 61 SLIYIKKPAEKENDTVGVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

Db 61 SLIYIKKPAEKENDTVGVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

Qy 121 HQPTPVYLGATAGMRLRMSEELADRLVDVRSLSNYPDFQCARIIITQCEGAYGWI 180

Db 121 HQPTPVYLGATAGMRLRMSEELADRLVDVRSLSNYPDFQCARIIITQCEGAYGWI 180

Qy 181 TINYLKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240

Db 181 TINYLKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240

Qy 241 LYGKDVNVYTHSFLCYGKQDALWKLAKDIQVASNEIILRDPCHFPGYKVVNSDLYKTP 300

Db 241 LYGKDVNVYTHSFLCYGKQDALWKLAKDIQVASNEIILRDPCHFPGYKVVNSDLYKTP 300

Qy 301 CTKRFEMTLFPQPEIIOGIGNYQCHOSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP 360

Db 301 CTKRFEMTLFPQPEIIOGIGNYQCHOSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP 360

Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420

Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420

Qy 421 SLILQGHFTADSWEHIFHTKIQGSDAGTGLGYMLNLTNMIPEAQPLSTPLSHSTYVFL 480

Db 421 SLILQGHFTADSWEHIFHTKIQGSDAGTGLGYMLNLTNMIPEAQPLSTPLSHSTYVFL 480

Qy 481 MVLFSLVFTVAIIGLLIFHKPSYFWKDMV 510

Db 481 MVLFSLVFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 9

ADR69210

ID ADR69210 standard; protein; 510 AA.

XX ADR69210;

AC ADR69210;

DT 04-NOV-2004 (first entry)

XX Human CD39 protein #3.

DE CD39-like protein; autoimmune deficiency disorder;

XX connective tissue disease; multiple sclerosis;

KW

KW systemic lupus erythematosus; rheumatoid arthritis;

KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;

KW autoimmune thyroiditis; insulin dependent diabetes mellitus;

KW myasthenia gravis; graft-versus-host disease;

KW autoimmune inflammatory eye disease; allergic disorder; asthma;

KW respiratory disorder; myeloid or lymphoid cell deficiency;

KW periodontal disease; tooth repair process; inflammatory bowel disease;

KW Crohn's disease; leukemia; nervous system disorder; anticoagulant;

KW food supplement; anti-tissue graft rejection; ATP neurotransmission;

XX gene therapy; human.

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 47. .68

FT /note= "Apyrase region (ACR) I "

FT Region 124. .142

FT /note= "Apyrase region (ACR)II"

FT Region 169. .191

FT /note= "Apyrase region (ACR) III "

FT Region 207. .228

FT /note= "Apyrase region (ACR) IV"

XX

PN US6780410-B1.

XX

XX 24-AUG-2004.

XX

XX 13-JUL-2001; 2001US-00905744.

XX

XX 29-JAN-1999; 99US-00240639.

PR

XX (NUVE-) NUVELO INC.

PA

XX Chadwick BP, Frischauf A;

PI

XX WPI; 2004-613270/59.

DR

XX

XX New isolated CD39LA polypeptide and polynucleotide, useful for

PT preventing, treating, or ameliorating multiple sclerosis, systemic lupus

PT erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-

PT host disease.

XX

XX Example; Fig 8; 103pp; English.

PS

XX The present invention relates to CD39-like polypeptide and its encoding

CC polynucleotide. The invention is useful for preventing, treating or

CC ameliorating autoimmune deficiency disorders including connective tissue

CC disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid

CC arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome,

CC autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia

CC gravis, graft-versus-host disease or autoimmune inflammatory eye disease,

CC allergic disorders including asthma and other respiratory problems,

CC myeloid or lymphoid cell deficiencies, periodontal diseases and other

CC tooth repair processes, inflammatory conditions including inflammatory

CC bowel disease and Crohn's disease, leukemias and nervous system

CC disorders. The invention is also useful as an anticoagulant for

CC inhibiting platelet aggregation, food supplement, anti-tissue graft

CC rejection agents, for regulating neurotransmission by ATP in smooth

CC muscle, peripheral ganglia or brain and in gene therapy. The present

CC sequence is a human CD39 protein. Note: This sequence is stated to be the

CC same as that shown as SEQ ID 13 in sequence listing, however these

CC sequences differ.

XX

SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;

Best Local Similarity 100.0%; Pred. No. 5.2e-262;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

QY	61	SLYIKWPAKENDTGVVHVQVECRVKGPGISKRVQKVEIGIYLTDCMERAREVIPRSQ	120
Db	61	SLYIKWPAKENDTGVVHVQVECRVKGPGISKRVQKVEIGIYLTDCMERAREVIPRSQ	120
QY	121	HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
Db	121	HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
QY	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNOTTIESPDNALQFR	240
Db	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNOTTIESPDNALQFR	240
QY	241	LYGKDVNVYTHSLFCYCKDQALWQKLAKDIQVNASNEILRDPCEHPGYKKVVNVDLYKTP	300
Db	241	LYGKDVNVYTHSLFCYCKDQALWQKLAKDIQVNASNEILRDPCEHPGYKKVVNVDLYKTP	300
QY	301	CTKRFEMTLFPQFQIEIGNYOQCHQSILELNTSYCPYSCAFNGIFLPPILQGDGFAG	360
Db	301	CTKRFEMTLFPQFQIEIGNYOQCHQSILELNTSYCPYSCAFNGIFLPPILQGDGFAG	360
QY	361	SAFYVNMKFLNLTSEKVSQKVTMMKKFCAQPKWEIKTSYAGVKEKYLSEYCFSGTYIL	420
Db	361	SAFYVNMKFLNLTSEKVSQKVTMMKKFCAQPKWEIKTSYAGVKEKYLSEYCFSGTYIL	420
QY	421	SLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480
Db	421	SLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480
QY	481	MVLPSLVFTVAIIGLLIFHPKPSYFWKDMV	510
Db	481	MVLPSLVFTVAIIGLLIFHPKPSYFWKDMV	510
RESULT 10			
ADR69042			
ID	ADR69042	standard; protein; 510 AA.	
XX	AC	ADR69042;	
XX	DT	04-NOV-2004 ; (first entry)	
XX	DE	Human CD39 protein #3.	
XX	KW	CD39-like protein; CD39-like nucleotide triphosphatase; NTPase; cancer;	
XX	KW	leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia;	
XX	KW	chronic leukaemia; autoimmune disorder; multiple sclerosis;	
XX	KW	rheumatoid arthritis; Guillain-Barre syndrome;	
XX	KW	insulin dependent diabetes mellitus; myasthenia gravis;	
XX	KW	graft-versus-host disease; GVHD; allergic disorder; asthma;	
XX	KW	respiratory disorder; inflammatory disorder; septic shock;	
XX	KW	systemic inflammatory response syndrome; SIRS; Crohn's disease;	
XX	KW	central nervous system disorder; peripheral nervous system disorder;	
XX	KW	ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea;	
XX	KW	systemic lupus erythematosus;	
XX	KW	human immunodeficiency virus-associated myelopathy;	
XX	KW	transverse myelopathy; nutritional disorder; vitamin B12 deficiency;	
XX	KW	folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;	
XX	KW	Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;	
XX	KW	nutritional supplement; ecto-ATPase activity; cytosolic; immunotherapy;	
XX	OS	human; enzyme.	
XX	OS	Homo sapiens.	
XX	PH	Key	Location/Qualifiers
FT	Region	47..68	
FT	FT	/note= "Apyrase (ACR) I"	
FT	Region	124..142	
FT	FT	/note= "Apyrase (ACR) II"	
FT	Region	169..191	
FT	FT	/note= "Apyrase (ACR) III"	
FT	Region	202..228	
FT	FT	/note= "Apyrase (ACR) IV"	
FT	FT		
XX	XX		

PN	US6780977-B1.		
XX	24-AUG-2004.		
XX	27-MAR-2002; 2002US-00107660.		
XX	29-JAN-1999; 99US-00240639.		
XX	13-JUL-2001; 2001US-00905589.		
XX	(NUVE-) NUVELO INC.		
XX	Chadwick BP, Frischauf A;		
XX	*WPI; 2004-613273/59.		
XX	GENBANK; S73813.		
XX	New antibody or its fragment that specifically binds to CD39L3		
XX	polypeptide, useful for detecting and purifying CD39L3 polypeptide, for		
XX	treating leukemia, and for detecting and preventing metastatic spread of		
XX	cancerous cells.		
XX	Example; Fig 8; 102pp; English.		
XX	The present invention provides novel CD39-like polypeptides (CD39-like		
XX	nucleotide triphosphatase; NTPase) and their encoding polynucleotides.		
XX	The invention is useful in treating cancer, leukaemia and related		
XX	disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia		
XX	and chronic leukaemia, autoimmune disorders such as multiple sclerosis,		
XX	rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes		
XX	mellitus, myasthenia gravis and graft-versus-host disease, allergic		
XX	disorders such as asthma, respiratory disorders, inflammatory disorders		
XX	such as septic shock, systemic inflammatory response syndrome (SIRS) and		
XX	Crohn's disease, central and peripheral nervous system disorders such as		
XX	ischaemia, Parkinson's disease, Alzheimer's disease, Huntington's chorea,		
XX	systemic lupus erythematosus, human immunodeficiency virus-associated		
XX	myelopathy and transverse myelopathy and nutritional disorders such as		
XX	vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-		
XX	alcohol amblyopia and Marchiafava-Bignami disease. The invention also has		
XX	haemostatic and thrombolytic activity, serve as nutritional supplements		
XX	and modulates ecto-ATPase activity. The invention acts as a cytosolic		
XX	agent and is useful in immunotherapy. The present sequence is human CD39		
XX	protein. Note: This sequence is described in the specification as being		
XX	the same as the human CD39 protein represented in SEQ ID NO: 13 of the		
XX	sequence listing, however the two sequences are different.		
XX	Sequence 510 AA;		
QY	Query Match	100.0%; Score 2698; DB 8; Length 510;	
Db	Best Local Similarity	100.0%; Pred. No. 5.2e-262;	
QY	Matches 510; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MEDTKSNVKTFCCKNLTALIGFSSIIATVALLAVGLTQNKALPENVKYGLVLDAGSSHT	60
Db	1	MEDTKSNVKTFCCKNLTALIGFSSIIATVALLAVGLTQNKALPENVKYGLVLDAGSSHT	60
QY	61	SLYIKWPAKENDTGVVHVQVECRVKGPGISKRVQKVEIGIYLTDCMERAREVIPRSQ	120
Db	61	SLYIKWPAKENDTGVVHVQVECRVKGPGISKRVQKVEIGIYLTDCMERAREVIPRSQ	120
QY	121	HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
Db	121	HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARIIITGQEGAYGWI	180
QY	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNOTTIESPDNALQFR	240
Db	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVQNOTTIESPDNALQFR	240
QY	241	LYGKDVNVYTHSLFCYCKDQALWQKLAKDIQVNASNEILRDPCEHPGYKKVVNVDLYKTP	300
Db	241	LYGKDVNVYTHSLFCYCKDQALWQKLAKDIQVNASNEILRDPCEHPGYKKVVNVDLYKTP	300
QY	301	CTKRFEMTLFPQFQIEIGNYOQCHQSILELNTSYCPYSCAFNGIFLPPILQGDGFAG	360
XX	XX	XX	XX

Db 301 CTKRFEMTLPPQOEIIOGNYQOCHOSILELFTNSYCPYSQCAFNGIFLPLQDGFAP 360
Qy 361 SAFYVNMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYVNMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLLOGHFTADSWEHIFHTGKIQSDAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLLOGHFTADSWEHIFHTGKIQSDAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 11
ADSI17924
ID ADSI17924 standard; protein; 510 AA.
AC ADSI17924;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human CD39 protein #3.
XX
KW CD39-like protein; gene mapping; food supplement; ecto-ATPase activity;
KW gene therapy; multiple sclerosis; rheumatoid arthritis;
KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
KW autoimmune inflammatory eye disease; osteoporosis; osteoarthritis;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW leukaemia; nervous system disorder; neuroprotective; antiarthritic;
KW antirheumatic; antithyroid; immunosuppressive; antidiabetic;
KW muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian;
KW cytostatic; human; CD39 protein.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Region 47..68
FT /note= "Apyrase region (ACR) I"
FT Region 124..142
FT /note= "Apyrase region (ACR) II"
FT Region 169..191
FT /note= "Apyrase region (ACR) III"
FT Region 207..228
FT /note= "Apyrase region (ACR) IV"
XX
PN US6787328-B1.
XX
PD 07-SEP-2004.
XX
XX 13-JUL-2001; 2001US-00905732.
XX
XX 29-JAN-1999; 99US-00240639.
XX
XX (NUVE-) NUVELO INC.
XX
XX Chadwick BP, Frischauf A;
XX
XX WPI; 2004-632929/61.
XX
XX New isolated CD39L4 polynucleotide, useful for preventing, treating, or
XX ameliorating multiple sclerosis, rheumatoid arthritis, diabetes,
XX osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or
XX leukemia.
XX
XX Example; Fig 8; 103pp; English.
XX
XX The present invention relates to a CD39-like polypeptides and the
XX encoding polynucleotides. The CD39L4 polynucleotide is useful as
XX hybridisation probes, as primers for PCR, for chromosome or gene mapping,
XX in the recombinant production of protein, and in generation of antisense
XX DNA or RNA. The protein of the invention is used as molecular weight

CC markers, and as food supplements and for modulating ecto-ATPase activity
CC and for identifying compounds that can be utilised for modulating ecto-
CC ATPase activity. The invention is useful for preventing, treating or
CC ameliorating a medical condition, e.g. multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,
CC autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC leukaemia or nervous system disorders and in gene therapy. The present
CC sequence is the human CD39 protein. Note: This sequence is stated to be
CC the same as that shown as SEQ ID 13 in sequence listing, however these
CC sequences differ.
XX
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSIIIAVALLAVGLTQNKALPENVKYIGVLGAGSSHT 60
Db 1 MEDTKESNVKTFCSKNILAILGFSIIIAVALLAVGLTQNKALPENVKYIGVLGAGSSHT 60
Qy 61 SLIYKWPAAEKENDTGVVHVVEECRVKPGISKFQVQKNEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYKWPAAEKENDTGVVHVVEECRVKPGISKFQVQKNEIGIYLTDCMERAREVIPSQ 120
Qy 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITTCQEEGAYGWI 180
Db 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITTCQEEGAYGWI 180
Qy 181 TINYLLGKFSOKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNTIESPDNALQFR 240
Db 181 TINYLLGKFSOKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNTIESPDNALQFR 240
Qy 241 LYKDYNNYTHSFLCYCKDQALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTP 300
Db 241 LYKDYNNYTHSFLCYCKDQALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTP 300
Qy 301 CTKRFEMTLPPQOEIIOGNYQOCHOSILELFTNSYCPYSQCAFNGIFLPLQDGFAP 360
Db 301 CTKRFEMTLPPQOEIIOGNYQOCHOSILELFTNSYCPYSQCAFNGIFLPLQDGFAP 360
Qy 361 SAFYVNMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYVNMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLLOGHFTADSWEHIFHTGKIQSDAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLLOGHFTADSWEHIFHTGKIQSDAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 12
ABO84674
ID ABO84674 standard; protein; 510 AA.
XX
XX ABO84674;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP20-011.5.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
XX Homo sapiens.
XX
XX WO2004074320-A2.
XX
XX 02-SEP-2004.

17-FEB-2004; 2004WO-US004730.
14-FEB-2003; 2003US-00367094.
14-MAR-2003; 2003US-00388838.
15-APR-2003; 2003US-00417375.
13-JUN-2003; 2003US-00461862.
15-SEP-2003; 2003US-00563431.
15-DEC-2003; 2003US-00737318.
(SAGR-) SAGRES DISCOVERY INC.
Morris DW, Morris DW, Malandro MS;
WPI: 2004-652914/63.
N-PSDB; ABD32958.
New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
claim 18; seqid 698; 310pp; English.
The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-associated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 95 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer cells (comprising the antibody cited above, methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 2698; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 510 AA;
1 MEDTKSNVKTFCCKNLAIGFSSIIATVALLAVGLTQNKALPENVKYGVLDAGSSHT 60
1 MEDTKSNVKTFCCKNLAIGFSSIIATVALLAVGLTQNKALPENVKYGVLDAGSSHT 60
61 SLYIYKWPAAKENDTGVVHVQVECRVKGPGISKVFQVKNVEIGIYLTDCMERAREVIPSQ 120
61 SLYIYKWPAAKENDTGVVHVQVECRVKGPGISKVFQVKNVEIGIYLTDCMERAREVIPSQ 120
121 HOETPVYLGATAGNRLRMESEELADRVLDVVERSLSNYPDFQCARIIITQOEGAYGWI 180
121 HOETPVYLGATAGNRLRMESEELADRVLDVVERSLSNYPDFQCARIIITQOEGAYGWI 180

181 TINYLLGKFSOKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNOTTIESPDNALQFR 240
181 TINYLLGKFSOKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNOTTIESPDNALQFR 240
241 LYGKDYNNVYTHSFLCYCKDQALWQKLAKDIQVNASNEILRDPCEFHPGKVKVNVSDLYKTP 300
241 LYGKDYNNVYTHSFLCYCKDQALWQKLAKDIQVNASNEILRDPCEFHPGKVKVNVSDLYKTP 300
301 CTRKFEMTLFPQPEIQIGNYQOCHOSILELNTSYCPYSQCAFNGIFLPLQDGFAP 360
301 CTRKFEMTLFPQPEIQIGNYQOCHOSILELNTSYCPYSQCAFNGIFLPLQDGFAP 360
361 SAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTYIL 420
361 SAFYFVNMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTYIL 420
421 SLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
421 SLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL 480
481 MWLPSLVLTVAIIGLLIFHKPSYFWKDMV 510
481 MWLPSLVLTVAIIGLLIFHKPSYFWKDMV 510
RESULT 13
ADR87821
ID ADR87821 standard; protein; 510 AA.
XX AC
XX ADR87821;
DT 18-NOV-2004 (first entry)
XX Human CD39 protein #3.
DE Human CD39 protein #3.
XX
XX CD39-like protein; CD39-like nucleotide-triphosphatase; NTPase;
XX HIV infection; hepatitis; multiple sclerosis;
XX systemic lupus erythematosus; rheumatoid arthritis;
XX Guillain-Barre syndrome; thyroiditis; diabetes; myasthenia gravis;
XX graft-versus-host disease; GHVD; asthma; human; human; enzyme; CD39.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Region 47..68
XX /note= "Apyrase region (ACR) I"
XX Region 125..142
XX /note= "Apyrase region (ACR) II"
XX Region 169..191
XX /note= "Apyrase region (ACR) III"
XX Region 207..228
XX /note= "Apyrase region (ACR) IV"
XX
XX US6783959-B1.
XX
XX 31-AUG-2004.
XX
XX 27-MAR-2002; 2002US-00107576.
XX
XX 29-JAN-1999; 99US-00240639.
XX 13-JUL-2001; 2001US-00908510.
XX
XX (NUVE-) NUVELO INC.
XX
XX Chadwick BP, Frischauf A;
XX WPI; 2004-623544/60.
XX GENBANK; S73813.
XX
XX New isolated CD39L3 polypeptide and polynucleotide, useful for
XX diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis,
XX systemic lupus erythematosus, arthritis, diabetes and asthma.

XX Example; Fig 8; 102pp; English.
 XX The invention relates to CD39-like polypeptides (CD39-like nucleotide-
 CC triphosphatase; NTPase) and their corresponding polynucleotides. The
 CC invention also relates to a method for making CD39L proteins. The methods
 CC and compositions of the invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the CD39-like polypeptide, such as HIV
 CC infection, hepatitis, multiple sclerosis, systemic lupus erythematosus,
 CC rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes,
 CC myasthenia gravis, graft-versus-host disease (GVHD) and asthma. The
 CC present sequence is the human CD39 protein. Note: This sequence is
 CC described in the specification as being the same as the human CD39
 CC protein represented in SEQ ID NO: 13 of the sequence listing, however the
 CC two sequences are different.

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;
 Best Local Similarity 100.0%; Pred. No. 5.2e-262;
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60
 DB 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60
 QY 61 SLIYKWPAAKENDTGVVHVQVEECRVKPGISKFKVQKVEIGIYLTDCMERAREVPRSQ 120
 DB 61 SLIYKWPAAKENDTGVVHVQVEECRVKPGISKFKVQKVEIGIYLTDCMERAREVPRSQ 120
 QY 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQCEGAYGWI 180
 DB 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQCEGAYGWI 180
 QY 181 TINVLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIETSPNALQFR 240
 DB 181 TINVLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIETSPNALQFR 240
 QY 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGKVVVNSDLYKTP 300
 DB 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGKVVVNSDLYKTP 300
 QY 301 CTKEFEMTLPPQOEIIOGIGNYQCHOSILELNTSYCPYQCAFNGIFLPPLOQDFGAF 360
 DB 301 CTKEFEMTLPPQOEIIOGIGNYQCHOSILELNTSYCPYQCAFNGIFLPPLOQDFGAF 360
 QY 361 SAFYFVWKFLNLTSEKVSQEKVTEMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGYVIL 420
 DB 361 SAFYFVWKFLNLTSEKVSQEKVTEMKKFCAPWEEIKTSYAGVKEKYLSEYCFSGYVIL 420
 QY 421 SLLQGVHFTADSWEHIFICKIOGSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHSYVFL 480
 DB 421 SLLQGVHFTADSWEHIFICKIOGSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHSYVFL 480
 QY 481 MVLFSVLVFTVAIIIGLLIFHKPSPFWKDMV 510
 DB 481 MVLFSVLVFTVAIIIGLLIFHKPSPFWKDMV 510

RESULT 14
 ID ADK60421

XX ADK60421 standard; protein; 511 AA.

XX AC ADK60421;

XX DT 06-MAY-2004 (first entry)

XX DE Angiogenesis differentially expressed protein #61.

XX KW vasotrophic; antirheumatic; antiarthritic; hypotensive; antianginal;
 KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;
 KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;

KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
 KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
 KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
 KW ischemia; angina; myocardial infarction; chronic heart disease;
 KW cardiac congestion; macular degeneration; osteoporosis.
 XX Homo sapiens.
 OS
 FN FR2836687-A1.
 XX
 PD 05-SEP-2003.
 XX
 PF 11-APR-2002; 2002FR-00004546.
 XX
 PR 04-MAR-2002; 2002FR-00002717.
 XX
 PA (GENE-) GENE SIGNAL.
 PA (ALMA/) AL MAHMOOD S.
 XX
 PI Colin S, Schneider C, Al Mahmood S;
 XX
 XX WPI: 2004-013912/02.
 DR N-PSDB; ADK60414.
 XX
 PT Compositions for diagnosing, prognosing and treating angiogenic disorders
 PT including tumor vascularization and heart disease, comprise nucleic acid
 PT or polypeptide differentially expressed in angiogenesis.
 XX
 PS Claim 7; SEQ ID NO 297; 424pp; French.
 XX

CC The invention relates to a novel pharmaceutical composition active on
 CC angiogenesis comprising an endothelial cell nucleic acid whose expression
 CC is induced by an angiogenic factor and inhibited by an angiostatic agent
 CC or its complement or fragment, a polypeptide sequence encoded by the
 CC nucleic acid or its fragment, a molecule capable of inhibiting expression
 CC of the nucleic acid or a molecule which binds to the polypeptide
 CC sequence. The invention is used to diagnose, prognose or treat an
 CC angiogenic disorder in a mammal, particularly a human. The disorder is
 CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
 CC endometriosis associated with neovascularization, restenosis due to
 CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
 CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
 CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
 CC myocardial infarction, chronic heart disease, cardiac congestion or
 CC macular degeneration due to age or osteoporosis. This sequence
 CC corresponds to a protein encoded by a differentially expressed DNA used
 CC in the composition of the invention.

XX Sequence 511 AA;

Query Match 100.0%; Score 2698; DB 8; Length 511;
 Best Local Similarity 100.0%; Pred. No. 5.3e-262;
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 60
 DB 2 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYIGVLDAGSSHT 61
 QY 61 SLIYKWPAAKENDTGVVHVQVEECRVKPGISKFKVQKVEIGIYLTDCMERAREVPRSQ 120
 DB 62 SLIYKWPAAKENDTGVVHVQVEECRVKPGISKFKVQKVEIGIYLTDCMERAREVPRSQ 121
 QY 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQCEGAYGWI 180
 DB 122 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQCEGAYGWI 181
 QY 181 TINVLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIETSPNALQFR 240
 DB 182 TINVLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIETSPNALQFR 241
 QY 241 LYGKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPFHPGKVVVNSDLYKTP 300

|||||
242 LYGKDYNYVTHSFLCYGKQDQWOKLAKDIQVAGNEILRDCFFHPGYKVVVNSDLYKTP 301
QY CTKRFEMTLPPQOEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOGDFGAF 360
Db CTKRFEMTLPPQOEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOGDFGAF 361
QY 361 SAFYFVVKFNLTLTSEKVSQEKVTEMKFKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 362 SAFYFVVKFNLTLTSEKVSQEKVTEMKFKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 421
QY 421 SLLQGYHFTADSWEHIFIKIQGSDAGWTLGYMLNLTNNIPAEQPLSTPLSHSTYVFL 480
Db 422 SLLQGYHFTADSWEHIFIKIQGSDAGWTLGYMLNLTNNIPAEQPLSTPLSHSTYVFL 481
QY 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 482 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 511

RESULT 15

ADK60722 ;
ID ADK60722 standard; protein; 511 AA.

XX AC
XX ADK60722;

XX DT 06-MAY-2004 (first entry)

XX DE Angiogenesis differentially expressed protein #61.

XX DX vasotrophic; antirheumatic; antiarthritic; hypotensive; antianginal;
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
KW ischemia; angina; myocardial infarction; chronic heart disease;
KW cardiac congestion; macular degeneration; osteoporosis.

XX OS Homo sapiens;

XX FR2836686-A1;

XX PD 05-SEP-2003.

XX PF 04-MAR-2002; 2002FR-00002717.

XX PR 04-MAR-2002; 2002FR-00002717.

XX PA (GENE-) GENE SIGNAL.

XX PA (ALMA/) AL MAHMOOD S.

XX PI Colin S, Schneider C, Al Mahmood S;

XX DR WPI; 2004-013911/02.

XX DR N-PSDB; ADK60715.

XX PS Compositions containing nucleic acid or polypeptide differentially

XX PT expressed in angiogenesis are useful to diagnose, prognose and treat

XX PT angiogenic disorders including tumor vascularization and heart disease.

XX PS Claim 7; SEQ ID NO 297; 405pp; French.

XX CC The invention relates to a novel pharmaceutical composition active on

XX CC angiogenesis comprising an endothelial cell nucleic acid whose expression

XX CC is induced by an angiogenic factor and inhibited by an angiostatic agent

XX CC or its complement or fragment, a polypeptide sequence encoded by the

XX CC nucleic acid or its fragment, a molecule capable of inhibiting expression

XX CC of the nucleic acid or a molecule which binds to the polypeptide

XX CC sequence. The invention is used to diagnose, prognose or treat an

XX CC angiogenic disorder in a mammal, particularly a human. The disorder is

XX CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,

CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
CC endometriosis associated with neovascularization, restenosis due to
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina
CC myocardial infarction, chronic heart disease, cardiac congestion or
CC macular degeneration due to age or osteoporosis. This sequence
CC corresponds to a protein encoded by a differentially expressed DNA used
CC in the composition of the invention.

XX SQ Sequence 511 AA;

Query Match 100.0%; Score 2698; DB 8; Length 511;

Best Local Similarity 100.0%; Pred. No. 5.3e-262;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

Db 2 MEDTKESNVKTFCSKNILAILGFSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 61

QY 61 SLTYIKWPAEKENDTGWHOVEECRVKPGISKFVQKVNEIGIYLTDCMERAREVIPSQ 120

Db 62 SLTYIKWPAEKENDTGWHOVEECRVKPGISKFVQKVNEIGIYLTDCMERAREVIPSQ 121

QY 121 HQETPVYLGTAGVRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 180

Db 122 HQETPVYLGTAGVRLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 181

QY 181 TINYLLGKFSQKTRWFSIVPEYTNNOETFGALDGGASTQVTFVQNOTTIESPDNALQFR 240

Db 182 TINYLLGKFSQKTRWFSIVPEYTNNOETFGALDGGASTQVTFVQNOTTIESPDNALQFR 241

QY 241 LYGKDYNYVTHSFLCYGKQDQWOKLAKDIQVAGNEILRDCFFHPGYKVVVNSDLYKTP 300

Db 242 LYGKDYNYVTHSFLCYGKQDQWOKLAKDIQVAGNEILRDCFFHPGYKVVVNSDLYKTP 301

QY 301 CTKRFEMTLPPQOEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOGDFGAF 360

Db 302 CTKRFEMTLPPQOEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOGDFGAF 361

QY 361 SAFYFVVKFNLTLTSEKVSQEKVTEMKFKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420

Db 362 SAFYFVVKFNLTLTSEKVSQEKVTEMKFKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 421

QY 421 SLLQGYHFTADSWEHIFIKIQGSDAGWTLGYMLNLTNNIPAEQPLSTPLSHSTYVFL 480

Db 422 SLLQGYHFTADSWEHIFIKIQGSDAGWTLGYMLNLTNNIPAEQPLSTPLSHSTYVFL 481

QY 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

Db 482 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 511

Search completed: March 7, 2005, 13:13:04

Job time : 85.4249 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 15.7384 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147A-2
Perfect score: 2698
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIGLLIFHKPSYFWKDMV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	2 I56242	lymphoid cell acti
2	511.5	19.0	483	2 D86276	hypothetical prote
3	465.5	17.4	405	2 E86276	hypothetical prote
4	455.5	16.9	630	2 S50463	hypothetical prote
5	435.5	16.1	572	2 T40856	probable nucleotid
6	421	15.6	516	2 G84442	probable nucleosid
7	413.5	15.3	485	2 T34147	hypothetical prote
8	402.5	14.9	508	2 C86276	7A19.33 protein -
9	397	14.7	557	2 T16696	hypothetical prote
10	381.5	14.1	556	2 T39109	probable guanosine
11	374.5	13.9	455	2 S48859	nucleoside triphos
12	352	13.0	1052	2 T04439	hypothetical prote
13	341.5	12.7	454	2 JC4616	aprase (EC 3.6.1.
14	332	12.3	479	2 T23508	hypothetical prote
15	322.5	12.0	518	2 A40732	guanosine-diphosph
16	318.5	11.7	628	2 A55421	nucleoside-triphos
17	145.5	5.4	369	2 S77299	C4-dicarboxylase-b
18	122.5	4.5	727	2 T47541	beta-galactosidase
19	113	4.2	665	2 T18979	hypothetical prote
20	107.5	4.0	307	2 T27332	hypothetical prote
21	101.5	3.8	417	2 S53410	hypothetical prote
22	101.5	3.8	451	2 G69859	Mg2+ transporter h
23	101.5	3.8	716	2 T21516	hypothetical prote
24	101	3.7	1415	2 A72369	(R)-2-hydroxygluta
25	100	3.7	3848	2 T17414	TipC protein - eli
26	99	3.7	473	2 T15986	hypothetical prote
27	99	3.7	1951	2 B43963	RNA viral polymera
28	98.5	3.7	536	2 B90195	hypothetical prote
29	98.5	3.7	590	2 AB1411	autolysin, N-acety

30	98.5	3.7	764	2 AB1695	p60-related protei
31	98.5	3.7	797	2 D86247	hypothetical prote
32	98.5	3.7	989	2 B84532	hypothetical prote
33	98.5	3.7	1509	2 B89985	hypothetical prote
34	98	3.6	371	2 T05213	hypothetical prote
35	97.5	3.6	392	2 A96738	hypothetical prote
36	97.5	3.6	402	2 A97743	penicillin-binding
37	97	3.6	494	2 T03774	probable histidine
38	97	3.6	4436	2 E71086	hypothetical prote
39	96.5	3.6	1013	2 JC2314	chitin synthase (E
40	96	3.6	883	2 B85725	probable fibribial
41	96	3.6	1028	2 T51173	myosin I beta - bu
42	96	3.6	1658	2 D86890	DNA-directed DNA p
43	95.5	3.5	461	2 G91228	probable permease
44	95.5	3.5	461	2 F86075	probable permease
45	95.5	3.5	591	2 P89770	hypothetical prote

ALIGNMENTS

RESULT 1
156242
Lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56242
R:Maliszewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;
J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A:Reference number: I56242; MUID:95015846; PMID:7930580
A:Accession: I56242
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: UNIPROT:P49961; GB:S73813; MID:g765255; PIDN:AAB32152.1; PID:g765255
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 100.0%; Score 2698; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIVLDAGSSHT	60
Db	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIVLDAGSSHT	60
Qy	61	SLYTYKWPAAEKENDTGWHQVEECRVKPGISKFQKNEIGIYLTDCMERAREVIPSQ	120
Db	61	SLYTYKWPAAEKENDTGWHQVEECRVKPGISKFQKNEIGIYLTDCMERAREVIPSQ	120
Qy	121	HOETPVVIGATAGMRLRMSEELADVLDDVVERSLSNYPDFQGARITTCQEEGAYGWI	180
Db	121	HOETPVVIGATAGMRLRMSEELADVLDDVVERSLSNYPDFQGARITTCQEEGAYGWI	180
Qy	181	TINYLLGKFSOKTWFISVPYETNNQETFGDALDGGASTQVTFVPPQNQTIESPDNALQFR	240
Db	181	TINYLLGKFSOKTWFISVPYETNNQETFGDALDGGASTQVTFVPPQNQTIESPDNALQFR	240
Qy	241	LYGKDYNNYTHSFICYGKDQALWOKLANDIQVASNEILRDCPFHPGYKKVNVNSLYKTP	300
Db	241	LYGKDYNNYTHSFICYGKDQALWOKLANDIQVASNEILRDCPFHPGYKKVNVNSLYKTP	300
Qy	301	CTKRFEMTLFPQOEIIGIGNYQCHOSILELNTSYCPYSCQAFNGIFLPLQDGFAG	360
Db	301	CTKRFEMTLFPQOEIIGIGNYQCHOSILELNTSYCPYSCQAFNGIFLPLQDGFAG	360
Qy	361	SAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEEIKTSYAGVKYKLSYCFSGTYIL	420
Db	361	SAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEEIKTSYAGVKYKLSYCFSGTYIL	420
Qy	421	SLLLQGVHFTADSWEHIFIKIQGSDAGWTGLYMLNLTNMIPAEQPLSTPLSHSTYVFL	480
Db	421	SLLLQGVHFTADSWEHIFIKIQGSDAGWTGLYMLNLTNMIPAEQPLSTPLSHSTYVFL	480

Query Match 16.9%; Score 455.5; DB 2; Length 630;
Best Local Similarity 25.0%; Pred. No. 5.4e-28;
Matches 139; Conservative 103; Mismatches 170; Indels 145; Gaps 25;

QY 46 NVKGVLDAGSSHTSLYIKWP-----AKENDTGV-----VHVEECRVK-GPGI 91
DB 7 NDRFGIVDAGSSGRHVFKNQDTESTLLHATNQDSQSILOSVPHIHOEKDWTFLNPL 66

QY 92 SKFVQKNE-IGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLD 150
DB 67 SSFEKKPDQAKSHIKPLDPAKNIIPESHSSCPVFIQATAGMRL---PDQIQSSILD 123

QY 151 VVERSLNYPDF-----QGARIITQEGEGAYGHITINYLKGFQSKTRWFSIVPVTN 204
DB 124 GLCOGL-KHPAEFLVEDCSAQIQVIGDTEGLYGLNLYLGHFNYP-----EVS 175

QY 205 NOETFGALDAGASTQVTFVQNO-----TIESPDNALQFRLYKQDVNVYTH 251
DB 176 DHFTFGMDMGASTQIAFAPHDSGEIARHDDIATIFLRVNGDLQ-----KWDVFS 229

QY 252 SFLCYGVKQDQWLAKDIOVA-----SNEILRDPFCHPGYKVVNVSDLYKT 299
DB 230 TWLFGANQARRYLQALINTLPENTNDYENDDFSTRNLNDPCMPRG-----SSTDF--- 281

QY 300 PCTKRFEMTLFQOFEIOGIGNYQCHOSILE-LFNTSYCPYSQCAFNGIFLPPLOGDF- 357
DB 282 ----EFKDTI----PHIAGSGNYEQTCKSIYPLLLKNMPCDDEPCLFNGVHAPRI--DFA 331

QY 358 ----GAFSAFVFMKFLNATSEKVSQEKVTMMKKFCAQWEEI-----KTSYAGVKEK 407
DB 332 NDKFTGTSEYWTANDVFKLGE-YNFKDKSKUREFCNSNWTQLANSDDGVNSIPEN 390

QY 408 YLSEYCFSGTYLSLLQY---HFTADSWEHIF---FIGKIQSGDAGWTLGYML-- 456
DB 391 FLKDACFKGNVNLHSGFDPMDRIDVA-ENVNDRPLFQSVKEVEBELSWTLGRILLY 449

QY 457 ----NLTNMIPAE-----OPLSTPLSHSTYVFLMVLV 484
DB 450 ASGSILAGNDDFMVGIAPSERRTKLTGKFKIPGKLLEDQLRKQSSLSNKGFLMWFALI 509

QY 485 SLVLFVTAIGLLIFHK 501
DB 510 CCIFY-----LIPHR 519

RESULT 5
T40856
Probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40856
R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21952
A:Accession: T40856
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-572 <RAM>
A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:
A:Experimental source: strain 972h-; cosmid cille10
C:Genetics:
A:Gene: SPDB:SPCC11E10.05C
A:Map position: 3

Query Match 16.1%; Score 435.5; DB 2; Length 572;
Best Local Similarity 26.7%; Pred. No. 1.8e-26;
Matches 144; Conservative 77; Mismatches 168; Indels 151; Gaps 22;

QY 48 KYGIVLDAGSSHTSLYIKWPAEKEN-----DTGVVHVQVEECRVKGRGIGSKFV 95
DB 4 KYGIFIDAGSSRLIYISWDYDTSLSDDKVKKPLIETIGDGGKRLKQVQGISFA 63

QY 96 QKVNEIG-IYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVER 154

DB 64 NNPKHVGRKKHLKLELDFAAHAIPKDVHKBETPVFLSATAGMRLLGVDQA---NKILSHACR 120

QY 155 SL-SNYPDF---QGARIITQEGEGAYGHITINYLKGFQSKTRWFSIVPVTNQTTF 209

DB 121 YIKKNYDFDIPNCSNIRVIDGKAEGMYGLWATNVLKLEEK-----DTSTV 168

QY 210 GALLDGGASTQVTF-VPONQTIESP-----NALQFRLYKQDVNVYTHSHFLCYGK 258

DB 169 GFLDMGGASVQIAFELPPSQLKNYKDSISTVHIGLQNGQOL-----EYFLFVTTWLGFCA 223

QY 259 DOALWQKLAKDIOVASNEI---LRDPCFHPGCKVKNVNVSDLYKTPCTKRFEMTLFPQOFE 315

DB 224 NEAYRRYGLLIESENGKVGNTLSDPCSLRG-----RTYDIDIGIE 263

QY 316 IQGIGNYQQCHQSILELFNTSY-CPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNITS 374

DB 264 FAGTGDLKQCLKLYTNLLNKDKPCMDPCNFDGIGSIPV--DF-ANTEFVGVSPEWYTTN 320

QY 375 EKVSO-----EKVTMMKKFCAQWEEI-----KTSYAGVKEKYLSEYCFSGTY 418

DB 321 DVFMGGSYHFPNFKYKVD---YCGTEWETMLSRLYNKELTPTSDENKLEKLCFKASW 376

QY 419 ILSLLQ-----VHFTADSWEHIFFIGKIQSGDAGWTLGYML 456

DB 377 ALNVLHEGFDVPKNTSSNDKQGLSVIPAYHSPTSLE-----KIBRTEVSWTLGQVL 430

QY 457 NLTN-----MIPAEQPLSTPLSH-----STYVFLMVLFSLVLF 489

DB 431 LYASNQQLAKPEYANYMDPYGLIASPSKHWRLFPNKLFFILSFIFCLFLESVLVLF 490

RESULT 6
G84442
Probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84442
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPROT:O80612; GB:AE002093; NID:G3461821; PIDN:AAC32915.1; GSPDB:GN
C:Genetics:
A:Gene: At2g02970
A:Map position: 2
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 15.6%; Score 421; DB 2; Length 516;
Best Local Similarity 26.5%; Pred. No. 2.2e-25;
Matches 136; Conservative 81; Mismatches 236; Indels 60; Gaps 15;

QY 8 NVKTFCSKNILAILGFSSIIAVIALVGLTQNALPENVKYGVLDAGSSHTSLYIKW 67

DB 27 NSKHAKNLLTGVSGISVVLGVFLCVSILFSGGNLRGLSLRYSVVVDGGSTGTRIHFVGY 86

QY 68 PAEKENDTGVVHVQVEECRVK-GPGISKFKVQKVEIGIYLTDCMERAREVIPSQHOETPV 126

DB 87 RIESGKPVFEPRGANYASLKLHPGLSAPADPDGASVSLTELVEFPAKGRVPKGMWIEFV 146

QY 127 YLGATAGMRLLRMESEELADRVLDVVERSL--SNYPDFQOGARIITQEGEGAYGHITIN 184

DB 147 RLMTATAGMRLLELPQOE---KILGVARRVLKSSGFLFRDEWASVISGDEGVYAMVANF 203

QY 185 LLGFQSKTRWFSIVPVTNQTTFGALDLCGASTQVTFVQNGTIESPDNALQFRLYK 244

DB 204 ALGSIG-----GDPLKTTGIVELGGASQVTFVSSEPM--PPEFSRTISFGNV 249

C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16696
R:Miller, N.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of *C. elegans* cosmid R07E4.
A:Reference number: Z18561
A:Accession: T16696
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-557 <MIL>
A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4.4
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R07E4.4
A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match	14.7%;	Score 397;	DB 2;	Length 557;
Best Local Similarity	25.0%;	Pred. No. 2e-23;		
Matches 133;	Conservative 96;	Mismatches 218;	Indels 86;	Gaps 21;
Qy	20	ILGSSIIAVIALLAUGLTQNKALPENV-----KYGIVLDAAGSSHTSLYIYKYPAKEN	73	
Db	9	ILAVSAMIFPVIIVFYVVEAHTSPKVIADQERSYGVICDAGSTGRLFFVYNWISTDS	68	
Qy	74	D-----TGVVHGVESCRVK-GPGISKFQKVNEIGIYLTDCMERAREVIPSQHQTVPVL	128	
Db	69	ELIQIEPVIYDKNPKMKISFGLSTFGTKPAQAAEYLRPLMELAEHPIPEKRPYTPVFI	128	
Qy	129	GATAGMRLLRMESELADRLVDVVVERSLN-----YPDFQGARITIQOEGAYGMIT	181	
Db	129	FAYAGMRLIPDEYVLIGQK--EAVLKNLRNLPKITSMQVLKEHIRIIEGKWEGIYSWIA	186	
Qy	182	INYLILGKFSQ-KTWFPSIVPVETNNQETFGALDGGASTQVTF-VPQNQITIES-----	232	
Db	187	VNYALGKFNKTATLDFPGTSPAHARQKTVMGDMGGASQIAFELPDTDFSINVENIN	246	
Qy	233	-----PDNALOPRLYKGDYNNVYTHSFLCVGKQDALWQ---KLAKDIOVASNEILLRDCPCHP	285	
Db	247	LGCHREDDSL-PK-----YKLFVITFLGVYGNEGIRKYEHHMLLSKLKDQONGTVITQDDCMLP	300	
Qy	286	GYKKVNVSDLYKTPCTKRPFMTLPFOOFELQIGIGNYOQQHQSILELFN-----TSYC--P	339	
Db	301	NLHKTVTLEN-----GENFVRRTGNNWTCNSNEVKLLNPESSESVECKAE	345	
Qy	340	YSCAENGIFLP--PLOG-DEGAFSAFYVMKFLNLTSEKVSQEKVTEMKKKCAQWEE	396	
Db	346	AARKCYGAVPAPSIPLNIENMGFSEYWIYTHDVLGQGYDAENIAKTKTQOYCSKRWST	405	
Qy	397	I-----KTSYAGVKREKYLSEYCFSGTYILSLLLQGYHFTADSMWEHIHF--IGTKQGS	449	
Db	406	IQAESKKQLYPRADEERLRTQCPSAMITSVLHDG--FSVDK-THNKFQSVSTIAGEVQ	462	
Qy	450	WTGLGYML-----NLNTMDPAEQPLSTPTLSHSTYVFLMWLFSVLVFTVA	492	
Db	463	WALGAMTYHMRFFPLRDOSSNLNIVKEHTSSSESLEWAPFLFLSAVFCFLVLVCA	515	

RESULT 10
T39109
probable guanosine-diphosphatase - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-556 <BAR>
A;Cross-references: UNIPROT:Q9UT35; EMBL:ALJ121741; PIDN:CAB57338.1; GSPDB:GN000066; SPDB:
A;Experimental source: strain 972h-; cosmid c824

C:Genetics:
A:Gene: SPDB:SPAC824.08
A:Map position: 1

Query Match 14.1%; Score 381.5; DB 2; Length 556;
Best Local Similarity 27.1%; Pred.No. 3.4e-22;
Matches 121; Conservative 71; Mismatches 181; Indels 73; Gaps 17;

Qy 48 KYGIVLDAGSSHTSYIYKWAPEKENDTGVVHQVEE--CRVKGGFGISKFKVQKVNEIGIYL 105
:
Db 133 QYVLMDIDAGSTGRVHVYQF-----NNCPNPKLEBEFFKWIEPLGLSLSFAGDPEGAAASL 187

Qy 106 TDCMERAREVIPRSQHQPETPVVILGATAGMRLLRMESEELADRVLDVVERSLSN-YPPDF- 163
:
Db 188 DPLLDYAMENVPEERYRCSPAIAKTAG---LRLTGSEAKAILKSVROHLENDYPFPPIV 244

Qy 164 -QGARIITQGEAGYGWITINVLKGFSOKTRWFISVPVTNNQOETFCALDLGCAGSTQVT 222
:
Db 245 KDGVSILSGSMGIYANITINVLTLGCKA-----THSTVAVMDLGARSQTUV 293

Qy 223 FVPQ-----NQTTESPDNALQFLRYKDYNVYTHSFLCYGKDQALMQLAKDIQVASNEIL 278
:
Db 294 FEPRFASDGESLVGDHKYVLDYNGEQVELYQSHLGYGLKEA--RKLIHKFVLNNAEAL 351

Qy 279 RD-----PCRHHPGYKKVVNVSDLYKTPCTKRFE-----TLPPQQFEIQGIG 320
:
Db 352 KESLELLGDSTSIIHPCULH-----LNASTLPDSKSEASEVFVGPSLAHLSQCRCIA 405

Qy 321 NYQOCHQSILEFNNTSCPYSCAQANGIFLPLPQGDGF-----AFSAFYFMKFLNLTSE 375
:
Db 406 E-----KALYDKDNKCPVRPCSNFVGHQPKFTFTDPSPIVLISFYDRMISLGMPF- 456

Qy 376 KVSOEKVTMMKKPCAOP--WEEIKTSYAGVKE-KYLSEYCFSGTYILSLLLQYHFHTAD 432
:
Db 457 TFTIEDMKYLANVCSGGTYWQDAFSLTDALKELKEEPCEWLCDLNYMISLSVGYEIFNN 516

Qy 433 SWEIHFIKTIQGS DAGWTLYMYMLN 458
:
Db 517 --RLHTAKKIDNKELGWCLGASLSM 540

RESULT 11
S48859
C:Nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S65147; S48859
R:Hsieh, H.-L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated nucleoside triphosphatase
A:Reference number: S65141; MUID:96197404; PMID:8616230
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <HS2>
A:Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:g563611; PID:CAA83655.1; PID:g5636
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: nucleus

	Query Match	13.9%	Score 374.5;	DB 2;	Length 455;
	Best Local Similarity	25.6%;	Pred. No. 9.1e-22;		
	Matches 120;	Conservative 80;	Mismatches 177;	Indels 91;	Gaps 19;
Qy	37	LTONKAL---	PENVKYIGIVLDSGSHTSIIYIKVPAEKENDTGVVH---OVEECRVKGPG	90	
				:	
Dd	29	LTSRKIFLKQBEISSYAVVFDPAGSTGSRIHVHF----	NQNLDLLHGKGYEYNNKITPG	84	
				:	
Qy	91	ISKFEVKQVNEIGIYLTDOMEAREVI	PRSQHOETPVVLGATACGMRLRMESEELADRVLD	150	
			:		
Dd	85	LSSVANNPEQAAKSLIPLEGEAEDVPDDLQPKTPVRLGATAGRLUNGDASE---	KILQ	141	
			:		
Qy	151	VVERSLSN-YPDFDQ--GARITGOEGAYGWITINYLGLKFQSOKTRWFSIVPYETNNQE	207		
Dd	142	SVRDMLNRSFTENFVOPDAVSIIIDGTORGSYLAVTVNYALGNLACK-----	YTK	189	

```
QY 208 TFGALDLGGASTQVTFPQNOTIETSDNAL-----OPRLYKGDVNVYTHSFLCYGKD 259
Db 190 TVGVIDLGGGVQWAVAYSKTAKNAKPVADGDDPYIKKVKLGIPDLDLVHSHYLFGR- 248
QY 260 QALMQKLAQIVASNEILR-----DPCFHPGYKKVNVVSDLYKTPCTKRFEMTLFPQQ 313
Db 249 -----EASRABILKLTSPSPNCPCLLAGFNIVTYSG-----BEFKAT----- 285
QY 314 FEIOGIGNYQCHOSILELFTNSY-CPYSQCAFNGFIFLPPLOQDFG-----AFSAFYF 365
Db 286 -AYTSGANFNKCKNTIRKALKNLNYPQYQNTFCGIW-----NGGGGNGQKNLFASSFFY 340
QY 366 VMKFLNLTSEK-----VSQEKVTMMKFCQAPWEEIKTSVAGVKEKYLSEY-CFSGTYI 419
Db 341 LPEDTGMVDASTPFIPLRPVDIETKAEACALNFEDAKSTTFPFDKKNVASVYCWMDLIYQ 400
QY 420 LSLLLQGYHFTADSWEHIFHFKIQGSD-----AGWTLGYMLNLTNMP 463
Db 401 YVLLVDG--FGLDPLQKITSGKEIEYQDAIVEAAWPLNGNAVEAISALP 446

RESULT 12
T04439
hypothetical protein T18B16.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04439
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15359
A:Accession: T04439
A:Molecule type: DNA
A:Residues: 1-1052 <BBV>
A:Cross-references: UNIPROT:O49676; EMBL:AL021687
A:Experimental source: cultivar Columbia; BAC clone T18B16
C:Genetics:
A:Map position: 4
A:Intron: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A:Note: T18B16.150

Query Match 13.0%; Score 352; DB 2; Length 1052;
Best Local Similarity 26.5%; Pred. No. 1.9e-19;
Matches 114; Conservative 81; Mismatches 165; Indels 70; Gaps 18;
QY 89 PGISKFKVQKNEIGIYLDCHMERAREVTPRQHQETPVYLGATAGMRLLR-WESEELADR 147
Db 578 PGFDKLVNVRTGLKTAIRKPLIQWAEKQIPKNAHRTTSLFVYATAGVRLRPA DSSWILGN 637
QY 148 VLDVVERSLSNYPDF--QGARIITGOEGEGAYGWITINY---LLGKFSQKTRWFSIVPYE 202
Db 638 VWSIIAKS-----PFTCRBWKIISGTBEAYFGWTALNYQTSMLGALPKKA----- 684
QY 203 TNNQETFGALDGLGGASTQVTFPQNOTIETSDNALQFRLYKGDVNVYTHSFLCYGKQQA- 261
Db 685 -----TFGALDGLGGSSLQTF--ENEERTHETNLNLRIGSNHLSAYSLAGYGLNDAF 737
QY 262 -----LNQKLA--KDIQVASNEILRDPCHPGYKKVNVVSDLYKTPCTKRFEMTLFPQ 312
Db 738 DRSVVHLKKLPNNVNSDLIEGKEMKHPCLNSGYN-----QGYTCQCASSVQGGKKGK 792
QY 313 ---QFEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGFIFLPPLOQDFGAFSAFYVMKF 369
Db 793 SGVSIKLVGAPNWGEC-----SALAKNAPCALPDGY-PRPHGQFVAYSGFVVYRF 842
QY 370 LNLTSKYSQEKVTMMKFCQAPWEEIKTSVAGVKEKYLSEYCPSGTYIISLLQGYHF 429
Db 843 FNLSAE-ASLDDVLEKGRFECADQAWARTSVS--PQPFIEQYCFRAPHYIVSLIREGLYI 899
QY 430 TADSWEHIFHFKIQGSDAGWTLGYMLNLTNMPAEQPLSTPLSHSTVVEL-VWLFSLVL 488
Db 900 T-----DKQIIIG---SGSITWTLGLVAL-----LESGKALSTLGLKSYETLSMKINPIL 947
```

```
QY 489 FTVAIIGLLI 498
Db 948 ISILILSLLL 957
```

RESULT 13

JC4616

apyrase (EC 3.6.1.5) precursor - potato

N:Alternate names: adenylylpyrophosphatase; ATP-diphosphohydrolase

C:Species: Solanum tuberosum (potato)

C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: JC4616; PC4147

R:Handa, M.; Guidotti, G.

Biochem. Biophys. Res. Commun. 218, 916-923, 1996

A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pot

A:Reference number: JC4616; MUID:96158985; PMID:8579614

A:Accession: JC4616

A:Molecule type: mRNA

A:Residues: 1-454 <HAN>

A:Cross-references: UNIPROT:P80595; GB:U58597; NID:gl381632; PIDN:AAB02720.1; PID:gi3816

A:Accession: PC4147

A:Molecule type: protein

A:Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>

A:Experimental source: tubers

A:Note: The authors translated the codon GCA for residue 215 as Gly

C:Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. The enzyme has nucleotide substrate specificity, divalent cation requirement, and is insensitive to stannous chloride. It is involved in starch synthesis.

C:Genetics:

A:Gene: rrop1

C:Superfamily: nucleoside triphosphatase chromatin-associated

C:Keywords: glycoprotein; hydrolase; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:8-25/Domain: transmembrane #status predicted <TM>

F:31-45/Product: ATP-diphosphohydrolase #status predicted <MAT>

F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding

F:192-212/Region: nucleotide binding #status predicted

F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding

F:390-410,427-446/Region: hydrophobic carboxyl end

F:151,262/binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match 12.7%; Score 341.5; DB 2; Length 454;
Best Local Similarity 24.6%; Pred. No. 3.8e-19;
Matches 118; Conservative 85; Mismatches 193; Indels 83; Gaps 19;
```

```
QY 26 IIAVIALAVGLTQ--NKAIP-----ENVKYGIVLDAGSSHTSLYIKWPAEKEND 74
Db 12 ILAIFLVLPLSLSKNVNAQIPLRHLHLSHSEHYAVIFDAGSTGSRVHVFRFD-EKLGL 70
```

```
QY 75 TGVVHVVECRVKPGISKFKVQKNEIGIYLDCHMERAREVTPRQHQETPVYLGATAGM 134
Db 71 LPTGNIEYFWATEFGLSSVAEDPKAAANSLEPLDGAEGVVPQELQSETPLELGATAGL 130
```

```
QY 135 RLLRMESEELADRLVDVVE---RSLSNYPDFQGARITGOEGEGAYGWITINYLLGKFSQ 191
Db 131 RMLKGDA---AEKILQAVRNLVKNQSTFHSKQDQVVTILDGTQEGSYMMAINYLNLGK 187
```

```
QY 192 KTRWFSIVPVTNNQETFGALDGLGGASTQVTFPQNT-OTIESPDN-----ALQFLYLGK 244
Db 188 -----DYKSTTATIDLGGGVQWAVAYSQFAPAKQNEGEPTVQOKHLMKSK 235
```

```
QY 245 DYNVYTHSFLCYGKQDALWQKLAQDIQVASNEILRDPCHPGYKKVNVVSDLYKTPCTKR 304
Db 236 DYNLYVHSHYLYNGQ-LAGRAEIFKASRNESNPCALEGC--DGYYSYGVD--YKVKAPKK 290
```

```
QY 305 FEMTLFPQFQFEIOGIGNYQCHOSILELFTN-TSCPYISQCAFNGFIFLPPLOQDFG----- 358
Db 291 G-----SSWKRCRLTRHALKINAKNIEECTFNQW-----NGGGGDDGQKN 332
```

```
QY 359 --AFSAFYVMKFLNLTSEKVSQ-----KVTEMMKFCQAPWEEIKTSVAGVKEKYLSE 411
Db 333 IHASSFFDYIGAQVGIQVDTFPFSAKAPIQVNLNAKACQTNVADIKSIFPKTDQNRNIPY 392
```

C>Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A40732; S30837; S50502
R/Abeijon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.; J. Cell Biol. 122, 307-323, 1993

A/Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A/Reference number: A40732; MUID:93308137; PMID:8391537
A/Accession: A40732
A/Molecule type: DNA
A/Residues: 1-518 <ABE>
A/Cross-references: UNIPROT:P32621; EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g3493
A/Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
A/Accession: B40732
A/Molecule type: protein
A/Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>
R/Mulligan, J.T.; Dietrich, F.S.; Hennessy, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor,
submitted to the EMBL Data Library, February 1993
A/Reference number: S30812
A/Accession: S30837
A/Molecule type: DNA
A/Residues: 1-518 <MUL>
A/Cross-references: GB:U18779; EMBL:L10830; NTD:g603625; PIDN:AAB65000.1; PID:g603637
R/Dietrich, F.S.
A/Description: The sequence of *S. cerevisiae* cosmid 8199, 8334, and 9871.
A/Reference number: S50491
A/Accession: S50502
A/Molecule type: DNA
A/Residues: 1-518 <DIE>
A/Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042w
C/Genetics:
A/Gene: SGD:GDAL
A/Cross-references: SGD:S0000768; MIPS:YEL042w
A/Map position: 5L
C/Function:
A/Description: hydrolase
C/Superfamily: nucleoside triphosphatase chromatin-associated
C/Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F/10-24/Domain: transmembrane #status predicted xTMM>
F/41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.0%; Score 322.5; DB 2; Length 518;
Best Local Similarity 26.6%; Pred. No. 1.5e-17;
Matches 123; Conservative 72; Mismatches 195; Indels 73; Gaps 20;

Qy 34 AVGLTONKALPENVKYGIVLDAGSSHTSLYIYKPAEKENDTGVVHQVBEVCRYKGPISK 93
||| : : : : : ||| : : : : : | : : : : :
Db 78 AVKSQTSCTEEHKYIMIDAGSTGSRVHIYKFVDVCTSPPTLL---DEKFDMLEPGLSS 134
||| : : : : : ||| : : : : : | : : : : :
Qy 94 PVQKNWIGI--YITDCMERAREVIPRSQHQTTPYLGTATGMRL--RMESBELADRVLD 150
||| : : : : : ||| : : : : : | : : : : :
Db 135 F--DTDSVGGAANSIDLPLKKVMNVYPFIARSCTPAVAKTAGLRLLGDASKSKILSAVRD 192
||| : : : : : ||| : : : : : | : : : : :
Qy 151 VVERSLSNYPE--DFQCARITGOEGAGYMITNYLLAGKFSQKTWFSPVVPETNNQE 207
||| : : : : : ||| : : : : : | : : : : :
Db 193 HLEK--DYPPPVGGDGVSMGGDEGFAMITNYLLGNIG-----ANGPK 237
||| : : : : : ||| : : : : : | : : : : :
Qy 208 --TFGALDLGGASTQVTVPQ---NOTIESPDNALQFLRYGKDYNVYTHSFLCYG----- 257
||| : : : : : ||| : : : : : | : : : : :
Db 238 LPTAAVFDLGGSGTOIVEPTPIPEKMDVGEHKFDLPKFGDENYTLYQPSHLGYGLKEGR 297
||| : : : : : ||| : : : : : | : : : : :
Qy 258 --KDOALWKLAKDIQVASNE-----ILRDPCFHGCKKVNVSDLYKTPCTRKFEMTL 310
||| : : : : : ||| : : : : : | : : : : :
Db 298 NKNSVLIVENALKDGKILKGDKNTKTHQLSSCLPP----KVNAENKVTLESK----- 346
||| : : : : : ||| : : : : : | : : : : :
Qy 311 FQOFEIOGIG---NYOOCHQSILEFN-TSVCPSYQCAFNGIFLPL-----QGDFGA 359
||| : : : : : ||| : : : : : | : : : : :
Db 347 -ETTYDFIGDEPSGAQRFLTDBILNKDAOCQSPPCSFNGVHQPSSLVTRTFKESNDIYI 405
||| : : : : : ||| : : : : : | : : : : :
Qy 360 FSAPFYVMKFLNLTSERKVSQKVTMMKKFC--AQPWEIKTSYAGVKKEYLSB--YCFS 415
||| : : : : : ||| : : : : : | : : : : :
Db 406 FSYFYDRTRPLCMPLSLFTLINE-LNDLARIVKGEETWNSVFSGIAGSLDLESDSHCLD 464
||| : : : : : ||| : : : : : | : : : : :
Qy 416 GTYILSLLLQGHYFTADSWEHIFGIKIQGS DAGMTLG YMLNL 458

Db 465 LSFQVSLHTGYDIPLQ--RELRTGKKIANKEIGWCLGASLPL 505

Search completed: March 7, 2005, 13:24:54
Job time : 17.7384 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 71.4475 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-2

Perfect score: 2698

Sequence: 1 MEDYKSNVTFCSKNILAI.....VAIIGLLIHFHKPSYFWKDMV 510

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	1 ENP1_HUMAN	P49961 homo sapien
2	2096	77.7	510	1 ENP1_MOUSE	P55772 mus musculus
3	2091	77.5	510	2 Q921Q6	Q921Q6 mus musculus
4	2077	77.0	539	2 Q8CDV7	Q8CDV7 mus musculus
5	2057.5	76.3	511	1 ENP1_RAT	P97687 rattus norv
6	2006	74.4	510	1 ENP1_PIG	Q9MYU4 sus scrofa
7	1993	73.9	372	2 Q86VW3	Q86VW3 homo sapien
8	1982.5	73.5	513	1 ENP1_BOVIN	O18956 bos taurus
9	1693	62.8	420	2 Q8CEB1	Q8CEB1 mus musculus
10	1552	57.5	508	2 Q6DFS1	Q6DFS1 xenopus tro
11	1530	56.7	508	2 Q6GP74	Q6GP74 xenopus lae
12	1373.5	50.9	492	2 Q8DC46	Q8DC46 brachydanio
13	1063.5	39.4	497	2 Q6UQ22	Q6UQ22 mus musculus
14	1029.5	38.2	493	1 ENP1_CHICK	Q93295 gallus gall
15	1014.5	37.6	493	2 Q90X66	Q90X66 gallus gall
16	1004	37.2	495	1 ENP2_RAT	Q35795 rattus norv
17	1001	37.1	495	1 ENP2_MOUSE	O55026 mus musculus
18	1001	37.1	495	2 Q921R1	Q921R1 mus musculus
19	982	36.4	454	2 Q6ZM69	Q6ZM69 brachydanio
20	981.5	36.4	494	1 ENP2_CHICK	P79784 gallus gall
21	981	36.4	526	2 Q6GNA4	Q6GNA4 xenopus lae
22	975	36.1	502	2 Q66L64	Q66L64 brachydanio
23	973.5	36.1	455	2 Q7T014	Q7T014 brachydanio
24	950	35.2	500	2 Q6NV19	Q6NV19 xenopus tro
25	942.5	34.9	529	1 ENP3_HUMAN	O75355 homo sapien
26	940	34.8	458	2 Q6UVZ0	Q6UVZ0 homo sapien
27	939.5	34.8	495	1 ENP2_HUMAN	Q9Y513 homo sapien
28	937.5	34.7	529	2 Q80Z26	Q80Z26 rattus norv
29	927	34.4	529	2 Q8BFW6	Q8BFW6 m mus muscu
30	860.5	31.9	453	2 Q6ZM68	Q6ZM68 brachydanio
31	843.5	31.3	452	2 Q8N6K2	Q8N6K2 homo sapien

RESULT 1	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
32	698.5	25.9	544	2 Q7YTA4
33	629.5	23.3	300	2 Q8K0L2
34	596.5	22.1	209	2 Q8UVX9
35	511.5	19.0	483	2 Q9XI62
36	510.5	18.9	488	2 Q6NQA8
37	499	18.5	503	2 Q94AP8
38	499	18.5	503	2 Q8H1D8
39	492	18.2	537	2 Q6Z543
40	490	18.2	336	2 Q8CCV2
41	488	18.1	634	2 Q6FRC2
42	486	18.0	555	2 Q94E22
43	482.5	17.9	611	2 Q6DH30
44	480	17.8	555	2 Q80612
45	469.5	17.4	405	2 Q9M9T7

ALIGNMENTS

ENP1_HUMAN STANDARD; PRT; 510 AA.

AC P49961; OSUQO9; Q9Y3Q9;

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)

DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).

GN Name=ENTPD1; Synonyms=CD39;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

EN [1]

RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).

RX MEDLINE=95015846; PubMed=7930580;

RA Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J., Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;

RT "The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization.";

RT J. Immunol. 153:3574-3583(1994).

RL [2]

RC SEQUENCE FROM N.A. (ISOFORM VASCULAR).

TISSUE=Umbilical vein;

RC MEDLINE=97149443; PubMed=8996251;

RA Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K., Millan M., Hancock W.W., Bach F.H.;

RT "Loss of ATP diphosphohydrolase activity with endothelial cell activation.";

RL J. Exp. Med. 185:153-163(1997).

RL [3]

RP SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).

TISSUE=Placenta;

RC MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;

RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T., Titani K., Fujimura Y., Narita N.;

RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II.";

RT FEBS Lett. 453:335-340(1999).

RL [4]

RC SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.

TISSUE=Placenta;

RC MEDLINE=96096723; PubMed=8529670;

RA Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;

RT "Purification and properties of human placental ATP diphosphohydrolase.";

RL Eur. J. Biochem. 234:66-74(1995).

RL [5]

RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND 399-405 (ISOFORM PLACENTAL I).

RC TISSUE=Placenta;

RX	MEDLINE=99062444; PubMed=9846014;	DR	GO: 0005887; C: integral to plasma membrane; TAS.
RA	Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,	DR	GO: 0007596; P: blood coagulation; TAS.
RA	Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.,	DR	InterPro: IPR000407; GDAL_CD39_NTPase.
RT	"Placental ecto-ATP diphosphohydrolase: its structural feature	DR	Pfam: PF01150; GDAL_CD39; 1.
RT	distinct from CD39, localization and inhibition on shear-induced	DR	PROSITE: PS01238; GDAL_CD39_NTPASE; 1.
RT	platelet aggregation.";	KW	Alternative splicing; Antigen; Calcium; Direct protein sequencing;
RL	Int. J. Hematol. 68:297-310 (1998).	KW	Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
RN	[6]	KW	Transmembrane.
RP	FUNCTION.	FT	DOMAIN 1 16 Cytoplasmic (Potential).
RX	MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;	FT	TRANSMEM 17 37 Potential.
RA	Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,	FT	DOMAIN 38 478 Extracellular (Potential).
RA	Beaudoin A.R., Bach F.H., Robson S.C.;	FT	TRANSMEM 479 499 Potential.
RT	"Identification and Characterization of CD39/vascular ATP	FT	DOMAIN 500 510 Cytoplasmic (Potential).
RT	diphosphohydrolase.";	FT	CARBOHYD 73 73 N-linked (GlcNAc..) (Potential).
RL	J. Biol. Chem. 271:33116-33122 (1996).	FT	CARBOHYD 227 227 N-linked (GlcNAc..) (Potential).
RN	[7]	FT	CARBOHYD 292 292 N-linked (GlcNAc..) (Potential).
RP	CHARACTERIZATION.	FT	CARBOHYD 334 334 N-linked (GlcNAc..) (Potential).
RX	MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;	FT	CARBOHYD 371 371 N-linked (GlcNAc..) (Potential).
RA	Wang T.F., Guidotti G.;	FT	CARBOHYD 457 457 N-linked (GlcNAc..) (Potential).
RT	"CD39 is an ecto-(Ca2+,Mg2+)-ATPase.";	FT	VARSPLIC 1 4 MEDT -> MKGTKDLTSQQ (in isoform Placental
RL	J. Biol. Chem. 271:9898-9901 (1996).	FT	I and isoform Placental II).
RN	[8]	FT	VARSPLIC 272 299 /FTId-VSP 003607.
RP	PALMITOYLATION.	FT	VASNEILRDFCFHFGKVKVNVSDLYKT -> ASITQSRPA
RX	MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;	FT	PFTSAPPAPTSCCFLFQIQ (in isoform Placental
RA	Kozlak K., Kaczmarek E., Kittel A., Sevigny J., Blusztajn J.K.,	FT	II).
RA	Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,	FT	/FTId-VSP 003608.
RA	Robson S.C.;	FT	Missing (in isoform Placental II).
RT	"Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to	FT	/FTId-VSP 003609.
RT	caveolae.";	FT	SS -> G (in Ref. 5).
RT	J. Biol. Chem. 275:2057-2062 (2000).	FT	D -> K (in Ref. 4).
CC	-!- FUNCTION: In the nervous system, could hydrolyze ATP and other	FT	D -> TGET (in Ref. 5).
CC	nucleotides to regulate purinergic neurotransmission. Could also	FT	V -> Y (in Ref. 5).
CC	be implicated in the prevention of platelet aggregation.	FT	SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;
CC	Hydrolyzes ATP and ADP equally well.	QY	1 MEDTKSNVKTFCNKILAILGPFSSIIAVIALAVGLTQNKALPENVKYGVILDGSSHT 60
CC	-!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.	DB	1 MEDTKSNVKTFCNKILAILGPFSSIIAVIALAVGLTQNKALPENVKYGVILDGSSHT 60
CC	-!- COFACTOR: Requires calcium and magnesium.	QY	61 SLVIYKWPAEKENDTGVMHQBECRVKPGISKFVQKVNIGIYLTDCMERAREVIPSQ 120
CC	-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).	DB	61 SLVIYKWPAEKENDTGVMHQBECRVKPGISKFVQKVNIGIYLTDCMERAREVIPSQ 120
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	QY	121 HOETPVYLGATAGMRLRMESEELADRLVDVRSLSNYFPDFQGARIIITGQEGAYGWI 180
CC	-!- ALTERNATIVE PRODUCTS:	DB	121 HOETPVYLGATAGMRLRMESEELADRLVDVRSLSNYFPDFQGARIIITGQEGAYGWI 180
CC	Event=Alternative splicing; Named isoforms=3;	QY	181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPNQTTIESPDNALQFR 240
CC	Name=Vascular;	DB	181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPPNQTTIESPDNALQFR 240
CC	ISOID=P49961-1; Sequences=Displayed;	QY	241 LYGKDYNNVTHSFICYGKQDALWQKLADIQVASNEILRDPCHPFGYKVVVSDLYKTP 300
CC	Name=Placental I;	DB	241 LYGKDYNNVTHSFICYGKQDALWQKLADIQVASNEILRDPCHPFGYKVVVSDLYKTP 300
CC	ISOID=P49961-2; Sequence=VSP_003607;	QY	301 CTKEFEMTLPPQOEIIGIGNYQOCHOSILELFNTSYCPYSQCAFNGIFLPLQDGFAG 360
CC	Name=Placental II;	DB	301 CTKEFEMTLPPQOEIIGIGNYQOCHOSILELFNTSYCPYSQCAFNGIFLPLQDGFAG 360
CC	ISOID=P49961-3; Sequence=VSP_003608, VSP_003609;	QY	361 SAFYFVNMKFLNLTSEKVSQEKVTEMKKFCAQPMEEIKTSYAGVKYKLYSEYCFSGYIIL 420
CC	-!- TISSUE SPECIFICITY: Expressed primarily on activated lymphoid	DB	361 SAFYFVNMKFLNLTSEKVSQEKVTEMKKFCAQPMEEIKTSYAGVKYKLYSEYCFSGYIIL 420
CC	cells. Also expressed in endothelial tissues. The vascular isoform	QY	421 SLLQGYHFTADSWEHIFTKIOGSDAGWTGLGYMLNTNMI PAEQPLSTPLSHSTYVFL 480
CC	and the placental isoform II are present in both placenta and	DB	421 SLLQGYHFTADSWEHIFTKIOGSDAGWTGLGYMLNTNMI PAEQPLSTPLSHSTYVFL 480
CC	umbilical vein, whereas placental isoform I is present in placenta	QY	481 MVLFSVLFTVAIIIGLIFHKPSYFWKDMV 510
CC	only.	DB	481 MVLFSVLFTVAIIIGLIFHKPSYFWKDMV 510
CC	-!- PTM: The N-terminus is blocked.		
CC	-!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and		
CC	7.5-8.0 with ADP.		
CC	-!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.		
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;		
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd39.htm".		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; S7813; AAB32152.1; -		
DR	EMBL; U87967; AAB47572.1; -		
DR	EMBL; AJ133133; CAB41886.1; -		
DR	EMBL; AJ133134; CAB41887.1; -		
DR	PIR; I56242; I56242.		
DR	Genew; HGNC:3363; ENTPD1.		
DR	MIM; 601752; -		

RESULT 2

ENP1_MOUSE
ID ENP1_MOUSE STANDARD; PRT; 510 AA.
AC P55772;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (Ecto-ATPase) (CD39 antigen).
DE Name=Entpdl; Synonyms=CD39;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Delepesse G.J.T., Schoenborn M.A., Armitage R.J.,
Fanelow W.C., Nakajima T., Baker E., Sutherland G.R., Polindexter K.,
Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III:
"The CD39 lymphoid cell activation antigen. Molecular cloning and
structural characterization.";
RL J. Immunol. 153:3574-3583(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=98399871; PubMed=9730622;
RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
Gayle R.B. III, Maliszewski C.R.;
RT "Gene structure and chromosome location of mouse Cd39 coding for an
ecto-ATPase.";
RL CytoGenet. Cell Genet. 81:287-289(1998).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
nucleotides to regulate purinergic neurotransmission. Could also
be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; AF037366; AAC82259.1; -;
DR EMBL; AF041818; AAC83203.1; -;
DR EMBL; AF041812; AAC83203.1; JOINED.
DR EMBL; AF041813; AAC83203.1; JOINED.
DR EMBL; AF041814; AAC83203.1; JOINED.
DR EMBL; AF041815; AAC83203.1; JOINED.
DR EMBL; AF041816; AAC83203.1; JOINED.
DR EMBL; AF041817; AAC83203.1; JOINED.
DR MGD; MGI:102805; Entpdl.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0004050; P:ATP catabolism; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1_NTPase.
DR PROSITE; PS02238; GDA1_CD39_NTPase; 1.
KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
DOMAIN 1 16
Cytoplasmic (Potential).

FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 478 Extracellular (Potential).
FT TRANSMEM 479 499 Potential.
FT DOMAIN 500 510 Cytoplasmic (Potential).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 428 428 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 510 AA; 57205 MW; 856A6113D2E13930 CRC64;
Query Match 77.7%; Score 2096; DB 1; Length 510;
Best Local Similarity 76.0%; Pred. No. 5.4e-150;
Matches 389; Conservative 53; Mismatches 66; Indels 4; Gaps 3;
Qy 1 MEDTKESNVKTFCSKNILAIIGFSSIIATVALLAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Db 1 MEDIKDSKVRKFCCKNIIILIGFTSIIAVIALIIVGLTQNKLPENVKYGIIVLDAGSSHT 60
Qy 61 SLIYKPAEKENDTVVHVQVEECRVKPGISKFVQVKEIGIYLTDCMERAREVIPSQ 120
Db 61 NLIYKPAEKENDTVVQQLBECQVKGPGISKYAKTDEIGAYLAECMELSTELIPTSK 120
Qy 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQCARITQOEGAYGWI 180
Db 121 HHQTPVYLGATAGMRLRMESEQSADEVLAAVSTSLKSYPDFQCAKIITQOEGAYGWI 180
Qy 181 TINYLLGKFSQKTFWSIVPVETNNQTFGALDGGASTQTVFVBNQTIESPDLQFR 240
Db 181 TINYLLGRFTQEQSWLSLIS--DSQKQTFGALDGGASTQITTFVFNQSTIESPNSLQFR 239
Qy 241 LYGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVAGNEILRDCPHPGYKVVNVDLYKTP 300
Db 240 LYGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVSGGVKDKPCFPGYKVVNVDLYKTP 299
Qy 301 CTRKPEMTLPQOPEIIOGNYOQCHOSILELFNTSYCPYSQCAFNGIFLPLQDQCAF 360
Db 300 CTRKFEKKLPDQPRIQCTGDEYEQHOSILELFNNSHCPSYQCAFNGVFLPLHGSFGAF 359
Qy 361 SAFYVNMKFLNLTSEK--VSQEKVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSTY 418
Db 360 SAFYVNMDFPKVAKNSVISOERKMTETKPNFCSKSWETKTSYPSVKEKYLSEYCFSGAY 419
Qy 419 ILSLLQGYHTADSWHIIHPIGKIQGSADAGWTGLYMLNTNMIPTAEOPLTSLSHSTYV 478
Db 420 ILS--LLQGYNTDSSWQIHPWGIKDSNAGWTGLYMLNTNMIPTAEQPLSPPLPHSTYI 478
Qy 479 FLMYLFSLVLTVAIIIGLIFHKPSYFWMKV 510
Db 479 GLMYLFSLLVAVAITGLIFTYKPSYFWMKEAV 510
RESULT 3
Q921Q6 PRELIMINARY; PRT; 510 AA.
AC Q921Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Entpdl protein.
GN Name=Entpdl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krawinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011278; AAH11278.1; -.
DR MGD; MGI:102805; Entpd.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; P:abzyme activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDA1 CD39; 1.
DR PROSITE; PS01238; GDA1 CD39 NTPASE; 1.
DR SEQUENCE 510 AA; 57176 NW; E77BB644AE1413A0 CRC64;
SQ
Query Match 77.5%; Score 2091; DB 2; Length 510;
Best Local Similarity 75.8%; Pred. No. 1.3e-149;
Matches 388; Conservative 53; Mismatches 67; Indels 4; Gaps 3;
QY 1 MEDYKSNVYKFCNKIIAIGFSSIIAIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60
DB 1 MEDIKDSVKRFRCSKNIILIIIGFTSILAVIALIIVGLTQNKPLPENVKYGVLDAGSSHT 60
QY 61 SLIYKVPKAEKNDGVVHVQVEECRVKPGISKFVQKVEIGIYLTDCMERAREVPRSQ 120
DB 61 NLIYKVPKAEKNDGVVQVEECRVKPGISKFVQKVEIGIYLTDCMERAREVPRSQ 120
QY 121 HOETPVYLGATAGMRLMESEELADRLVDVVERSLSNYPDFQCARITQCEBAGYGI 180
DB 121 HHQTPVYLGATAGMRLMESEELADRLVDVVERSLSNYPDFQCARITQCEBAGYGI 180
QY 181 TINYLLGFESQKTRFVSIVPVTNNOETFGALDGGASTQVTFPQNTIESPNDALQFR 240
DB 181 TINYLLGRTFQBSWLSLS-DSQKQETFGALDGGASTQVTFPQNTIESPNSJQFR 239
QY 241 LYGDYVYVTHSFLCYGKQDQALWQKLDIOVASNEIIRLDPFCFPGYKVVNSLYKTP 300
DB 240 LYGEYVYVTHSFLCYGKQDQALWQKLDIOVSSGCVLKDFCFPGYKVVNSLYKTP 299
QY 301 CTKRFEMTLPPQFPIQIGNYQQCHQSILELFTNTSYCPYSCAPFNGIFLPLQDGFAG 360
DB 300 CTERFEKKLPPQFPIQIGNYQQCHQSILELFTNTSYCPYSCAPFNGIFLPLQDGFAG 359
QY 361 SAFYFVNFNLITSEK--VSQKVTMMKKCAQPEIKTSYAGVKEKYLSEYCFSGTY 418
DB 360 SAFYFVMPDFKKVAKNSVISQKMTETITKNFCSKSWETKTSYPSVKREKYLSEYCFSGAY 419
QY 419 ILSLLQGYHTADSWEHFTKIQGSDAGWTLGMLNLTNMIPEAQPLSTPLSHSTYV 478
DB 420 ILS-LLQGYHTADSWEHFTKIQGSDAGWTLGMLNLTNMIPEAQPLSTPLSHSTYI 478
QY 479 FLMLVLSLVFTVAIIGLIFHFKPSYFWKDMV 510
DB 479 FLMLVLSLVFTVAIIGLIFHFKPSYFWKDMV 510

Db 479 GLMVLFSLLLVAIVAITGLFIYKSPSYFWKEAV 510
RESULT 4
Q8CDV7
ID Q8CDV7 PRELIMINARY; PRT; 539 AA.
AC Q8CDV7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:492151C05 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence.
GN Name=Entpd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,
RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.,
RA Konno H.; Akiyama Y.; Nishi K.; Kiteunai T.; Tashiro H.; Itoh M.,
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.,
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.,
RA Fujiwara S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watahiki M.,
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.,
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.,
RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.,
RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.,
RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.,
RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Konno H.; Kouda M.; Koya S.,
RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.,
RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohsato N.; Okazaki Y.,

Db 300 CTRRLTSLPPELEIQGTGDFOKQSQSIRPLPNTSYCPYRCSPDGVFLPLPQGDFAAP 359
Qy 361 SAFYFVFMKFLNLTSEKVS-QEKVTEMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYI 419
Db 360 SAFYVVMGFLNLTSEGSFQSKSTLEAFCSRPAWELQMYFGDVKEKYLSEYCFSGTYI 419
Qy 420 LSLILQGHFTADSWEHIFHTKIGQSDAGWTLGYMLNLTNMIAPQPLSTPLSHSTYVF 479
Db 420 LTLSSGYHFTABTWKNLHFGKVGQSTSVGWTGLGYMLNLTNMIAPSEPSRLSHSTYVF 479
Qy 480 LMLVFLSLVFTVAIIGLILFHKPSYFWKDMV 510
Db 480 LMLVFLSLVFTVAIIGLILFHKPSYFWKDMV 510
RESULT 7
Q86VV3
ID Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettunen M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; ABB1DE1366356EE3 CRC64;
Query Match 73.9%; Score 1993; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.3e-142;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 139 MESELDRLVLDVVERSLSNYPFDQGIITGQEGAGYWTITNLLGKFSQKTRWFSI 198
Db 1 MESELDRLVLDVVERSLSNYPFDQGIITGQEGAGYWTITNLLGKFSQKTRWFSI 60
Qy 199 VPYETNNQETFGALDLGGASTQVTFVQNTIESPDNALQRLYKGVKNVYTHSFLCYGK 258

Db 61 VPYETNNQETFGALDLGGASTQVTFVQNTIESPDNALQRLYKGVKNVYTHSFLCYGK 120
Qy 259 DQALWQKLAKDIQVNASNEILRDPCHFGYKGVKNVSDLYKTPCTKRFEMTLFPQOFEIQG 318
Db 121 DQALWQKLAKDIQVNASNEILRDPCHFGYKGVKNVSDLYKTPCTKRFEMTLFPQOFEIQG 180
Qy 319 IGNTQQCHQSITLLEFNTSYCPYSQCAFNGIFLPLQDGFAGAFSAFYFWKFLNLTSEKVS 378
Db 181 IGNTQQCHQSITLLEFNTSYCPYSQCAFNGIFLPLQDGFAGAFSAFYFWKFLNLTSEKVS 240
Qy 379 QEKVTEMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIILSLILQGHFTADSWEHIFH 438
Db 241 QEKVTEMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIILSLILQGHFTADSWEHIFH 300
Qy 439 FIGKIQSDAGWTLGYMLNLTNMIAPQPLSTPLSHSTYVFLMVLFSVLFTVAIIGLIL 498
Db 301 FIGKIQSDAGWTLGYMLNLTNMIAPQPLSTPLSHSTYVFLMVLFSVLFTVAIIGLIL 360
Qy 499 FHKPSYFWKDMV 510
Db 361 FHKPSYFWKDMV 372
RESULT 8
ENPI_BOVIN
ID ENPI_BOVIN STANDARD; PRT; 513 AA.
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPD1; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
diphosphohydrolase";
RL J. Biol. Chem. 271:33116-33122 (1996).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
nucleotides to regulate purinergic neurotransmission. Could also
be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COPACTOR: Requires calcium and magnesium.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
or send an email to license@ebi.ac.uk).
CC EMBL; AF005940; AAB62382.1; -
DR InterPro; IPR000407; GDAI_CD39_NTPase.

DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
FT Magnesium; Transmembrane.
FT DOMAIN 1 16 Cytoplasmic (Potential).
FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 481 Extracellular (Potential).
FT TRANSMEM 482 502 Potential.
FT DOMAIN 503 513 Cytoplasmic (Potential).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 336 336 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 373 373 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 460 460 N-linked (GlcNAc...) (Potential).
FT CONFLICT 97 97 K -> N (in Ref. 2).
FT CONFLICT 101 103 INV -> GGF (in Ref. 2).
FT CONFLICT 464 464 K -> V (in Ref. 2).
SQ SEQUENCE 513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;

Query Match 73.5%; Score 1982.5; DB 1; Length 513;
Best Local Similarity 70.8%; Pred. No. 2.1e-141;
Matches 364; Conservative 73; Mismatches 72; Indels 5; Gaps 3;

QY 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
DB 1 MEDRESSEKLVKFCNSKILSILGFSIIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60

QY 61 SLIYKVAEKENDGVVHVQVECKVPGKIGKFKVQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLIYKVAEKENDGVVHVQVECKVPGKIGKFKVQKNEIGIYLTDCMERAREVIPSQ 120

QY 121 HOETPVVLGATAGMELLMESEELADRVLDVVERSLSNVPRDQAGRIITQGESGAYGI 180
DB 121 HMETPVVLGATAGMELLMESEELADRVLDVVERSLSNVPRDQAGRIITQGESGAYGI 180

QY 181 TINYLLGKFSQTRFVSVPTVETNNQETFGALDLGGASTQVTFVFPQNTIESPNALQFR 240
DB 181 TVNYLLGKFTQKLSWFLNPKSKDDQTEYTGALDLGGASTQVTFVFPQNTIESPNALQFR 240

QY 241 LYGDQNYVTHSFLCYGKQDLQWKLQKIDQVANSNEIURDPCFHPGYKVVVNSDLYKTP 300
DB 241 LYGKNYSVYTHSFLCYGKQDLQWKLQKIDQVANSNEIURDPCFHPGYKVVVNSDLYKTP 300

QY 301 CTKRPEMT--LPPQOFRIQIGNYQCHQSTLELFTNSYCPYSCAFNGIFLPLQGD 357
DB 300 CTKRHELNSSFYPLVDIIRGAGNFQRCQSLIQLFNTSYCPYSCSFGNGLPLPLHGQF 359

QY 358 GAFSAFYFVKRFLNLTSEK-VSQEKVTEMMKKFCAQPWEEIKTSYAGVKYLSYCFSG 416
DB 360 GAFSAFYFVKRFLNLTSEKVSVEQLTEKREFCARWEEVQKNGFGEVKYLSYCFSG 419

QY 417 TYILSLILQGHFTADSHWEHHTFKIGSAGWTGLVNLMTNMPAEQPLSTPLSHST 476
DB 420 TYIIVLLNGHYHTAESVKNHFMKVRSTDVGTGLVNLMTNMPAEQPLSTPLSHST 479

QY 477 YVFLMLVLSLVLFTVAIIIGLIFHKPSYFVKDMV 510
DB 480 YVFLMLVLSLILLAVIIVGVVFKPSYFVKDMV 513

RESULT 9
Q8CEB1 PRELIMINARY; PRT; 420 AA.
AC Q8CEB1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732419M16 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence. (Fragment).
GN Name=Entpd1;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hirozane T.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1; -.
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:apyrase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.

Qy	66	KWPAEKENDTGVVHQVECBKVGPGISKFPQKVNNEIGIYITDCMERAREVIPSRSQHOETP	125
Db	62	KWPAEKENNTGMVQOHHTCNTYKGGKISSYPDKPHGAGASLEECWKEAKEKIPAHRHSETP	121
Qy	126	VYLGATAGNRLRLRMESESLADRLVDVVRBSLSNTPDPFOGARIITQOEGEGAYGMITVYL	185
Db	122	VYLGATAGNRLLLKMEDEWASEKVLTSVAHSLKTPPSYQGARILSQOEGEGAFGMITVYL	181
Qy	186	LKGFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQNTIESPDNALQFRUYLXKD	245
Db	182	-----SENLR-----KPACTLGALDGGASTQITFVPQ-QIIESSDNSIDFLRYGND	227
Qy	246	YNVYTHSFICYGKDOALWQKLAKIOVASNE-----ILRDPCFHPGYKVVNVUSDLYKTCB	301
Db	228	YHLYTHSFICYGKDOALWAEKRTDPDKTDAILRLDPCFHPGYNTTKTLESV-NTPC	286
Qy	302	TKRFEMTLFPFOFEIGIGNYQOCHSILELNTSYCPYSQCAFNGIFLPPLOQDFGARS	361
Db	287	MKPLKN--PKEQFSHVGLGNNSQOQESIRKVFNTSHCPYSGCSFNGVFPQTVBEGKEGARS	344
Qy	362	APYFUNKFLNLTSEKVSQEKYTEMKKFCAQPWSEIKTSYAGVKEKYLSEYCSGTYILS	421
Db	345	APFFVMDFLNLRKND--SLDKTKQRLAMYCSTPWQKIVQDHPKVKYKYLSEYCSFATYILT	402
Qy	422	LRLTQGYHTADSWEHIFGTIGKIOSDAGWTLGYMLNLTNMI PAEQPLSTPLSHSTTVFLM	481
Db	403	LELHGYNFTSDNWDIKEFKKIGDSAGWTLGYMLNLTNMI PAEDPDKPLMPHGGVTFM	462
Qy	482	VLPFLVLTVAIIGLLIFHK	501
Db	463	ILFSLILVLIIMAYIVFR	482

RESULT 13

Q6U022	Q6U022	PRELIMINARY;	PRT;	497 AA.
ID	Q6U022;			
AC	Q6U022;			
DT	05-JUL-2004	(TReMBLrel. 27, Created)		
DT	05-JUL-2004	(TReMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TReMBLrel. 27, Last annotation update)		
DE	Nucleoside triphosphate diphosphohydrolase-8 (EC 3.6.1.5).			
GN	Name=Entpd8;			
OS	Mus musculus	(Mouse).		
OC	Eukaryota;	Metazoa;	Chordata;	Craniata;
OC	Mammalia;	Eutheria;	Rodentia;	Sciurognathi;
OC	NCBI_TaxID=10090;			Muridae; Mus.
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;	TISSUE=Liver;		
RA	Bignonnesse F.;	Levesque S.A.;	Kukulski F.;	Robson S.C.;
RA	Fernandes M.J.G.;	Sevigny J.;		
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.			
RL	EMBL;	AY364442;	AAQ84519.1;	
DR	GO;	GO:0004050;	F.apyrase activity;	IEA.
DR	GO;	GO:0016787;	F.hydrolase activity;	IEA.
DR	InterPro;	IPR000407;	GDAL_CD39_NTPase.	
DR	Pfam;	PF01150;	GDAL_CD39;	1.
DR	PROSITE;	PS01238;	GDAL_CD39_NTPASE;	1.
DR	Hydrolase.			
KW	SEQUENCE	497 AA;	54650 MW;	00DE822B6EEB1BDF CRC64;
SQ				

Query Match	39.4%;	Score 1063.5;	DB 2;	Length 497;
Best Local Similarity	45.1%;	Pred. No. 7.1e-72;		
Matches 227;	Conservative 82;	Mismatches 157;	Indels 37;	Gaps 14

Qy	23	PSIIIAVIALAVGQTQ-----	NKALPENVKYGI	VLDDAGSSHTSLVIYKWP	AEKN 73
		:::	:::	:::	:::
Db	10	FWALLGVAA--ASGLTMLVLILVKAINVLLPADTKFGIVDFDAGSSHTSLFVYQWP	PANK 67		
		:::	:::	:::	:::
Qy	74	DTGVVHQVEECRVKGGISKFKVQKNEIGIVLTDCMERAREVIPRSOQSTPVPV	LGA 133		
		:::	:::	:::	:::
Db	68	DTGVWSOALTCTOIEGGFISVTSDDPTOAGESLSKCLREALALIPAOCHPTPTFL	STAG 127		
		:::	:::	:::	:::

[illegible]

RESULT 14

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ENR1_CHECK
ID ENPI_CHECK STANDARD; PRT; 493 AA.
AC
O93295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) Ecto-ATP diphosphohydrolase (ATPase) (lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
DE
DE Name=ENTPD1; Synonyms=CD39;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE=Oviduct;
RC MEDLINE=98298108; PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RA "Molecular cloning of the chicken oviduct ecto-ATP-
RA diphosphohydrolase";
RL J. Biol. Chem. 273:16043-16049 (1998).
RN [2]
RN SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RC MEDLINE=97442428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
RA Lewis-Carl S., Kireley T.L.;
RA "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RA gizzard and stomach. Purification and N-terminal sequence of the
RA stomach ecto-apyrase.";
RL J. Biol. Chem. 272:23645-23652 (1997).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

```

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF041355; AAC26491.1; -- CD39_NTPase.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39; 1.
 DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
 KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Magnesium; Transmembrane.
 FT DOMAIN 1 7 Cytoplasmic (Potential).
 FT TRANSMEM 8 28 Potential.
 FT DOMAIN 29 463 Extracellular (Potential).
 FT TRANSMEM 464 486 Potential.
 FT DOMAIN 487 493 Cytoplasmic (Potential).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 16 16 C -> W (in Ref. 2).
 FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
 SQ SEQUENCE 493 AA; 54034 MW; F1AFFC3AA2F3603 CRC64;

Query Match 38.2%; Score 1029.5; DB 1; Length 493;
 Best Local Similarity 42.1%; Pred. No. 2.6e-69;
 Matches 211; Conservative 91; Mismatches 176; Indels 23; Gaps 11;

QY 15 KNILAILGFSSIIAVIALAVGL-TONKALPENVKYGVLDAGSSHTSLYIKWPAEKEN 73
 DB 6 KVVAGLLTATCVFSIIALISAVDKVFLPPGTYGLVDFDAGSTHTALYVYQWPAKEN 65
 QY 74 DTGVVHVQVECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAG 133
 DB 66 GTGIVSQVESCTVNGSGISSYADDPAGAGASLKPCLDKAMAVIPVEQWQPTVYLGATAG 125
 QY 134 MRLLRMESEELADRLVDVVERSLSNYPDFQGAIRITQBEQAGYWTINYLIG---KFS 190
 DB 126 MRLLRQNSTKAEQVFAEVSKAIRFEPVDFRGAQILTNGEESFGWITVNYLLETIKFS 185
 QY 191 QKTRFWSIVPVTNNQETFGALDGGASTQVTFVPQNTIESPDNALQFRLYKDYNYVT 250
 DB 186 FAGKW-----EHPQNTFVLGALDGGASTQITFP-GVTIEDKNTSLFRLYGTNYSLYT 239
 QY 251 HSFLCYGKDOA---LWQKLAKDIQVASNEILRDPFCFHPGKYKVVNSDLYKTPCTKRFEM 307
 DB 240 HSYLCYGOIQASKRLMAALHODGSYVQN--ISHPCYPKGYRITIAIYDSCPVPPTSM 297
 QY 308 TLPFQOFEIIGNTYQQCHQSILEFNFTSYCPYSCAFNGIFLPLPLOGDGFASAFYFVM 367
 DB 298 LSPAQILVTGTGNPAACPTAILKLFNLTCGANRTCGFDGVVQPPVRGQFFAFAGFYTF 357
 QY 368 KFLNLTSEKVSQEKVTEMMKKFCAQWEEIKTSYAGVKEKYLSEYCFSGTYILSLIQGY 427
 DB 358 SFNLNLTQQ-SLSHVNATVWDFCNKNWSELVETFPQNK-HLHTYCVGVLYLTLLVDGY 415
 QY 428 HFTADSWEHIFHTGKIQGSADAGWTGLGYMLNLTNMPAEQPLSTPLSHSTYVFLMVLFSLV 487
 DB 416 KFDEHTWSNIHFSQKAGNADIGWTLGFMNLTNMTPT-ALEHVKGHPSPSLWAGASIFV 474
 QY 488 LFTVA-IIGLLIFHKPSYFWK 507
 DB 475 LAIVAGLVAILL-----QCFWK 491

Db 475 LAIVAGLVAILL-----QCFWK 491
 RESULT 15
 Q90X66 PRELIMINARY; PRT; 493 AA.
 AC Q90X66
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=21982040; PubMed=11985621;
 RA Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
 RT "Purification, characterization, cloning, and expression of the
 RT chicken liver ecto-ATP-diphosphohydrolase";
 RL Eur. J. Biochem. 269:2373-2382 (2002).
 DR EMBL; AF426405; AAL25086.1;
 DR GO; GO:0004050; F:apyrase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR Pfam; PF01150; GDAI_CD39; 1.
 DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
 KW Hydrolase.
 SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;

Query Match 37.6%; Score 1014.5; DB 2; Length 493;
 Best Local Similarity 41.9%; Pred. No. 3.6e-68;
 Matches 210; Conservative 90; Mismatches 178; Indels 23; Gaps 11;

QY 15 KNILAILGFSSIIAVIALAVGL-TONKALPENVKYGVLDAGSSHTSLYIKWPAEKEN 73
 DB 6 KVVAGLLTATCVFSIIALISAVDKVFLPPGTYGLVDFDAGSTHTALYVYQWPAKEN 65
 QY 74 DTGVVHVQVECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAG 133
 DB 66 GTGIVSQVESCTVNGSGISSYADDPAGAGASLKPCLDKAMAVIPVEQWQPTVYLGATAG 125
 QY 134 MRLLRMESEELADRLVDVVERSLSNYPDFQGAIRITQBEQAGYWTINYLIG---KFS 190
 DB 126 MRLLRQNSTKAEQVFAEVSKAIRFEPVDFRGAQILTNGEESFGWITVNYLLETIKFS 185
 QY 191 QKTRFWSIVPVTNNQETFGALDGGASTQVTFVPQNTIESPDNALQFRLYKDYNYVT 250
 DB 186 FAGKW-----EHPQNTFVLGALDGGASTQITFP-GVTIEDKNTSLFRLYGTNYSLYT 239
 QY 251 HSFLCYGKDOA---LWQKLAKDIQVASNEILRDPFCFHPGKYKVVNSDLYKTPCTKRFEM 307
 DB 240 HSYLCYGOIQASKRLMAALHODGSYVQN--ISHPCYPKGYQENITIAIYDSCPVPPTSM 297
 QY 308 TLPFQOFEIIGNTYQQCHQSILEFNFTSYCPYSCAFNGIFLPLPLOGDGFASAFYFVM 367
 DB 298 LSPAQILVTGTGNPAACPTAILKLFNLTCGANRTCGFDGVVQPPVRGQFFAFAGFYTF 357
 QY 368 KFLNLTSEKVSQEKVTEMMKKFCAQWEEIKTSYAGVKEKYLSEYCFSGTYILSLIQGY 427
 DB 358 SFNLNLTQQ-SLSHVNATVWDFCNKNWSELVETFPQNK-HLHTYCVGVLYLTLLVDGY 415
 QY 428 HFTADSWEHIFHTGKIQGSADAGWTGLGYMLNLTNMPAEQPLSTPLSHSTYVFLMVLFSLV 487
 DB 416 KFDEHTWSNIHFSQKAGNADIGWTLGFMNLTNMTPT-ALEHVKGQPSLWAGASIFV 474
 QY 488 LFTVA-IIGLLIFHKPSYFWK 507
 DB 475 LAIVAGLVAILL-----QCFWK 491

Search completed: March 7, 2005, 13:22:43
Job time : 73.4475 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 59.831 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-2

Perfect score: 2698

Sequence: 1 MEDTKSNVKTFCRSKNILAI.....VAIIGLLIFHKSYFWKDMV 510

Scoring table: BLOSUM62

Gap: 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2698	100.0	510	9	US-09-835-147-2
2	2698	100.0	510	9	US-09-374-586-1
3	2698	100.0	510	10	US-09-781-796B-1
4	2698	100.0	510	16	US-10-646-308-30
5	2650	98.2	502	13	US-10-092-063-38
6	2358	87.4	464	9	US-09-835-147-27
7	2348	87.0	439	9	US-09-374-586-2
8	2348	87.0	454	9	US-09-835-147-6
9	2348	87.0	463	9	US-09-835-147-30
10	2348	87.0	473	9	US-09-835-147-29
11	2348	87.0	474	9	US-09-835-147-28
12	2348	87.0	476	9	US-09-835-147-3
13	2348	87.0	478	9	US-09-835-147-8

14	2348	87.0	487	9	US-09-835-147-26
15	2297	85.1	476	9	US-09-835-147-4
16	1042.5	38.6	495	9	US-09-823-356-4
17	942.5	34.9	529	9	US-09-923-304-4
18	940	34.8	458	13	US-10-052-586-496
19	940	34.8	458	14	US-10-174-590-496
20	940	34.8	458	14	US-10-176-758-496
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26	940	34.8	458	14	US-10-176-915-496
27	940	34.8	458	14	US-10-173-706-496
28	940	34.8	458	14	US-10-175-738-496
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31	940	34.8	458	14	US-10-176-757-496
32	940	34.8	458	14	US-10-176-913-496
33	940	34.8	458	14	US-10-180-552-496
34	940	34.8	458	14	US-10-180-557-496
35	940	34.8	458	14	US-10-173-700-496
36	940	34.8	458	14	US-10-174-572-496
37	940	34.8	458	14	US-10-174-573-496
38	940	34.8	458	14	US-10-174-582-496
39	940	34.8	458	14	US-10-174-588-496
40	940	34.8	458	14	US-10-175-739-496
41	940	34.8	458	14	US-10-175-740-496
42	940	34.8	458	14	US-10-175-743-496
43	940	34.8	458	14	US-10-176-488-496
44	940	34.8	458	14	US-10-176-492-496
45	940	34.8	458	14	US-10-176-747-496

ALIGNMENTS

RESULT 1
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US200200227A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match 100.0%; Score 2698; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-234;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEDTKSNVKTFCRSKNILAILGFFSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60
DB 1 MEDTKSNVKTFCRSKNILAILGFFSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60

QY 61 SLVIYKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
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DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQFR 240
QY 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300
DB 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300
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DB 301 CTKRFEWTLFPQOFEIQQIGNYQOCHOSILELFNTSYCPYSQCAFNGIFLPLQGDGFGAF 360
QY 361 SAFYFVMKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFVMKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
QY 421 SLLAQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNLTNMIAPBQPLSTPLSHSTYVFL 480
DB 421 SLLAQGYHFTADSWEHIFIGIKIQGSDAGWTLYGMLNLTNMIAPBQPLSTPLSHSTYVFL 480
QY 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
DB 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 2
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD35/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match 100.0%; Score 2698; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-234;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEDTKESNVKTCCKNLAIALGFSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
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QY 61 SLVIYKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
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QY 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVVERSLSNYPDFQGARIIITGOEGAYGWI 180
DB 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVVERSLSNYPDFQGARIIITGOEGAYGWI 180
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QY 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300
DB 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300
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DB 361 SAFYFVMKFLNLTSEKVSQEKVTMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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DB 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 3
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 100.0%; Score 2698; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-234;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEDTKESNVKTCCKNLAIALGFSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
DB 1 MEDTKESNVKTCCKNLAIALGFSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60
QY 61 SLVIYKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLVIYKPAEKENDTGTVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVVERSLSNYPDFQGARIIITGOEGAYGWI 180
DB 121 HQETPVYLGATAGMRLRMESEBELADRVLDVVVERSLSNYPDFQGARIIITGOEGAYGWI 180
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQFR 240
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQFR 240
QY 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300
DB 241 LYGKDVNVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTP 300

QY 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
DB 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
QY 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
QY 421 SLLQGYHTADSWEHIFIGIKQSDAGWTGMLNLTNMIAPAEQPLSTPLSHSTYVFL 480
DB 421 SLLQGYHTADSWEHIFIGIKQSDAGWTGMLNLTNMIAPAEQPLSTPLSHSTYVFL 480
QY 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
DB 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
RESULT 4
US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 100.0%; Score 2698; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-234;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEDTKESNVKTCCKNLAAILGFSSIIAIVALLAVGLTONKALPENVKYGI VLDAGSSHT 60
DB 1 MEDTKESNVKTCCKNLAAILGFSSIIAIVALLAVGLTONKALPENVKYGI VLDAGSSHT 60
QY 61 SLIYIKWPAEKENDTGTVHVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQONQITIESPDNALQPR 240
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQONQITIESPDNALQPR 240
QY 241 LYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPHGPKYKVVNSDLYKTP 300
DB 241 LYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPHGPKYKVVNSDLYKTP 300
QY 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
DB 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
QY 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHTADSWEHIFIGIKQSDAGWTGMLNLTNMIAPAEQPLSTPLSHSTYVFL 480
DB 421 SLLQGYHTADSWEHIFIGIKQSDAGWTGMLNLTNMIAPAEQPLSTPLSHSTYVFL 480
QY 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
DB 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
RESULT 5
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110735908
; CURRENT APPLICATION NUMBER: US/10/092,063
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-38

Query Match 98.2%; Score 2650; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 2e-229;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEDTKESNVKTCCKNLAAILGFSSIIAIVALLAVGLTONKALPENVKYGI VLDAGSSHT 60
DB 1 MEDTKESNVKTCCKNLAAILGFSSIIAIVALLAVGLTONKALPENVKYGI VLDAGSSHT 60
QY 61 SLIYIKWPAEKENDTGTVHVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKGGISKFVKQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQONQITIESPDNALQPR 240
DB 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQONQITIESPDNALQPR 240
QY 241 LYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPHGPKYKVVNSDLYKTP 300
DB 241 LYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEILRDCPHGPKYKVVNSDLYKTP 300
QY 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
DB 301 CTKRPEMTLPFOQFEIQIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPLQGDGFAG 360
QY 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
DB 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLQGYHTADSWEHIFIGIKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHTADSWEHIFIGIKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480

QY 481 MVFLSLVLTVAIIGLIFHPK 502
Db 481 MVFLSLVLTVAIIGLIFHPK 502

RESULT 6

US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 87.4%; Score 2358; DB 9; Length 464;
Best Local Similarity 97.8%; Pred. No. 3.4e-203;
Matches 443; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 24 SSIIVALLAVGLTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVEE 83
Db 12 SCIALSLAVTNSATQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVEE 71
QY 84 CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPRSQHOETPVYLKATAGMELLRWSEEE 143
Db 72 CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPRSQHOETPVYLKATAGMELLRWSEEE 131
QY 144 LADRVLDDVVERSLNYPFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYET 203
Db 132 LADRVLDDVVERSLNYPFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYET 191
QY 204 NQOETFGALDLGGASTQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALW 263
Db 192 NQOETFGALDLGGASTQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALW 251
QY 264 QKLAKDIOVASNEILRDCPFHGYKVVNVSDLYKTPCTKRFEMTLPPQOFIQQIGNYQ 323
Db 252 QKLAKDIOVASNEILRDCPFHGYKVVNVSDLYKTPCTKRFEMTLPPQOFIQQIGNYQ 311
QY 324 QCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVT 383
Db 312 QCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVT 371
QY 384 EMWKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKI 443
Db 372 EMWKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKI 431

QY 444 QGSDAGWTGLGYMLNTNMIPAEQPLSTPLSHST 476
Db 432 QGSDAGWTGLGYMLNTNMIPAEQPLSTPLSHST 464

RESULT 7

US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 87.0%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.5e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVEEYKRGKIGSKFVQK 97
Db 1 TONKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVEEYKRGKIGSKFVQK 60
QY 98 VNEIGIYLTDCMERAREVIPRSQHOETPVYLKATAGMELLRWSEELADRVLDDVVERSLS 157
Db 61 VNEIGIYLTDCMERAREVIPRSQHOETPVYLKATAGMELLRWSEELADRVLDDVVERSLS 120
QY 158 NYPDFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217
Db 121 NYPDFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 180
QY 218 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 277
Db 181 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 240
QY 278 LRDCPFHGYKVVNVSDLYKTPCTKRFEMTLPPQOFIQQIGNYQCHQSILELNTSY 337
Db 241 LRDCPFHGYKVVNVSDLYKTPCTKRFEMTLPPQOFIQQIGNYQCHQSILELNTSY 300
QY 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEI 397
Db 301 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEI 360
QY 398 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLGYMLN 457
Db 361 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLGYMLN 420
QY 458 LTNMIPAEQPLSTPLSHST 476
Db 421 LTNMIPAEQPLSTPLSHST 439

RESULT 8

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 87.0%; Score 2348; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.6e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TQKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQBECRVKGPISKPVOK 97
DB 16 TQKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQBECRVKGPISKPVOK 75

QY 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 157
DB 76 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 135

QY 158 NTPPFDQAGARIITGEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217
DB 136 NTPPFDQAGARIITGEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 195

QY 218 STQVTFVQNPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQALWQKLAKDIQVASNEI 277
DB 196 STQVTFVQNPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQALWQKLAKDIQVASNEI 255

QY 278 LRDPCHFGPKYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTSY 337
DB 256 LRDPCHFGPKYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTSY 315

QY 338 CPYSQCAFNGIFLPPQQDGFAGSAFYFVWKPLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
DB 316 CPYSQCAFNGIFLPPQQDGFAGSAFYFVWKPLNLTSEKVSQEKVTMMKKFCAQPWEEI 375

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFGIKQSDAGWTLGYMLN 457
DB 376 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFGIKQSDAGWTLGYMLN 435

QY 458 LTNMIPAEQPLSTPLSHST 476
DB 436 LTNMIPAEQPLSTPLSHST 454

RESULT 9
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 87.0%; Score 2348; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 2.7e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TQKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQBECRVKGPISKPVOK 97
DB 25 TQKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQBECRVKGPISKPVOK 84

QY 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 157
DB 85 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 144

QY 158 NTPPFDQAGARIITGEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217
DB 145 NTPPFDQAGARIITGEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 204

QY 218 STQVTFVQNPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQALWQKLAKDIQVASNEI 277
DB 205 STQVTFVQNPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQALWQKLAKDIQVASNEI 264

QY 278 LRDPCHFGPKYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTSY 337
DB 265 LRDPCHFGPKYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTSY 324

QY 338 CPYSQCAFNGIFLPPQQDGFAGSAFYFVWKPLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
DB 325 CPYSQCAFNGIFLPPQQDGFAGSAFYFVWKPLNLTSEKVSQEKVTMMKKFCAQPWEEI 384

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFGIKQSDAGWTLGYMLN 457
DB 385 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFGIKQSDAGWTLGYMLN 444

QY 458 LTNMIPAEQPLSTPLSHST 476
DB 445 LTNMIPAEQPLSTPLSHST 463

RESULT 10
US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13

;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 29
;; LENGTH: 473
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Fusion
;; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 87.0%; Score 2348; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.8e-202; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGCVHQAECRCVKGPGISKFKVQK 97
Db 35 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGCVHQAECRCVKGPGISKFKVQK 94

QY 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 157
Db 95 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 154

QY 158 NYPDFQGARITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
Db 155 NYPDFQGARITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 214

QY 218 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 277
Db 215 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 274

QY 278 LRDPCHPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFTSY 337
Db 275 LRDPCHPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFTSY 334

QY 338 CPYSQCAFNGIFLPPQDGFAGSAFYFVWKFNLTSEKVSQEKVTEMMKKFCAQPWEI 397
Db 335 CPYSQCAFNGIFLPPQDGFAGSAFYFVWKFNLTSEKVSQEKVTEMMKKFCAQPWEI 394

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLN 457
Db 395 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLN 454

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 455 LTNMIPAEQPLSTPLSHST 473

RESULT 11
US-09-835-147-28
;; Sequence 28, Application US/09835147
;; Patent No. US20020002277A1
;; GENERAL INFORMATION:
;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.
;; APPLICANT: Price, Virginia L.
;; APPLICANT: Gimpe, Steven D.
;; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
;; FILE REFERENCE: 2879-US
;; CURRENT APPLICATION NUMBER: US/09/835,147
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: US 60/104,585
;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1999-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 28
;; LENGTH: 474
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Fusion
;; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 87.0%; Score 2348; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.8e-202; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGCVHQAECRCVKGPGISKFKVQK 97
Db 36 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGCVHQAECRCVKGPGISKFKVQK 95

QY 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 157
Db 96 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 155

QY 158 NYPDFQGARITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
Db 156 NYPDFQGARITGQEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 215

QY 218 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 277
Db 216 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 275

QY 278 LRDPCHPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFTSY 337
Db 276 LRDPCHPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFTSY 335

QY 338 CPYSQCAFNGIFLPPQDGFAGSAFYFVWKFNLTSEKVSQEKVTEMMKKFCAQPWEI 397
Db 336 CPYSQCAFNGIFLPPQDGFAGSAFYFVWKFNLTSEKVSQEKVTEMMKKFCAQPWEI 395

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLN 457
Db 396 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLN 455

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 456 LTNMIPAEQPLSTPLSHST 474

RESULT 12
US-09-835-147-3
;; Sequence 3, Application US/09835147
;; Patent No. US20020002277A1
;; GENERAL INFORMATION:
;; APPLICANT: Maliszewski, Charles R.
;; APPLICANT: Gayle III, Richard B.
;; APPLICANT: Price, Virginia L.
;; APPLICANT: Gimpe, Steven D.
;; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
;; FILE REFERENCE: 2879-US
;; CURRENT APPLICATION NUMBER: US/09/835,147
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: US 60/104,585
;; PRIOR FILING DATE: 1998-10-16
;; PRIOR APPLICATION NUMBER: US 60/107,466
;; PRIOR FILING DATE: 1998-11-06
;; PRIOR APPLICATION NUMBER: US 60/149,010
;; PRIOR FILING DATE: 1999-08-13
;; PRIOR APPLICATION NUMBER: PCT/US99/22955
;; PRIOR FILING DATE: 1999-10-13
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 476
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

QY 38 TQNKALPENVKYIGIVLDAGSSHTSLYIYKWPAPKENDTGVVHVQVEECRVKPGISKFVQK 97
DB 49 TQNKALPENVKYIGIVLDAGSSHTSLYIYKWPAPKENDTGVVHVQVEECRVKPGISKFVQK 108
QY 98 VNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSL 157
DB 109 VNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSL 168
QY 158 NYPPDFQAGRIITGOBEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGA 217
DB 169 NYPPDFQAGRIITGOBEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGA 228
QY 218 STQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFCLCYGKDQALWOKLAKDIQVASNEI 277
DB 229 STQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFCLCYGKDQALWOKLAKDIQVASNEI 288
QY 278 LRDPCHFGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQIGIYQCHOSILELFTSY 337
DB 289 LRDPCHFGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQIGIYQCHOSILELFTSY 348
QY 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWBEI 397
DB 349 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWBEI 408
QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIIHFICKIQGSDAGWT 451
DB 409 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIIHFICKIQGSDAGWT 451
QY 458 LTNMIPAEQPLSTPLSHST 476
DB 469 LTNMIPAEQPLSTPLSHST 487

QY 36 GLTQNKALPENVK-----YGIVLDAGSSHTSLYIYKWPAPKENDTGVVHVQVEECRVKPGI 91
DB 32 GILSSMKPINVSASTLYIGIVLDAGSSHTSLYIYKWPAPKENDTGVVHVQVEECRVKPGI 91
QY 92 SKFVQKNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMESEELADRLDV 151
DB 92 SKFVQKNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMESEELADRLDV 151
QY 152 VERSLSNYPDFQAGRIITGOBEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGA 211
DB 152 VERSLSNYPDFQAGRIITGOBEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGA 211
QY 212 LDLGGASTQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFCLCYGKDQALWOKLAKDIQ 271
DB 212 LDLGGASTQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFCLCYGKDQALWOKLAKDIQ 271
QY 272 VASNEILRDPCHFGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQIGIYQCHOSILE 331
DB 272 VASNEILRDPCHFGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQIGIYQCHOSILE 331
QY 332 LFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 391
DB 332 LFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 391
QY 392 QPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIIHFICKIQGSDAGWT 451
DB 392 QPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIIHFICKIQGSDAGWT 451
QY 452 LGYMLNLTNMIPAEQPLSTPLSHST 476
DB 452 LGYMLNLTNMIPAEQPLSTPLSHST 476

Search completed: March 7, 2005, 14:12:36
Job time : 61.831 secs

RESULT 15
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: {39}
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 85.1%; Score 2297; DB 9; Length 476;
Best Local Similarity 97.1%; Pred.No. 1.1e-197;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

GenCore version 5.1.6
: Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: March 7, 2005, 12:59:07 ; Search time 13.6708 Seconds
(without alignments)
3117.881 Million cell updates/sec
Title: US-09-835-147A-2_COPY_36_478
Perfect score: 2369
Sequence: 1 GLTQNKALPENVKYIVLDA.....TNMIPASQPLSTPLSHSTYV 443
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	2369	100.0	510	2	I56242
2	505	21.3	483	2	D86276
3	469.5	19.8	405	2	E86276
4	453	19.1	630	2	S50463
5	417	17.6	572	2	T40856
6	406.5	17.2	516	2	G84442
7	402.5	17.0	485	2	T34147
8	394.5	16.7	508	2	C86276
9	383.5	16.2	557	2	T16696
10	381.5	16.1	556	2	T39109
11	374.5	15.8	455	2	S48859
12	336.5	14.2	1052	2	T04439
13	334	14.1	454	2	JC4616
14	330	13.9	479	2	T23508
15	320.5	13.5	518	2	A40732
16	167	7.0	628	2	A55421
17	103.5	4.4	369	2	S77299
18	101.5	4.3	716	2	T21516
19	100	4.2	307	2	T27332
20	99	4.2	1951	2	B43963
21	98.5	4.2	590	2	A81411
22	98.5	4.2	797	2	D86247
23	98.5	4.2	989	2	B84532
24	98.5	4.2	1509	2	B89985
25	98	4.1	371	2	T05213
26	98	4.1	665	2	T18979
27	98	4.1	3848	2	T17414
28	97.5	4.1	392	2	A96738
29	97	4.1	494	2	T03774

probable fimbrial
myosin I beta - bu
(R)-2-hydroxygluta
hypotheical prote
serine/threonine k
spore germination
Mg2+ transporter h
hypotheical prote
lactacin 481/lacto
probable permease
probable permease
hypotheical prote
hypotheical 51.7
probable dnaK prot
probable dnaK-type
beta-galactosidase

30 96 4.1 883 2 B85725
31 96 4.1 1028 2 I51173
32 96 4.1 1415 2 A72369
33 95.5 4.0 591 2 F89770
34 95.5 4.0 1900 2 AG2391
35 95 4.0 288 1 B48583
36 95 4.0 451 2 G89859
37 95 4.0 564 2 S15962
38 95 4.0 927 2 T43110
39 94.5 4.0 461 2 G91228
40 94.5 4.0 461 2 F86075
41 92.5 3.9 404 2 T21251
42 92.5 3.9 468 2 H65192
43 92.5 3.9 556 2 A90715
44 92.5 3.9 556 2 H64799
45 92.5 3.9 727 2 T47541

ALIGNMENTS

RESULT 1
I56242
lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56242
R:Maliszewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;
J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A:Reference number: I56242; MUID:95015846; PMID:7930580
A:Accession: I56242
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: UNIPROT:P49961; GB:S73813; MID:9765255; PIDN:AAB32152.1; PID:9765255
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	Best Local Similarity	Score	DB 2	Length	510;
Matches	443;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Qy	1	GLTQNKALPENVKYIVLDA	GSSHTSLYYIKWPAEKENDTGVVHQVEECRVKGPISKPV	60	
Db	36	GLTQNKALPENVKYIVLDA	GSSHTSLYYIKWPAEKENDTGVVHQVEECRVKGPISKPV	95	
Qy	61	QKVNIEGILYTDCEMERAREVIPSQHOETPVYLCATAGMRLRMESELRADRVLDVVERS	120		
Db	96	QKVNIEGILYTDCEMERAREVIPSQHOETPVYLCATAGMRLRMESELRADRVLDVVERS	155		
Qy	121	LSNYPFDFQGARIIITGQEEGAYGMITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG	180		
Db	156	LSNYPFDFQGARIIITGQEEGAYGMITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG	215		
Qy	181	GASTQVTFVPOQNTIESPDNALQRLYKGVKNVYTHSPLCYGKQALWQKLAKDIQVASN	240		
Db	216	GASTQVTFVPOQNTIESPDNALQRLYKGVKNVYTHSPLCYGKQALWQKLAKDIQVASN	275		
Qy	241	EILRDCPHGPKYKKNVNSDLYKTPCTKRPMTLPFOQFEIQGIGNYQCHOSILELFT	300		
Db	276	EILRDCPHGPKYKKNVNSDLYKTPCTKRPMTLPFOQFEIQGIGNYQCHOSILELFT	335		
Qy	301	SYCPYSQCAFNGIIFLPLOQDFGAFSAFYFMKFLNLTSEKVSQKVTMMKKFCAQPWE	360		
Db	336	SYCPYSQCAFNGIIFLPLOQDFGAFSAFYFMKFLNLTSEKVSQKVTMMKKFCAQPWE	395		
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKTQGSAGWTLGYM	420		
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKTQGSAGWTLGYM	455		
Qy	421	LNLTNMIIPASQPLSTPLSHSTYV	443		
Db	456	LNLTNMIIPASQPLSTPLSHSTYV	478		

RESULT 2
D86276
hypochemical protein F7A19.34 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L.
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9XI62; GB:AE005172; NID:G5080801; PIDN:AAD39311.1; GSPDB:GN
C:Genetics:
C:Superfamily: nucleoside triphosphatase chromatin-associated
Query Match 21.3%; Score 505; DB 2; Length 483;
Best Local Similarity 31.3%; Pred. No. 4.8e-33;
Matches 135; Conservative 70; Mismatches 164; Indels 62; Gaps 18;
Qy 12 VKYGVLDAGSSHTSLYIKVPAKEN---DTGVVHVQVECRVK-GPGISKFVKVNEIG 67
Db 68 LKYSVLIDAGSGTRVHVGWFGESGKVPDFGEKHY---ANLKTPLGSSIANPEGAS 124
Qy 68 IYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRLDVVERSL--SNYP 125
Db 125 VSVTKLVEFAKQRIKPMFRERSDIRLMATAGMRLLEVPVQGE--QILEVTRVLRSSGFM 181
Qy 126 PDFQARIITGOEGAYGWITINYLKFGSKQTRWFSIVPVETNNQETFGALDILGGASTQ 185
Db 182 FRDEWANVIGSDEGIYSWITANYALGSLG-----TDPLETTGTIVELGGASAQ 229
Qy 186 VTFVPQNTIESPINALQFLRYGK-DYNNVTHSFLCYGKQOALWQKLAKDIOVASNE--- 241
Db 230 VTFVSSEHV---PPEYSRTIAYGNISYTIYSHSFLDYGKDAAAL-KKGLKQLNSANSTVD 285
Qy 242 -ILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLFPQOFEIQG----IGNYQOCHQSILE 296
Db 286 GVVEDPCTPKGY-----IYDTN-SKNYSSGFLADSSKLKGLSQAAGNFSKCRSATFA 336
Qy 297 LF-NTSYCPYSCAFNGIFLPPQGDGFGAFSAFYVNMKFLNLTSEKVSQEKVTEMKKF 354
Db 337 LLKEGKCNLYEHCSIGSTFTPDQLGGSFLATASFYTTAKFPPEL-EKGLWSELIPAGKRY 395
Qy 355 CAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLILQGHVFTADSWEHIFHFGIKQGSAG 414
Db 396 CGEWSKILLEYPTTDEBYLRGYCFSAAYTISMLHDSLGIALDD-ESITYASK-----AG 449
Qy 415 -----WTLG 418
Db 450 EKHIPLDWALG 460

RESULT 3
E86276
hypochemical protein F14L17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L.

anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:G7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1
Query Match 19.8%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 2.9e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;
Qy 54 PGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRV 113
Db 29 PGLSSYADNPPEGASVSVTKLVEFAKGRIPKGLKKSDIRLMATAGMRLLDVFPVQGE--QI 85
Qy 114 LDVVERSILSNYPDFQG--ARIITGOEGAYGWITINYLKFGSKQTRWFSIVPVETNNQ 171
Db 86 LDVTRRVLRSSGFKFQDEWATVISTDEGIYAVVNVANHLGSLG-----GDPL 133
Qy 172 ETFGALDILGGASTQVTFVPQNTIESPINALQFLRYGK-DYNNVTHSFLCYGKQOAL--L 227
Db 134 KTTGIVELGGASAQVTFVPSEHV---PPEFSRTISYGNVSYTIYSHSFLDFGQDAAEDKL 190
Qy 228 WQKLAKDIOVASNE-ILRDPCHPGYKVVNVSDLYKTPCTK-----RREMTLPF 276
Db 191 LESLQNSVAASTGDIVEDPCTPKGY-----IYDTHSQKSSGLSESKFKASL-- 240
Qy 277 QQFEIQIGNYQOCHQSILELF--NTSYCPYSCAFNGIFLPPQGDGFGAFSAFYVNMKF 334
Db 241 ---QVQAGDFTKCRSATLMLQEGKENCAYKHCISGSTFTPNQGSFLATENFHTSKF 297
Qy 335 LNLTSKVSQEKVTEM---KKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLILQ 391
Db 298 FGL-GEK---EWLSEMLAGKFCGEEWSKLKKEYPKTKDKLHRYCFSSAYIISMLHDS 353
Qy 392 YHFTADSWEHIFHFGIKI--QGS DAGWTLG-YMLN 422
Db 354 LGVALDD-ERIKYASKAGKENIPLDWALGAPILN 386
RESULT 4
S50463
hypochemical protein YER005w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DJE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:G603592; PID:G603597; GSPDB:GN00005
C:Genetics:
A:Gene: SGD:YND1; MIPS:YER005w
A:Cross-references: SGD:S0000807
A:Map position: 5R
Query Match 19.1%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1.2e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

Db	224	NEAYRRYGLLIISENGKVGNTSLDPCSLRG-----RTYDIDGIE	263
Qy	281	IQGIGNYQQCHQSILELFNTSY-CPYSOCAPNGIFLPLOGDFGAFSAFYFVKFLNLTS	339
Db	264	PAGTGDLKQCLKLTNYLLNKDKPCSPDNFGISIPV--DF-ANTEFVGUSEFWYTN	320
Qy	340	EKVSQ-----EKVTENMKKFCQAQPWBEI-----KTSYAGVKEKYILSEYCFSGRY	383
Db	321	DVFDMGGSYHFPNPKYKVD-----YCCTWETMLSRLYNKKELTPSDENKLEKLCKFKASW	376
Qy	384	ILSLLOG-----YHFTADSWEHHTFGTKIOGSDAGWTGLGYML	421
Db	377	ALANVLHEGFDPVKSTNSDAKDGLSVIPAYHSPPTSL-----KIERTEVSWTGLQVL	430
Qy	422	NLTNMIPAEOPLSTPLSHSTY	442
Db	431	----LYASNQQLAKPEYANY	447
 RESULT 6 G84442			
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana			
C;Species: Arabidopsis thaliana (mouse-ear cress)			
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004			
C;Accession: G84442			
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuj			
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.			
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.;			
Nature 402, 761-768, 1999			
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalia			
A;Reference number: A84420; MUID:20083487; PMID:10617197			

A:Status: preliminary

A:	Molecule type: DNA
A:	Residues: 1-516 <STO>
A:	Cross-references: UNIPROT: O80612; GB: AE002093; NID: G3461821; PIDN: AAC32915.1
C:	Genetics:
A:	Gene: At2g02970
A:	Map position: 2
C:	Superfamily: nucleoside triphosphatase chromatin-associated
Query Match	17.2%; Score 406.5; DB 2; Length 516;
Best Local Similarity	27.5%; Pred. No. 5.3e-25;
Matches 117; Conservative	68; Mismatches 187; Indels 53; Gaps 13
Qy	11 NVKXGIVLDAGSSHTSLIYKNPAEKENDTGVHVQECERVK-GPGISKFKVQNVEIGY 69 :: :: : : : : : : :
Dd	65 SLRYVVVIDGGSTRIHVLGYRISYGKPVFPEFRGANYSKLHLFGSAFADDPDGASVS 124 : : : : : : : : : : :
Ov	70 LTDCMERAREVIPRSOHETPVYLGCATGMELLRWSESELADRVLVDVVVERSL--SNYPD 127 : : : : : : : : : : :

125	Db	LTELVEFAKRGVKGMMIETVRUMATAGMKLLELPVQE---	125	Db	KLUGVARRVLKSSGFLPR
128	Qy	FOGARIITGOBEGAYGMITNYLLGKFSQKTRWFSIV	128	Qy	VEYTNNOETFGALDIGGASTQVT
182	Db	DEWASVSGSGDEGYAVWVANFALGSLG---	182	Db	GDPLKTTGIVELGGSAAQVT
188	Qy	FVPQNOTIESPDNALQFRLYCKDYNVYTHSFLCYCKDQA---	188	Qy	LW-OKLAKD---IOVAS
230	Db	FVSEPM--PPEFERTISFGNVYTNLYKSHSLHFGQNAAHKLWGSLLSRDHSNAVEPTR	230	Db	---
240	Qy	NEILRDCPHFGYKXVNVNVDLYKTPCTKRFEMTLPPQOFBIQIGIGNYQQCHQSILELPN	240	Qy	---
288	Db	EKIPTDCAPKGYNLDANTOKHLSGLLAEESRLSDSF---	288	Db	QAGNGYSQCRSAALTILQ
300	Qy	TSYCPYSCAFNGIFLPPLOQDFCAFSAFYFMVKFLNLTSEKVSQEKVTEMKKFKCAQPW	300	Qy	---
343	Db	-----NGRILIIAG---FSLPFLGL-----	343	Db	GEKAWLSNMISAGERFCGEDW
360	Qy	BEIKTSYAGVKEKYSBVCFSGTYILSLLOGYHFTADSWBHIHFIGIKQSGDAGWTLOY	360	Qy	---
384	Db	SKLRKDPKSLHEEDLLRYCFSSAYIVSLHDTLGLPLDD--	384	Db	ERIGYANQAGDIFLOWALGA

Qy 420 MLNLT 424
Db 443 FIQOT 447

RESULT 7
T34147
hypothetical protein C33H5.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34147
R:Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C33H5.
A:Reference number: Z21482
A:Accession: T34147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485

A:Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C33H5.14
A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C:Superfamily: nucleoside triphosphatase chromat-in-associated

Query Match 17.0%; Score 402.5; DB 2; Length 485;
Best Local Similarity 26.7%; Pred. No. 1e-24;
Matches 116; Conservative 69; Mismatches 187; Indels 63; Gaps 15;

Qy 11 NVKYGIVLDAGSSHTSLIYKPAEKENDTCV---VHGVCECRVK-GPGISKFKVQKNEI 66
Db 22 NIKYGVICDAGSSGTRLVYTLKPLSGGLTIDILIHSEPVVKVTPGLSFGDKPEQV 81
Qy 67 GYILTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSLNYPF 126
Db 82 VEYLTPLLRFAEHIPIYEQLGSETDLLIPATAGMRLPEAKQDAIKNLQGLKSVTLRV 141
Qy 127 DFOGARIITQEGAGYGHITINLLKFSQKTRWFISVYPYTNQETFGALDLGASTOV 186
Db 142 SDSNIRIIDGAWEGIYSIAVNIILGFRDKE-----NDSKGMIDMGASVOI 189
Qy 167 TFPVQNOTIESPD--NALQFLYKGD-----YNNVTHSFLCYGKDOALWOKLAKDIOVA 238
Db 190 AFEIANEK-ESVNGNVVNIINLSGTETNEDYKIKYSTTFILGYGANGL-KKYENSLVKS 247
Qy 239 SNEILRDCPFHFGYKVVNVDLYKTPCTKRFEMTLPPQFEIOGIGNYQOCHOSILELF 298
Db 248 GNS--NDSGSPRLNRLIG-----EFTVNGTGEWDVCLAQVSSLI 285
Qy 299 NTS-----YCPYQCAENGFLPPLQ---GDFGAFSAFYFMKFLNLTSEKVSQEKVTMMK 352
Db 286 GDKAQPCFNPCTFLRNVIAPSVNLSTVQLYGFSEYWTTSNFGSGGE-YHYQKPTDEVR 344
Qy 353 KFCAPQWEI-----KTSVAGVKEKYLSEYCFSGVYILSLLLQGYHFTADSWEHIFIG 406
Db 345 KYCQKQWMDIQDFRNEFPNADIERTLNTCNKAAWTVSVLHDG--FNVDKTKHLFQSVL 402
Qy 407 KIQGS DAGWTLLGYML 421
Db 403 KIAGEQMQLGAML 417

RESULT 8
C86276
7A19.33 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <STO>
A:Cross-references: UNIPROT:Q9X163; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: nucleoside triphosphatase chromat-in-associated

Query Match 16.7%; Score 394.5; DB 2; Length 508;
Best Local Similarity 28.2%; Pred. No. 4.9e-24;
Matches 123; Conservative 71; Mismatches 171; Indels 71; Gaps 20;

Qy 11 NVKYGIVLDAGSSHTSLIYKPAEKENDTCV---VHGVCECRVK-GPGISKFKVQKNEI 69
Db 63 SLHYSVIIIDGSSGTRVHVFYRIESGKPVDFDGEENYASLKLSPGLSAYADNPEGVSES 122
Qy 70 LTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSLNYPFDFQ 129
Db 123 VTEIYEFKRVHKGKLSKSDIRLMATAGWRLLELPQE---QILDVTRVLRSSGPDF- 178
Qy 130 GARIITQEGAGYGHITINLLKFSQKTRWFISVYPYTNQ-ETFGALDLG-----GA 182
Db 179 -----RDWASVISILENFQDLMKVYMLGLLIMRSV 211
Qy 183 STQVTFVQNOTIESPDNALQFLYK-GDNNVTHSFLCYGKDOALWOKLAKDI-OVASN 240
Db 212 RLEVTFV---STELVSEFSERTLAYGNVSNLHSHFLDFGQD-AAQEKLSSELYNSAAN 267
Qy 241 E-----ILRDCPFHFGYKVVNVDLYKTPCTK-RFEMTLPPQFEIOGIGNYQOCHOSI 294
Db 268 STGEGIVDPDIPKGYIETNLQKLPGLADKGFATL-----QAAGNFSECRSAA 320
Qy 295 LEIF--NTSCYPSQCAFNGIFLPPLOGDFGASAFYFMKFLNLTSEKVSQEKVTMM- 351
Db 321 FAMLQEBKGTCTKRCISIGSIFTPNLQGSFLATENPFHTSKFFGL-GEK---EWLSEML 376
Qy 352 --KKFCAQPEEIKTSYAGVKEKYLSEYCFSGVYILSLLLQGYHFTADSWEHIFIGIKI 409
Db 377 AGKRFCEEHSKLVKVPYTFKDNLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
Qy 410 GSD--AGWTLLG-YMLN 422
Db 436 EEDIPLDQWALGAFIN 451

RESULT 9
T16696
hypothetical protein R07E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16696
R:Miller, N.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid R07E4.
A:Reference number: Z18561
A:Accession: T16696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-557 <Mil>
A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R07E4.4
A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match	15.8%;	Score 374.5;	DB 2;	Length 455;
Best Local Similarity	25.6%;	Pred. No. 1.8e-22;		
Matches	120;	Conservative	80;	Mismatches 177; Indels 91; Gaps 19
Qy	2	LTQNKAL----	PENVKYGIVLDAGSHTSLTYIKYKPA	KENDTGVH-----QVEECKVKGPG 55
Db	29	LTSRKIFLKOEI	SSYAVVFDAGSTGRIHYHF----	NQLDLLHLHGKGYEVYVYKNIITPG 84
Qy	56	ISKFPQVKNEIGI	YLTDCMERARVIPSQHOETPVVIGATAG	MRLLRMESEELADRVLD 115
Db	85	LSSYANNPEQA	AKSLIPLLEQAEADVDDLPQKTPVRLG	ATAGURLUNDASE---KITLQ 141
Qy	116	WVERSLN-YP	FDQ--GARIITQEBEGAYCWIINVL	LKGFOSKTRWFSIVPVETNNQE 172
Db	142	SVRDMLSNRST	FNVQPDVAVSIIDTQSGSYLVVTVN	YALGNLKK-----YTK 189
Qy	173	TFGALDGG	ASTQTVTFVQNOTTIESPNAL-----	QFRLYKGNVNVYTHSFLCYGKD 224
Db	190	TGVVIDLGG	GSQVAYAVSKTAKNPKVADGDDPYIK	VKKVYLGIPDYLYVHSYLHFGK- 248
Qy	225	QALWQKLAK	DIQVANSILR-----DPCFHPG	YKVVNVSDLYKTPTCKRFEMTLFPQQ 278
Db	249	-----EAS	RABILKLTPRSPNPLL	AGNGIYTSG-----EEFKAT----- 285
Qy	279	FEIQGIGNY	QOCHOSILELFNTSY-CFYSOCARNGI	FLPPLQDFG-----AFSAFVF 330
Db	286	-AYTSGANF	NKKNITIRKALKNTPCYQNTCFGGI	W-----NGGGNGQKNLFPASSPFY 340
Qy	331	VMKFLNLT	SBK-----VSQBKVTEMMKKFCAQ	PWEEIKTSYAGVKYEKLSEY-CFSGFYI 384
Db	341	LPEDTGM	VDASTPNFILRPVDIETKAEACALN	FEADAKSTYFPLDKKNVASYVCMDLIYQ 400
Qy	385	LSLILQYH	TTAASWEHHIFGKI	QSGD-----AGWTLGYMLNLNMP 428
Db	401	YVLLIVD	G--FGLDPLOKITSGKEIT	EYQDATVEAAAPLGNVAEALSAIP 446

RESULT 12

T04439
hypothetical protein T18B16.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04439
R:Bayan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15359
A:Accession: T04439
A:Molecule type: DNA
A:Residues: 1-1052 <REV>
A:Cross-references: UNIPROT:O49676; EMBL:AL021687
A:Experimental source: cultivar Columbia; BAC clone T18B16
C:Genetics:
A:Map position: 4
A:Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A:Note: T18B16.150

Query Match 14.2%; Score 336.5; DB 2; Length 1052;
Best Local Similarity 26.5%; Pred. No. 7.2e-19;
Matches 108; Conservative 75; Mismatches 156; Indels 69; Gaps 17;
Qy 54 PGISKFKVQVNEIGIYLTDCMERAREVTPRSOHOETPVYLGATAGMILLR-MESEELADR 112
Db 578 PGFKLVNRTGLTKTAIKPLQWAEKQIPKNAHTTSLFVYATAGVRLRPADSSWILGN 637
Qy 113 VLDVVERSLSNYPDF--QGARIITQOEAGYGMITINY---LLGKFSQKTRWFSIVPYE 167
Db 638 VWSILAKS---PTCRREWKIISGTEAYFGWALTALNYQTSMLGALPKKA----- 684
Qy 168 TNNDETGCALDLGASQTQVTPVONQITSPDNLQFLRYGKDYNVVTHSFLCYGKQQA- 226
Db 685 ---TFGALDLGSSLSQVTF--EENERTHETNLRLRIGSVNHLAYSAGYGLNDAF 737
Qy 227 -----LWOKLA---KDIQVANSILRDPCHPGKVKVNVVSDLYKTPCTKRFEMTLFPQ 277
Db 738 DRSVVHLKKLPNVNKSLDIEKLEMKHPCLNSGVN-----GVYICQCASSVGGKKGK 792
Qy 278 ---QFEIQIGIGNYQOCHSILELFTNTSYCYSCAFNGIFLPPLOQDFGAFSAFYVWKF 334
Db 793 SGVSIKLVGAPNWGEC-----SALAKNAPCALPDGY-PRPHGQFYAVSGFVVRVF 842
Qy 335 LNTISEKVSQKRYTEMKMKFCAQPWEEKITSYAGVKEKYLSEYCFSGTYILSILLQGHF 394
Db 843 FNLSAE-ASLDDVLEKRGFCDAWQARTSVS--POPFIEQYCFRAPYIVSLLREGLYI 899
Qy 395 TADSWEHIFTKIGQSDAGWTGLGYMLNLTWNIPAEQPLSTPLSHSTY 442
Db 900 T-----DKQIIIG---SGSITWTLGVAL-----LESGLALSTLGLKSY 935

RESULT 13

JC4616
apyrase (EC 3.6.1.5) precursor - potato
N:Alternate names: adenylypyrophosphatase; ATP-diphosphohydrolase
C:Species: Solanum tuberosum (potato)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4616; PC4147
R:Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A:Reference number: JC4616; MUID:96158985; PMID:8579614
A:Accession: JC4616
A:Molecule type: mRNA
A:Residues: 1-454 <HAN>
A:Cross-references: UNIPROT:P80595; GB:U58597; NID:gl381632; PIDN:AA02720.1; PID:gl3816
A:Accession: PC4147
A:Molecule type: protein
A:Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A:Experimental source: tubers

A:Note: The authors translated the codon GCA for residue 215 as Gly
C:Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate, a reaction that requires a divalent cation requirement, and insensitive to vanadate.
C:Genetics:
A:Gene: rrop1

C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; hydrolase; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:8-25/Domain: transmembrane #status predicted <TM>
F:31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F:44-65/Region: nucleotide binding #status predicted
F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F:192-212/Region: nucleotide binding #status predicted
F:390-410,427-446/Region: hydrophobic carboxyl end
F:151,262/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 334; DB 2; Length 454;
Best Local Similarity 24.9%; Pred. No. 3.4e-19;
Matches 112; Conservative 80; Mismatches 185; Indels 72; Gaps 17;
Qy 10 ENVKYGVILDAGSHSTSLYIKWPAEKENDTGVVHVECRVKPGIGSKFVKQVNEIGIY 69
Db 42 ESEHYAVIFDAGSTGSRVHFRFD-EKLGLLPTGNNIEYFMATEPGLSSVAEDPKAAANS 100
Qy 70 LTDCMERAREVTPRSOHOETPVYLGATAGMILLRMESEELADRVLDDVE---RSLSNYPF 126
Db 101 LEPLLDGAEVVPQELQSETPLELGATGLMLKGDA---AEKILQAVRLNVKNQSTFHS 157
Qy 127 DFGARIITQOEAGYGMITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGASTQV 186
Db 158 KDQWVTLLDGTQEGSYWMAAINVLLGNLKG-----DYKSTTATIDLGGSVQM 205
Qy 187 TFPVQN-OTTESPDN-----ALQFRLYGKDYNVVTHSFLCYGKQDQALWQKLADIQVAS 239
Db 206 AYAINSEQFAKQNEDEGEFVQOQKHLMSKDYLYVHSYLYNYGO-LAGRAEIFKASRNES 264
Qy 240 NEILRDPCHPGKVKVNVVSDLYKTPCTKRFEMTLFPQFEIQIGNYQOCHQSILELFN 299
Db 265 NPCALEGC--DGYYSYGVVD--YKVPKKG-----SSWKRCRLTRHALK 306
Qy 300 -TSYCPYSQCAFNGIFLPPLOQDFG-----AFSAFYVWKFLNLTSEKVSQE-----K 346
Db 307 INAKCNIEECTFNGW-----NGGGGQGNTHASSFFYDICAQVGIQVDTKPPSALAKPIQ 362
Qy 347 VTEMKKFCAQPWEEKITSYAGVKEKYLSEYCFSGTYILSILLQGHYHFTADSWEHIFIG 406
Db 363 YLNAARVACQTNVADIKSIFPKTDNRNIPYLCMDLIYEYTLVDG--FGLNPHKEITVIH 420
Qy 407 KIQGSD---AGWTLGYMLNL---TNMI 427
Db 421 DVQYKNYLVAAMPGLGCAIDLVSSTTKKI 449

RESULT 14

T23508
hypothetical protein K08H10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23508
R:Gardner, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19750
A:Accession: T23508
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-479 <WIL>
A:Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; CESP:K0
C:Genetics:
A:Gene: CESP:K08H10.4
A:Map position: 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 62.0612 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-2_COPY_36_478

Perfect score: 2369

Sequence: 1 GLTQKALPENVKYIVLDA.....TNMIPAEQPLSTPLSHSTYV 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2369	100.0	510	1 ENP1_HUMAN	P49961 homo sapien
2	1855	78.3	510	1 ENP1_MOUSE	P55772 mus musculus
3	1855	78.3	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1850	78.1	510	2 Q921Q6	Q921q6 mus musculus
5	1829	77.2	372	2 Q86VW3	Q86vw3 homo sapien
6	1814.5	76.6	511	1 ENP1_RAT	P97687 rattus norv
7	1736	73.3	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1711.5	72.2	513	1 ENP1_BOVIN	O18956 bos taurus
9	1584	66.9	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1456	61.5	508	2 Q6DFS1	O6dfs1 xenopus tro
11	1426	60.2	508	2 Q6GP74	Q6gp74 xenopus lae
12	1316.5	55.6	492	2 Q6DC46	Q6dc46 brachydanio
13	1046.5	44.2	497	2 Q6UQ22	Q6uq22 mus musculus
14	1004	42.4	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	42.1	493	2 Q90X66	Q90x66 gallus gall
16	974	41.1	454	2 Q6ZM69	Q6zm69 brachydanio
17	971.5	41.0	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	40.7	495	1 ENP2_MOUSE	O55026 mus musculus
19	964.5	40.7	495	2 Q921R1	Q921r1 mus musculus
20	962	40.6	455	2 Q7T014	Q7t014 brachydanio
21	953	40.2	494	1 ENP2_CHICK	P79784 gallus gall
22	939	39.6	526	2 Q6GN44	Q6gna4 xenopus lae
23	937.5	39.6	502	2 Q6GL64	Q6gl64 brachydanio
24	933	39.4	500	2 Q6NV19	Q6nv19 xenopus tro
25	913.5	38.6	529	2 Q80Z26	Q80z26 rattus norv
26	911	38.5	529	1 ENP3_HUMAN	O75355 homo sapien
27	907.5	38.3	495	1 ENP2_HUMAN	Q9y5l3 homo sapien
28	906.5	38.3	458	2 Q6UVZ0	Q6uvz0 homo sapien
29	902.5	38.1	529	2 Q8BFW6	Q8bfw6 m mus muscu
30	854	36.0	453	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	34.8	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	27.8	544	2 Q7YTA4	Q7yta4 schistosoma
33	620.5	26.2	300	2 Q8KOL2	Q8kol2 mus musculus
34	596.5	25.2	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	505	21.3	483	2 Q9X162	Q9x162 arabidopsis
36	504	21.3	488	2 Q6NQA8	Q6nqa8 arabidopsis
37	491	20.7	503	2 Q94AP8	Q94ap8 arabidopsis
38	491	20.7	503	2 Q8H1D8	Q8h1d8 arabidopsis
39	485	20.5	537	2 Q6Z543	Q6z543 oryza sativ
40	483	20.4	634	2 Q6FRC2	Q6frc2 candida gla
41	482.5	20.4	336	2 Q8CCV2	Q8ccv2 mus musculus
42	471.5	19.9	555	2 Q94EZ2	Q94ez2 arabidopsis
43	469.5	19.8	405	2 Q9M9T7	Q9m9t7 arabidopsis
44	466	19.7	611	2 Q6DH30	Q6dh30 brachydanio
45	465.5	19.6	555	2 Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1

ID	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
AC	P49961; Q9UQ09; Q9Y3Q9;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)			
DE	(NTPDase1) (ecto-ATP diphosphohydrolase) (ATPDase) (lymphoid cell			
DE	activation antigen) (ecto-apyrase) (CD39 antigen).			
GN	Name=ENTPD1; Synonyms=CD39;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Deleseppe G.J.T., Schoenborn M.A., Armitage R.J.,			
RA	Fanslow W.C., Nakajima T., Baker E., Sucherland G.R., Polindexter K.,			
RA	Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;			
RT	"The CD39 lymphoid cell activation antigen. Molecular cloning and			
RT	structural characterization."			
RL	J. Immunol. 153:3574-3583(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	TISSUE=Umbilical vein;			
RC	MEDLINE=97149443; PubMed=8996251;			
RX	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Koziak K.,			
RA	Millan M., Hancock W.W., Bach F.H.;			
RT	"Loss of ATP diphosphohydrolase activity with endothelial cell			
RT	activation."			
RL	J. Exp. Med. 185:153-163(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).			
RX	TISSUE=Placenta;			
RC	MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;			
RX	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,			
RA	Titani K., Fujimura Y., Narita N.;			
RT	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I			
RT	and II."			
RL	FEBS Lett. 453:335-340(1999).			
RN	[4]			
RP	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96096723; PubMed=8529670;			
RA	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;			
RT	"Purification and properties of human placental ATP			
RT	diphosphohydrolase."			
RL	Eur. J. Biochem. 234:66-74(1995).			
RN	[5]			
RP	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND			
RP	399-405 (ISOFORM PLACENTAL I).			
RC	TISSUE=Placenta;			

RA RX MEDLINE=99062444; PubMed=9846014;
RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.,
RT "Placental ecto-ATP diphosphohydrolase: its structural feature
RT distinct from CD39, localization and inhibition on shear-induced
RT platelet aggregation.";
RL Int. J. Hematol. 68:297-310(1998).
RN [6]
RP FUNCTION.
RX MEDLINE=97115858; PubMed=955160; DOI=10.1074/jbc.271.51.33116;
RX Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase.";
RL J. Biol. Chem. 271:33116-33122(1996).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;
RX Wang T.F., Guidotti G.;
RT "CD39 is an ecto-(Ca²⁺, Mg²⁺)-ATPase.";
RL J. Biol. Chem. 271:9898-9901(1996).
RN [8]
RP PALMITOYLATION.
RX MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
RX Koziak K., Kaczmarek E., Kittel A., Sevigny J., Blusztajn J.K.,
RA Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,
RA Robson S.C.;
RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
RT caveolae.";
RL J. Biol. Chem. 275:2057-2062(2000).
CC -!- FUNCTION. In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Vascular;
CC IsoId=P49961-1; Sequence=Displayed;
CC Name=Placental I;
CC IsoId=P49961-2; Sequence=VSP_003607;
CC Name=Placental II;
CC IsoId=P49961-3; Sequence=VSP_003608, VSP_003609, VSP_003609;
CC TRISUE SPECIFICITY: Expressed primarily on activated lymphoid
CC cells. Also expressed in endothelial tissues. The vascular isoform
CC and the placental isoform II are present in both placenta and
CC umbilical vein, whereas placental isoform I is present in placenta
CC only.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and
CC 7.5-8.0 with ADP.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
CC
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CC
CC EMBL; S73813; AAB32152.1; -;
CC EMBL; U07967; AAB4752.1; -;
CC EMBL; A0133133; CAB41886.1; -;
CC EMBL; A0133134; CAB41887.1; -;
CC PIR; I56242; I56242.
CC Genew; HGNC:3363; ENTPD1.
CC MIM; 601752; -;

DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO:0007596; P:blood coagulation; TAS.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
KW Transmembrane.
FT DOMAIN 1 16 Cytoplasmic (Potential).
FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 478 Extracellular (Potential).
FT TRANSMEM 479 499 Potential.
FT DOMAIN 500 510 Cytoplasmic (Potential).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 1 4 MEDT -> MKGTDKLTSQQ (in isoform Placental I and isoform Placental II).
FT VARSPPLIC 272 299 VASNEILRDCEFHFGYKVVNSDLYKT -> ASITQSRPA
PFTSAPPAPPTSCCLFQIQ (in isoform Placental II).
FT VARSPPLIC 300 510 Missing (in isoform Placental II).
FT CONFLICT 57 58 SS -> G (in Ref. 5).
FT CONFLICT 162 162 D -> K (in Ref. 4).
FT CONFLICT 208 208 T -> TGEE (in Ref. 5).
FT CONFLICT 248 248 V -> Y (in Ref. 5).
SQ SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;
Query Match 100.0%; Score 2369; DB 1; Length 510;
Best Local Similarity 100.0%; Pred. No. 66-178;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLTNKALPENVKYGVLDAGSHTSLYIYKPAEKENDGVVHVQVECRVKGPGISKFV 60
Db 36 GLTNKALPENVKYGVLDAGSHTSLYIYKPAEKENDGVVHVQVECRVKGPGISKFV 95
Qy 61 QKVNIEGILYTDCEMERAREVIPSQHOETPVYLGATAGMELLRMESEBELADRLDVVVERS 120
Db 96 QKVNIEGILYTDCEMERAREVIPSQHOETPVYLGATAGMELLRMESEBELADRLDVVVERS 155
Qy 121 LSNYPDFQGARITGOEGAGYGVITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 180
Db 156 LSNYPDFQGARITGOEGAGYGVITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 215
Qy 181 GASTQVTFVFNQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASN 240
Db 216 GASTQVTFVFNQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASN 275
Qy 241 EILRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFIEQIGNTQOCHQSILELPNT 300
Db 276 EILRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFIEQIGNTQOCHQSILELPNT 335
Qy 301 SYCPSQCAFNGIFLPLQGDGFGAFSIFYVMKFLNLTSEKVSQEKVTEMMKKFCAQDWE 360
Db 336 SYCPSQCAFNGIFLPLQGDGFGAFSIFYVMKFLNLTSEKVSQEKVTEMMKKFCAQDWE 395
Qy 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGIKQSDAGWTILGYM 420
Db 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGIKQSDAGWTILGYM 455
Qy 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 2
ENP1_MOUSE

DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 78.1%; Score 1850; DB 2; Length 510;
Best Local Similarity 76.2%; Pred. No. 4.5e-137;
Matches 339; Conservative 46; Mismatches 56; Indels 4; Gaps 3;

Qy 1 GLTKQKALPENKVGIVLDAGSSHTSLYIKWPAEKENDTGTVQVQVCEKRVKGGISKFV 60
Db 36 GLTKQKALPENKVGIVLDAGSSHTSLYIKWPAEKENDTGTVQVQVCEKRVKGGISK 95
Qy 61 QKNEIGYLTDCHERAREVTPROHSTPVYLGATAGMRLRMESEBELADVLDDVRS 120
Db 96 QKTEIGAYLAECHELSTELPTSKHQTPVYLGATAGMRLRMESEBELADVLAAVTS 155
Qy 121 LSNYPFDFQGAARIITGOEAGYGHITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 180
Db 156 LKGYPFDFQGAARIITGOEAGYGHITINYLGRFTQGSWLSLS-DSQKQETFGALDLG 214
Qy 181 GASTQVTFVPPQNTIESPDNALQRLYKGVNVTSHFLCYGKQDALWQKLAKIOVASN 240
Db 215 GASTQITFVPPQNTIESPDNALQRLYKGVNVTSHFLCYGKQDALWQKLAKIOVSSG 274
Qy 241 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQGNVQCHOSILELFNT 300
Db 275 GVLKDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQGNVQCHOSILELFNT 334
Qy 301 SYCPYSQACAFNGIFLPPQDGFAGSAPFYFVWDFPKKAKNSVISQEKWTITKNFCSK 358
Db 335 SHCPYSQACAFNGIFLPPQDGFAGSAPFYFVWDFPKKAKNSVISQEKWTITKNFCSK 394
Qy 359 WEETKTSYAGVKEKYLESCYSGYIISLLQGHFTADSWEHIHFTGKIQGSAGWTLG 418
Db 395 WEETKTSYAGVKEKYLESCYSGYIISLLQGHFTADSWEHIHFTGKIQGSAGWTLG 453
Qy 419 YMLNLTNMIPAEQPLSTPLSHSTYV 443
Db 454 YMLNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 5
Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356E83 CRC64;

Query Match 77.2%; Score 1829; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 MESEBELADVLDDVRSLSNYPFDFQGAARIITGOEAGYGHITINYLKGFSQKTRWFSI 163
Db 1 MESEBELADVLDDVRSLSNYPFDFQGAARIITGOEAGYGHITINYLKGFSQKTRWFSI 60
Qy 164 VPYETNNQETFGALDLGASTQVTFVPPQNTIESPDNALQRLYKGVNVTSHFLCYGK 223
Db 61 VPYETNNQETFGALDLGASTQVTFVPPQNTIESPDNALQRLYKGVNVTSHFLCYGK 120
Qy 224 DQALWQKLAKIOVASNEILRDCPHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQG 283
Db 121 DQALWQKLAKIOVASNEILRDCPHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQG 180
Qy 284 IGVNQQCHQSILELFNTSYCPYSQACAFNGIFLPPQDGFAGSAPFYFVWDFPKKAKNSVISQEKWTITKNFCSK 343
Db 181 IGVNQQCHQSILELFNTSYCPYSQACAFNGIFLPPQDGFAGSAPFYFVWDFPKKAKNSVISQEKWTITKNFCSK 240
Qy 344 QEKVTENMKKFCAPWEEIKTSYAGVKEKYLESCYSGYIISLLQGHFTADSWEHIH 403
Db 241 QEKVTENMKKFCAPWEEIKTSYAGVKEKYLESCYSGYIISLLQGHFTADSWEHIH 300
Qy 404 FIGKIQGSAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYV 443
Db 301 FIGKIQGSAGWTGLGYMLNLTNMIPAEQPLSTPLSHSTYV 340

RESULT 6
ENP1_RAT STANDARD; PRT; 511 AA.
ID ENP1_RAT
AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase)
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Ectpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=9221928;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]

RP	SEQUENCE FROM N.A.
RC	STRAIN=Wistar; TISSUE=Cochlea;
RC	MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
RA	Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
RA	"Evidence for alternative splicing of ecto-ATPase associated with
RT	Termination of purinergic transmission";
RL	Brain Res. Mol. Brain Res. 73:85-92(1999).
RN	[3]
RP	SEQUENCE OF 432-511 FROM N.A.
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;
RC	MEDLINE=38031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
RA	Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
RA	"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
RT	rat brain.";
RL	Neuropharmacology 36:1189-1200(1997).
CC	-1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC	nucleotides to regulate purinergic neurotransmission. Could also
CC	be implicated in the prevention of platelet aggregation.
CC	Hydrolyzes ATP and ADP equally well.
CC	-1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC	-1- COFACTOR: Requires calcium and magnesium.
CC	-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC	-1- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
CC	kidney, liver, muscle, thymus, lung and spleen.
CC	-1- PTM: N-glycosylated.
CC	-1- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC	-----
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CC	-----
DR	EMBL; U81295; AAC53195.1; --
DR	EMBL; Y15685; CAA75730.1; --
DR	RGD; 694265; Entpdl.
DR	InterPro; IPR000407; GDAL_CD39_NTPase.
DR	Pfam; PF01150; GDAL_CD39_1.
DR	PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW	Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
FT	DOMAIN 1 16 Cytoplasmic (Potential).
FT	TRANSMEM 17 37 Potential.
FT	DOMAIN 38 478 Extracellular (Potential).
FT	TRANSMEM 479 499 Potential.
FT	DOMAIN 500 511 Cytoplasmic (Potential).
FT	CARBOHYD 73 73 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 226 226 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 291 291 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 333 333 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 374 374 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 429 429 N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD 458 458 N-linked (GLCNAC. .) (Potential).
FT	CONFLICT 332 332 F -> L (in Ref. 2).
SEQ	SEQUENCE 511 AA; 57408 MW; 4CC123D3B644C193 CRC64;
Query Match	
Best Local Similarity 74.4%; Score 1814.5; DB 1; Length 511;	
Matches 331; Conservative 52; Mismatches 59; Indels 3; Gaps 3;	
QY	1 GLTONKALPENVKYGIIVLDAGSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVF 60
Db	
36	GLTHNKLPLPENVKYGIIVLDAGSHTTLYIKWPAEKENDTGVVQLLEECQVRKPGISKYA 95
QY	61 QKWEITGIVLTDGWERAREVIPRSORQETPVYLGATAGMRLLRMESEELADRLVDVVERS 120
Db	
96	QKTDEIAAYLAECMKMSTERIPASKQHQPVIYLGATAGMRLLRMESEKQSADEVLAIVRS 155
QY	121 LSNYPDFOGARIITQGEAGYGIWITNYLLGKFSQKTRFISFVYETYNQETFFGALDIG 180
Db	
156	LKSYPPDFGAKIITQGEAGYGIWITNYLLGRTQESWLNPFIS-DSQKATFFGALDIG 214

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CC EMBL; AJ133746; CAB95871.1; -
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Mgnesium; Transmembrane.
FT CHAIN 1 510
FT Ectonucleoside triphosphate
FT diposphohydrolase 1.
FT CHAIN 1 201
FT Ectonucleoside triphosphate
FT diposphohydrolase 1 27 kDa subunit.
FT CHAIN 202 510
FT Ectonucleoside triphosphate
FT diposphohydrolase 1 54 kDa subunit.
FT DOMAIN 1 16
FT Potential.
FT TRANSMEM 17 37
FT Extracellular (Potential).
FT DOMAIN 38 477
FT Potential.
FT TRANSMEM 478 498
FT Cytoplasmic (Potential).
FT DOMAIN 499 510
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 73 73
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 245 245
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 274 274
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 291 291
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 333 333
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 370 370
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 457 457
FT N-linked (GlcNAc. .) (Potential).
FT CONFLICT 203 203
FT G -> S (in Ref. 2).
SQ SEQUENCE 510 AA; 57757 MW; 82F8686940D7735 CRC64;

Query Match 73.3%; Score 1736; DB 1; Length 510;
Best Local Similarity 70.9%; Pred. No. 4.3e-128;
Matches 315; Conservative 63; Mismatches 64; Indels 2; Gaps 2;

Qy 1 GLTQNKALPENVKYGVILVDAGSSHTSLYIYKWPAAKENDTGWHQVHRCVKPGISKFV 60
Db 36 GLTQNKALPENVKYGVILVDAGSSHTSLYIYKWPAAKENDTGWHQVHRCVKPGISFV 95
Qy 61 OKVNEIGYLTDCMERAREVTPRSQHQETPVVLGATAGMRLLRSEBELADRVLDVVERS 120
Db 96 KKLGEIDIYLEACMERATVPKSOHAETPVVLGATAGMRLLRSEBELADRVLDVVERS 155
Qy 121 LSNYPFDFQAGRIITQEGEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG 180
Db 156 ITRYPDFQAGRIITQEGEGAYGWTITNYLLDKFIQKSGWFLKPRKGDGTOSTYGALDLG 215
Qy 181 GASTQVTPVQNTIESPDNALQPLRYKGVNVTYTHSLCYGKQALWQKLAKDIQVANS 240
Db 216 GASTQITVPVQNVLESPELTHFLRYGKNSVYTHSLCYGKQALWQKLAKDIQVANS 274
Qy 241 EILRDPCHFGKVKVNVSDLYKTPCTKRFEWTLPPQOFGIGNYQOCHQSILLEPNT 300
Db 275 GTIHEPCFHSQVQRKMNVSUHYEAPCTRRFLTSLFPPELEIQGTGDFKQOQSIRPLENT 334
Qy 301 SYCPSQCAFNGIFLPLQGFAGFSAFYFMKFLNLTSEKVS-QEKYTEMMKFKCAQPW 359
Db 335 SYCPSRCSFGVFLPLQGFAGFSAFYFMKFLNLTSEKVSFQSKVTSTLEAFCSRPW 394
Qy 360 BEIKTSYAGVKEKYLSEYCFSGTSTYLSLLQGYHTADSWBHIPIGKIQQSDAGWTLYG 419
Db 395 AELQMYGDMVKEKYLSEYCFSGTSTYLSLLQGYHTADSWBHIPIGKIQQSDAGWTLYG 454
Qy 420 MLNLTNMTIPAEQPLSTPLSHSTYV 443
Db 455 MLNLTNMTIPSEPSSTRLSHSTYV 478

RESULT 8

ENP1_BOVIN

ID ENP1_BOVIN STANDARD; PRT; 513 AA.

AC O18956;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diposphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase) (Ecto-ATP diposphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPD1; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.F.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diposphohydrolase";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -----
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DR EMBL; AF005940; AAB62382.1; -
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Mgnesium; Transmembrane.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT Cytoplasmic (Potential).
FT DOMAIN 38 481
FT Extracellular (Potential).
FT TRANSMEM 482 502
FT DOMAIN 503 513
FT Potential.
FT CARBOHYD 73 73
FT Cytoplasmic (Potential).
FT CARBOHYD 227 227
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 245 245
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 307 307
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 336 336
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 373 373
FT N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 460 460
FT N-linked (GlcNAc. .) (Potential).
FT CONFLICT 97 97
FT INV -> N (in Ref. 2).
FT CONFLICT 101 103
FT K -> V (in Ref. 2).
FT CONFLICT 464 464
FT K -> V (in Ref. 2).
SQ SEQUENCE 513 AA; 58113 MW; 20F898F27B6D2F96 CRC64;

Query Match 72.2%; Score 1711.5; DB 1; Length 513;
Best Local Similarity 70.0%; Pred. No. 3.7e-126;
Matches 313; Conservative 64; Mismatches 65; Indels 5; Gaps 3;

Qy 1 GLTQNKALPENVKYGVILVDAGSSHTSLYIYKWPAAKENDTGWHQVHRCVKPGISKFV 60

Db 36 GLTQNKALPENVKYGVILVDAGSSHTSLYIYKWPAAKENDTGWHQVHRCVKPGISGFA 95

RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Liver;
RC Bigonnesse F., Levesque S.A., Kukulski F., Lecka J., Robson S.C.,
RD Fernandes M.J.G., Sevigny J.,
RE Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY364442; AAQ84519.1; F:aprase activity; IEA.
DR GO; GO:0004050; F:aprase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase.
SQ SEQUENCE 497 AA; 54550 MW; 00DE822BEEB1BDF CRC64;

Query Match 44.2%; Score 1046.5; DB 2; Length 497;
Best Local Similarity 47.2%; Pred. No. 8.5e-74;
Matches 213; Conservative 75; Mismatches 133; Indels 31; Gaps 11;

Qy 1 GLTQ-----NKALPENVKYGLVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRV 51
Db 21 GLTMLVLILVKAINVLLPADTKFGIVFDAGSSHTSLFYQWPAEKEDTGTVSQALTQCI 80

Qy 52 KPGIGSKFQVKWNEIGVLTDCMERAREVIPSQHOETPVVLGATAGMRLLRMESEELAD 111
Db 81 EGPGLSSVTSPTQAGESLKSCEALALIPQAQHPETPTFLGSTAGMRLLSQKNSSQAR 140

Qy 112 RVLVDVVERSLSNYPDFQARIITQGEAGYCWITINLLG---KFSQKTRWFSIVPYET 168
Db 141 DILAASVSTLSKSPVDFNGAKILAGQDSGAFGWITINVLGMLLKYS-SGQW--ILPPE- 196

Qy 169 NNQETFGALDGGASTQTVTFPQNTIESPDNALQFRLYGKDYNVYTHSFLCYKQDQALW 228
Db 197 --GMLVGALDGGASTQISFVPGQILDQ-STQVTFRLYGANYSVYTHSLYLCFGDRDQILN 253

Qy 229 QKIAK-----DIOVASNEILRDCPFHPGYKVVNVSPLYTCTCKREMTLPQQFPIQ 282
Db 254 RLLAKLAQRLSSQVAP---VRHPTCHSGYQAILPLSLSDSPCLHTTDSLNHTQNLTV 310

Qy 283 GIGNYQCHQSHLELNTSYCP-YSQAFNGIFLPLQDGFCAFSAFYVFMKFLNLITSEK 341
Db 311 GTDPPGNCVVALRSLEFNFSCKGQKDCAFNGIYQPPVHGQFVAFSNFYTHFLNLSRQ 370

Qy 342 VSQKVTWKKKFCQAPWEEIKTSVAGVKEKYLSEYCFSGYVILSLLLQGHVFTADSWEH 401
Db 371 -SLNTVNDVTKVFCQKPKLVEVSPG-QERWLRDYCASGLYILVLLLEGYKFSSEETWPN 428

Qy 402 IHFTICKIOGSDAGWTLGYMLNLTMMIPAEQ 432
Db 429 IQQKQAGDTDGTGTLGFMNLMTGMIPAEAP 459

RESULT 14
ENPL_CHICK STANDARD; PRT; 493 AA.
ID _ENPL_CHICK STANDARD; PRT; 493 AA.
AC O93295; .
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (Ecto-aprase) (CD39 antigen).
GN Name=ENTPD1; Synonyms=CD39;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE=Oviduct;
RE MEDLINE=98298108; PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RT "Molecular cloning of the chicken oviduct ecto-ATP-

diphosphohydrolase."; J. Biol. Chem. 273:16043-16049 (1998).
[2]
RP SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RX MEDLINE=97442428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
RA Lewis-Carl S., Kirley T.L.;
RT "Immunolocalization of the ecto-ATPase and ecto-aprase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-aprase."; J. Biol. Chem. 272:23645-23652 (1997).
CC 1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC 1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC 1- COFACTOR: Requires calcium and magnesium (By similarity).
CC 1- SUBUNIT: Homodimer, disulfide-linked (Probable). (Potential).
CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC 1- PTM: N-glycosylated.
CC 1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

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DR EMBL; AF041355; AAC26491.1; -.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 7 Cytoplasmic (Potential).
FT TRANSMEM 8 28 Potential.
FT DOMAIN 29 463 Extracellular (Potential).
FT TRANSMEM 464 486 Potential.
FT DOMAIN 487 493 Cytoplasmic (Potential).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
FT CONFLICT 16 16 C -> W (in Ref. 2).
FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
SQ SEQUENCE 493 AA; 54034 MW; F14FF43AA2F3603 CRC64;

Query Match 42.4%; Score 1004; DB 1; Length 493;
Best Local Similarity 45.7%; Pred. No. 1.9e-70;
Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

Qy 8 LPENVKYGLVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRVKPGFISKVKVNEIG 67
Db 35 LPQTKYGLVFDAGSTHTALYVYQWPAKNGTGVISQVESCCTVNGSGISSYVADDPACAG 94

Qy 68 IYLTDCMERAREVIPSQHOETPVVLGATAGMRLLRMESEELADRVLDVVERSLNYPFD 127
Db 95 ASLKPCLDKAMAVIPVEQOMQTPTLYGATAGMRLLRMESEELADRVLDVVERSLNYPFD 154

Qy 128 FQGAIRITGOEGAYGWITINLLG---KFSQKTRWFSIVPYETNNOTFCALDGGAST 184
Db 155 FRGAQITGNEEGSGFWITINLLTLLKFSFAGW-----EHPQNTVLGALDGGAST 209

```
QY 185 QVTFVFPQNTIESPDNALQFRLYGKDYNNVYTHSFCLYCKDOA---LWOKLAKDIQVAGNE 241
Db 210 QITFQP-GVTIEDKNTSVLFRLYGNTSYLSYLYCYGQIQASKELMAALHQDGSYVQN- 267
QY 242 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOPEIQGIGNYQOCHOSILELFNTS 301
Db 268 -ISHPCYKGYRRIITIAEIVDSPCVTPPSMLSPAQLTGTGNPAACPTAILKLFNLT 326
QY 302 YCPYSQCAFNGIFLPPLOQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 361
Db 327 CGANRTCGFDGVYQPPVRGQFFAFAGFYTFSLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
QY 362 IKTSVAGVKEKYLSEYCFSGTYILSLILQGYHFTADSWEHIHFICKIQGSDAGWTLGYML 421
Db 386 LVETFPQKE-HLHTYCVUGLYILTLVDGYKDFDEHTWSNIHFSQKAGNADIGWTLGFML 444
QY 422 NLTNMIPAE 430
Db 445 NLTNMIPTE 453

RESULT 15
Q90X66 PRELIMINARY; PRT; 493 AA.
AC Q90X66;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=21982040; PubMed=11985621;
RA Knowles A.F.; Nagy A.K.; Strobel R.S.; Wu-Weis M.;
RT "Purification, characterization, cloning, and expression of the
RT chicken liver ecto-ATP-diphosphohydrolase.";
RL Eur. J. Biochem. 269:2373-2382(2002).
DR EMBL; AF426405; AAL25086.1; -.
DR GO; GO:0004050; P:ATPase activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;
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Query Match 42.1%; Score 997; DB 2; Length 493;
Best Local Similarity 45.7%; Pred. No. 6.6e-70;
Matches 196; Conservative 72; Mismatches 145; Indels 16; Gaps 7;

QY 8 LPENVKYGIVLDAGSHTSLIYKWPAAKENDTVVHVEECRVKPGISKRFVQKNEIG 67
Db 35 LPPGTGYGLVFDAGTHTALIVYQWPAKNGTGVSVQVSTVNGSGISSYADDPAGAG 94
QY 68 IYLTDCMERAREVIPSQHQETPVYLGATAGNRLRMESEBLADRLVDVRSLSNYPFD 127
Db 95 ASLKPCLDKAMAVIPEVQWQWTPYLGATAGNRLRMESEBLADRLVDVRSLSNYPFD 154
QY 128 FQGARIIITQOEGAGWTINVLG---KFSQKTFWFSIVYETNNQTFGALDGGAST 184
Db 155 FRGAQILTNGEGSGFQITVNVYLLTLTKFSPAGKW-----EHPQNTFVLGALDGGAST 209
QY 185 QVTFVFPQNTIESPDNALQFRLYGKDYNNVYTHSFCLYCKDOA---LWOKLAKDIQVAGNE 241
Db 210 QITFQP-GVTIEDKNTSVLFRLYGNTSYLSYLYCYGQIQASKELMAALHQDGSYVQN- 267
QY 242 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOPEIQGIGNYQOCHOSILELFNTS 301
Db 268 -ISHPCYKGYQENITIAEIVDSPCVTPPSMLSPAQLTGTGNPAACRTAILKLFNFT 326
```

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QY 302 YCPYSQCAFNGIFLPPLOQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 361
Db 327 CGANRTCGFDGVYQPPVRGQFFAFAGFYTFSLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
QY 362 IKTSVAGVKEKYLSEYCFSGTYILSLILQGYHFTADSWEHIHFICKIQGSDAGWTLGYML 421
Db 386 LVETFPQKE-HLHTYCVUGLYILTLVDGYKDFDEHTWSNIHFSQKAGNADIGWTLGFML 444
QY 422 NLTNMIPAE 430
Db 445 NLTNMIPTE 453
```

Search completed: March 7, 2005, 13:22:40
Job time : 65.0612 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 72.3686 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147A-2_COPY_36_478

Perfect score: 2369

Sequence: 1 GLTQNKALPENVKYGVILDA.....TNMIPAEQLSTPLSHSTYV 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2369	100.0	510	2	AAW04334 Human lym
2	2369	100.0	510	2	AAW04264 Human CD3
3	2369	100.0	510	3	AAW0910 Human sol
4	2369	100.0	510	3	AAW0887 Human sol
5	2369	100.0	510	4	AAW71917 Human CD3
6	2369	100.0	510	7	ADJ57262 Human CD3
7	2369	100.0	510	8	ADL24295 Human CD3
8	2369	100.0	510	8	ADQ99453 Human CD3
9	2369	100.0	510	8	ADQ69210 Human CD3
10	2369	100.0	510	8	ADR69042 Human CD3
11	2369	100.0	510	8	ADL17924 Human CD3
12	2369	100.0	510	8	ABO84674 Human can
13	2369	100.0	510	8	ADR87821 Human CD3
14	2369	100.0	511	8	ADK60421 Angiogene
15	2369	100.0	511	8	ADK60722 Angiogene
16	2369	100.0	511	8	ADP73345 CD39 lymph
17	2369	100.0	517	7	ADN95839 Human BEC
18	2369	100.0	517	8	ADK60221 Angiogene
19	2369	100.0	517	8	ADK60522 Angiogene
20	2369	100.0	517	8	ADP73145 Angiogene
21	2369	100.0	522	8	ABO84672 Human can
22	2348	99.1	439	4	AAW71918 Soluble h
23	2348	99.1	454	3	AAW70913 Human sol
24	2348	99.1	454	3	AAW70890 Protein e
25	2348	99.1	463	3	AAW70925 Human sol

26	2348	99.1	463	3	AAW70902	Aay70902 Protein e
27	2348	99.1	464	3	AAW70922	Aay70922 Human sol
28	2348	99.1	464	3	AAW70899	Aay70899 Protein e
29	2348	99.1	473	3	AAW70924	Aay70924 Human sol
30	2348	99.1	473	3	AAW70901	Aay70901 Protein e
31	2348	99.1	474	3	AAW70923	Aay70923 Human sol
32	2348	99.1	474	3	AAW70900	Aay70900 Protein e
33	2348	99.1	476	3	AAW70911	Aay70911 Human CD3
34	2348	99.1	476	3	AAW70888	Aay70888 Protein e
35	2348	99.1	478	3	AAW70914	Aay70914 Human sol
36	2348	99.1	478	3	AAW70891	Aay70891 Protein e
37	2348	99.1	487	3	AAW70921	Aay70921 Human sol
38	2348	99.1	487	3	AAW70898	Aay70898 Protein e
39	2305	97.3	529	8	ABM83376	Abm83376 Human dia
40	2297	97.0	476	3	AAW70912	Aay70912 Human CD3
41	2297	97.0	476	3	AAW70889	Aay70889 Protein e
42	2147	90.6	503	8	ABM83377	Abm83377 Human dia
43	1980	83.6	402	8	ABO84671	ABO84671 Human can
44	1852	78.2	377	7	ADI62735	ADI62735 Human apo
45	1129	47.7	311	8	ABO84673	ABO84673 Human can

ALIGNMENTS

RESULT 1
AAW04334
ID AAW04334 standard; protein; 510 AA.
XX AC AAW04334;
XX XX 29-DEC-1996 (first entry)
XX XX Human lymphoid cell activation antigen CD39.
DE ATP diphosphohydrolase; ATPase; bovine aorta; pig pancreas; apyrase;
XX CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;
KW thrombogenicity; anti-haemostatic.
KW Homo sapiens.
OS WO9632471-A2.
FN 17-OCT-1996.
PD 10-APR-1996; 96WO-CA000223.
PF 10-APR-1995; 95US-00419204.
XX PR (UYSH) UNIV SHERBROOKE.
XX PI Beaudoin AR, Sevigny J;
XX WPI; 1996-477122/47.
XX N-PSDB; AAT38516.
PT Isolated ATP di-phospho-hydrolase enzymes - have anti-haemostatic
PT activity, useful for reducing platelet aggregation and thrombogenicity.
XX Claim 17; Page 42-44; 60pp; English.

The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine pancreatic (AAW04339) ATPases have been partially sequenced. The sequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Maliszewski et al. (1994) . J. Immunol. : 3574-3583). The complete sequences of the ATPases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPases using the CD39 sequence (AAT38516)

Sequence 510 AA;
SQ

Query Match 100.0%; Score 2369; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGVVHQVEECRVKGGISKFV 60
DB 36 GLTONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGVVHQVEECRVKGGISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDRLVDVVERS 120
DB 96 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDRLVDVVERS 155
QY 121 LSNYPDFQGARITITGOEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPDFQGARITITGOEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVPOQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDAQALWQKLAKDIQVASN 240
DB 216 GASTQVTFVPOQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDAQALWQKLAKDIQVASN 275
QY 241 EILRDCPFHGPYKVVNSDLYKTPCTKRFEMTLPFQOFEIQQIGNYQOCHOSILELFNT 300
DB 276 EILRDCPFHGPYKVVNSDLYKTPCTKRFEMTLPFQOFEIQQIGNYQOCHOSILELFNT 335
QY 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWE 360
DB 336 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYM 420
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYM 455
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 2
AAW04264
ID AAW04264 standard; protein; 510 AA.
XX AC AAW04264;
XX DT 29-MAY-1997 (first entry)
XX DE Human CD39 protein.
XX Human; lymphocyte activation marker; gene therapy;
KW ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;
KW transplantation; endothelial cell; prosthetic device;
KW platelet aggregation; inhibition; intravascular.
XX Homo sapiens.
XX WO9630532-A1.
XX PD 03-OCT-1996.
XX PF 22-MAR-1996; 96WO-EP001270.
XX PR 24-MAR-1995; 95US-00410371.
XX PR 12-FEB-1996; 96US-00600383.
XX PA (SANO) SANDOZ LTD.
XX PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX Bach FH, Robson S;
XX WPI; 1996-455377/45.
XX DR N-P8DB; AAT33966.
XX Gene therapy of inflammatory or immunological stimulation of platelet
PT aggregation - using CD39 protein with ATP di:phospho:hydrolase activity,
PT

PT useful for preventing or alleviating thrombotic condition in mammalian
PT subject.
XX Claim 3; Page 39; 65pp; English.
XX Non-human transgenic or somatic recombinant mammals, whose cells contain
CC a heterologous DNA encoding a polypeptide (especially human CD39 protein)
CC having ATP-diphosphohydrolase activity under cellular activating
CC conditions is claimed. In particular the animal is a pig and its cells
CC (or tissues or organs) can be used for transplantation. DNA coding for
CC human CD39 is also useful for genetically modifying a mammalian cell to
CC render it less susceptible to an inflammatory or immunological stimulus
CC and platelet aggregation. The modified cells can be used to prevent or
CC alleviate a thrombotic condition. The present sequence is that of the
CC human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-
CC 3584
XX SQ Sequence 510 AA;
Query Match 100.0%; Score 2369; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGVVHQVEECRVKGGISKFV 60
DB 36 GLTONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGVVHQVEECRVKGGISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDRLVDVVERS 120
DB 96 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDRLVDVVERS 155
QY 121 LSNYPDFQGARITITGOEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPDFQGARITITGOEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVPOQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDAQALWQKLAKDIQVASN 240
DB 216 GASTQVTFVPOQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDAQALWQKLAKDIQVASN 275
QY 241 EILRDCPFHGPYKVVNSDLYKTPCTKRFEMTLPFQOFEIQQIGNYQOCHOSILELFNT 300
DB 276 EILRDCPFHGPYKVVNSDLYKTPCTKRFEMTLPFQOFEIQQIGNYQOCHOSILELFNT 335
QY 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWE 360
DB 336 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYM 420
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYM 455
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 3
AAW70910
ID AAW70910 standard; protein; 510 AA.
XX AC AAW70910;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 protein.
XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;

KW cardiant; vástotropic; thrombolytic.
XX Homo sapiens.
PH Key
XX Domain
FT Location/Qualifiers
FT 17..37
FT /label= Transmembrane domain
FT /note= "N-terminal end"
FT Modified-site
FT 73..75
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT 227..229
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT 292..294
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT 334..336
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT 371..373
FT /note= "Asn is N-glycosylated"
FT Modified-site
FT 457..459
FT /note= "Asn is N-glycosylated"
FT Domain
FT 477..499
FT /label= Transmembrane domain
FT /note= "C-terminal end"
XX WO200023459-A1.
XX 27-APR-2000.
XX 13-OCT-1999; 99WO-US022955.
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX (IMMV) IMMUNEX CORP.
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX N-PSDB; NAD00205.
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX Claim 1a; Fig 1; 122pp; English.
XX The present sequence is the human soluble CD39 protein, a cell surface
XX molecule, having apyrase activity. It is derived from a human B cell line
XX cDNA library, referred to as MP-1. Soluble CD39 is constructed by
XX removing the N- and C-terminal transmembrane domains. It retains the
XX capacity to metabolise ATP and ADP at relevant concentrations and the
XX ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
XX embolism, platelet-associated ischaemic disorders including lung,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis, intracardiac and venous
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX Sequence 510 AA;
XX Query Match 100.0%; Score 2369; DB 3; Length 510;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-233;
XX Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 GLTNKALPENVKYIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVF 60
|||||

Db 36 GLTNKALPENVKYIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVF 95
Qy 61 QKVNEIGIYLTDCMERAREVIPRSQHQTTPVYLGCATAGMRLLRMESEELADRVLDVVERS 120
Db 96 QKVNEIGIYLTDCMERAREVIPRSQHQTTPVYLGCATAGMRLLRMESEELADRVLDVVERS 155
Qy 121 LSNYPDFQOGARIITGOEBGAYGHITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG 180
Db 156 LSNYPDFQOGARIITGOEBGAYGHITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG 215
Qy 181 GASTQVTFVQONQTIESPNDALQPLRYGKDVVYTHSFCLCYGKQDQALWOKLAKDIQVASN 240
Db 216 GASTQVTFVQONQTIESPNDALQPLRYGKDVVYTHSFCLCYGKQDQALWOKLAKDIQVASN 275
Qy 241 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFOQFEIQGIGNYQQCHOSILELFT 300
Db 276 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFOQFEIQGIGNYQQCHOSILELFT 335
Qy 301 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFLNLTSEKVSQEKVTEMKKFCAQPWE 360
Db 336 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFLNLTSEKVSQEKVTEMKKFCAQPWE 395
Qy 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTLCYM 420
Db 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTLCYM 455
Qy 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db 456 LNLTNMIPAEQPLSTPLSHSTYV 478
RESULT 4
AAV70887
ID AAV70887 standard; protein; 510 AA.
XX AC AAV70887;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 protein.
XX KW Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
XX coronary ischaemia; vascular occlusion.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Domain 17..37
XX /label= Transmembrane domain
FT Modified-site 73..75
FT /note= "Asn is N-glycosylated"
FT Modified-site 227..229
FT /note= "Asn is N-glycosylated"
FT Modified-site 292..294
FT /note= "Asn is N-glycosylated"
FT Modified-site 334..336
FT /note= "Asn is N-glycosylated"
FT Modified-site 371..373
FT /note= "Asn is N-glycosylated"
FT Modified-site 457..459
FT /note= "Asn is N-glycosylated"
FT Domain 477..499
FT /label= Transmembrane domain
XX FX

PN WO200023094-A2.
 XX 27-APR-2000.
 XX 13-OCT-1999; 99WO-US023641.
 XX 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX (IMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 DR N-PSDB; AAD00200.
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.
 XX Claim 2; Fig 1; 118pp; English.
 PS The present sequence is soluble CD39 having apyrase activity. Soluble
 CC CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at
 CC physiologically relevant concentrations as well as the ability to block
 CC and reverse ADP-induced platelet activation and recruitment including
 CC platelet aggregation. This is used in the treatment of unstable angina,
 CC myocardial infarction, stroke, coronary artery disease or injury,
 CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,
 CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
 CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
 CC peripheral artery thrombosis, venous thrombosis, thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke
 XX Sequence 510 AA;
 SQ
 Query Match 100.0%; Score 2369; DB 3; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.5e-233;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 60
 DB 36 GLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 95
 QY 61 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 120
 DB 96 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 155
 QY 121 LSNYPDFQGARITGOEGAGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 180
 DB 156 LSNYPDFQGARITGOEGAGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 215
 QY 181 GASTQVTFVPPNQNTIESPDNALQPLRYGKDYNYVTHSFLCYGKQDALWQKLAKDIQVASN 240
 DB 216 GASTQVTFVPPNQNTIESPDNALQPLRYGKDYNYVTHSFLCYGKQDALWQKLAKDIQVASN 275
 QY 241 EILRDPCHPGYKVVNVDLYKTPCTKRFEMTLPPQOFQIGTGNVQCHQSILELFT 300
 DB 276 EILRDPCHPGYKVVNVDLYKTPCTKRFEMTLPPQOFQIGTGNVQCHQSILELFT 335
 QY 301 SYCPSQCAFNGIFLPPLOQDFGAFSAFYVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE 360
 DB 336 SYCPSQCAFNGIFLPPLOQDFGAFSAFYVWKFNLNTSEKVSQEKVTEMMKKFCAQPWE 395
 QY 361 EIKTSYAGVKKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTLGYM 420
 DB 396 EIKTSYAGVKKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTLGYM 455
 QY 421 LNLNMIAPAEQPLSTPLSHSTYV 443
 DB 456 LNLNMIAPAEQPLSTPLSHSTYV 478
 RESULT 5
 AAB71917
 ID AAB71917 standard; protein; 510 AA.
 XX AC AAB71917;
 XX DT 09-MAY-2001 (first entry)
 XX DE Human CD39.
 XX Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
 KW stroke; thrombotic disorder; ischaemic disorder.
 XX Homo sapiens.
 OS WO200111949-A1.
 FN 22-FEB-2001.
 PD 11-AUG-2000; 2000WO-US022060.
 PF 13-AUG-1999; 99US-00374586.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA Pinsky DJ;
 PI WPI; 2001-202805/20.
 DR Treating stroke in a subject susceptible to intracranial hemorrhaging and
 XX an ischemic disorder, involves administering a CD39 polypeptide which
 XX inhibits ADP-mediated platelet aggregation or leukocyte accumulation.
 PS Claim 1; Page 14; 118pp; English.
 XX The present sequence is the human CD39 polypeptide. The present sequence
 CC or its active fragment may be administered to treat or prevent stroke in
 CC a subject susceptible to intracranial haemorrhaging or an ischaemic
 CC disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
 CC or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
 CC subject. It is useful for treating or preventing stroke, thrombotic
 CC disorders and ischaemic disorders such as peripheral vascular disorder,
 CC pulmonary embolus, venous thrombosis, myocardial infarction, transient
 CC ischaemic attack, unstable angina, reversible ischaemic neurological
 CC deficit and sickle cell anaemia. It is also useful for treating or
 CC preventing a stroke disorder in a subject undergoing heart surgery, lung
 CC surgery, spinal surgery, brain surgery, vascular surgery, abdominal
 CC surgery, or organ transplantation surgery
 XX Sequence 510 AA;
 SQ
 Query Match 100.0%; Score 2369; DB 4; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.5e-233;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 60
 DB 36 GLTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 95
 QY 61 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 120
 DB 96 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 155
 QY 121 LSNYPDFQGARITGOEGAGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 180
 DB 156 LSNYPDFQGARITGOEGAGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 215

QY 181 GASTQVTFVFNQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 240
 DB 216 GASTQVTFVFNQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 275
 QY 241 EILRDPCHFGYKVVNVDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELNT 300
 DB 276 EILRDPCHFGYKVVNVDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELNT 335
 QY 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 360
 DB 336 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
 QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSAGWTGLYM 420
 DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSAGWTGLYM 455
 QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
 DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 6

ADJ57262
 ID ADJ57262 standard; protein; 510 AA.

XX AC ADJ57262;

XX DT 06-MAY-2004 (first entry)

XX DE Human CD39 polypeptide.

XX CD39; nucleoside diphosphate; thrombolytic; anticoagulant;
 KW cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;
 KW cardiant; angiogenic; antiarteriosclerotic; gynaecological;
 KW cerebroprotective; cancer; human; apyrase; enzyme.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 55..61

FT Domain /note = ACR1

FT Domain 125..135

FT Domain /note = ACR2

FT Domain 171..183

FT Domain /note = ACR3

FT Domain 213..220

FT Domain /note = ACR4

FT Domain 447..454

FT Domain /note = ACR5

PN WO2003070823-A2.

XX 28-AUG-2003.

XX 19-FEB-2003; 2003WO-US004845.

XX 20-FEB-2002; 2002US-0358303P.

XX (GEHO) GEN HOSPITAL CORP.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Elmaleh DR, Robson SC, Papisov MI;

XX WPI; 2003-778966/73.

XX N-PSDB; ADJ57261.

XX New enzyme polymer conjugate used for treating abnormal levels of
 FT extracellular nucleotides or platelet aggregation, graft transplant,
 FT cardiovascular disease, cancer and sepsis.

XX Claim 20; SEQ ID NO 2; 82pp; English.

XX

CC The invention relates to a conjugate (I) comprising an enzyme and a
 CC biodegradable polymer, where (i) enzymatic activity of the enzyme is
 CC higher relative to that of the enzyme in the absence of the biodegradable
 CC polymer, or (ii) the half life of the enzyme is longer than that of the
 CC enzyme in the absence of the polymer. The enzymatic activity (i) is at
 CC least 10 (preferably at least 100) times higher in the presence of the
 CC polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,
 CC preferably an apyrase, especially a soluble form of CD39 and catalyzes
 CC hydrolysis of nucleoside diphosphate. The conjugate can be used to treat
 CC diseases relating to abnormal levels of extracellular nucleotides or
 CC abnormal aggregation of platelets, particularly cardiovascular disease,
 CC cancer, sepsis or a disease related to graft transplant. (I) is also used
 CC for treating coronary artery disease or injury following myocardial
 CC infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,
 CC platelet associated ischaemic disorders including lung, coronary and
 CC cerebral ischaemia, reocclusion following thrombosis, thrombotic
 CC disorders, and thrombosis and coagulopathies associated with exposure to
 CC a foreign or injured tissue surface, in combination with angioplasty,
 CC carotid endarterectomy, anastomosis of vascular grafts and chronic
 CC cardiovascular devices. The present sequence represents a human CD39
 CC polypeptide.

XX SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 7; Length 510;

Best Local Similarity 100.0%; Pred. No. 2.5e-233;

Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGGISKFPV 60

DB 36 GLTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGGISKFPV 95

QY 61 QKNEIGIYITDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVWVERS 120

DB 96 QKNEIGIYITDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVWVERS 155

QY 121 LSNYPDFQGARITGQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLG 180

DB 156 LSNYPDFQGARITGQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLG 215

QY 181 GASTQVTFVFNQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 240

DB 216 GASTQVTFVFNQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 275

QY 241 EILRDPCHFGYKVVNVDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELNT 300

DB 276 EILRDPCHFGYKVVNVDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELNT 335

QY 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 360

DB 336 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395

QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSAGWTGLYM 420

DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSAGWTGLYM 455

QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443

DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 7

ADL24295

ID ADL24295 standard; protein; 510 AA.

XX AC ADL24295;

XX DT 03-JUN-2004 (first entry)

XX DE Human CD39.

XX KW cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;

XX antagonist.

XX OS Homo sapiens.
XX PN WO2004019866-A2.
XX PD 11-MAR-2004.
XX PF 21-AUG-2003; 2003WO-US026354.
XX PR 28-AUG-2002; 2002US-0406418P.
XX PA 12-AUG-2003; 2003US-0494457P.
XX PI (IMMV) IMMUNEX CORP.
XX PI Burton PB, Deisher TA;
XX DR WPI; 2004-239107/22.
XX DR N-PSDB; ADL24294.
XX PT Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a
XX PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart
XX PT failure, aneurysm, angina, embolism, restenosis, ischemia or
XX PT thrombocytopenic purpura.
XX PS Disclosure; Page 133-134; 135pp; English.
XX CC The present invention relates to a method of treating cardiovascular
XX CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,
XX CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40
XX CC antagonists are useful for treating cardiovascular disorders, e.g.
XX CC (chronic immune) myocarditis, congestive heart failure, aneurysms,
XX CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The
XX CC present sequence is a polypeptide used in the exemplification of the
XX CC invention.
XX SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVF 60
DB 36 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVF 95
QY 61 QKVAEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRSEBELADRVLDVVYRS 120
DB 96 QKVAEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRSEBELADRVLDVVYRS 155
QY 121 LSNYPFDQFQARIITGQEGAYGMITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPFDQFQARIITGQEGAYGMITINYLKGFESQKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTPVQNTIESPDNALQRLYKGVKNVYTHSFLCYGKQDALWQKLAKDIQVASN 240
DB 216 GASTQVTPVQNTIESPDNALQRLYKGVKNVYTHSFLCYGKQDALWQKLAKDIQVASN 275
QY 241 EILRDPCHPGYKVVNVSDLYKTPCTKRPFMTLPFOQFETQGGTGNVQOCHQSILELFNT 300
DB 276 EILRDPCHPGYKVVNVSDLYKTPCTKRPFMTLPFOQFETQGGTGNVQOCHQSILELFNT 335
QY 301 SYCPYSQCAFNGIFLPLQGDGFAFSAFYFMWKFNLNTSEKVSQEKVTENMKKFCAPWE 360
DB 336 SYCPYSQCAFNGIFLPLQGDGFAFSAFYFMWKFNLNTSEKVSQEKVTENMKKFCAPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGSTYILSLLOQYHTADSWEHIPGIKQSDAGWTILGYM 420
DB 396 EIKTSYAGVKEKYLSEYCFSGSTYILSLLOQYHTADSWEHIPGIKQSDAGWTILGYM 455
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 8
ADQ99453
ID ADQ99453 standard; protein; 510 AA.
XX AC ADQ99453;
XX DT 23-SEP-2004 (first entry)
XX DE Human CD39 protein.
XX KW CD39-like protein; gene mapping; molecular weight marker;
XX KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
XX KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
XX KW NTPase; human; enzyme.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 47..68
XX FT /note= "Apyrase region (ACR) I"
XX FT Region 124..142
XX FT /note= "Apyrase region (ACR) II"
XX FT Region 169..191
XX FT /note= "Apyrase region (ACR) III"
XX FT Region 207..228
XX FT /note= "Apyrase region (ACR) IV"
XX FN US6759214-B1.
XX PN 06-JUL-2004.
XX PD 13-JUL-2001; 2001US-00908510.
XX PF 29-JAN-1999; 99US-00240639.
XX PR (NUVE-) NUVELO INC.
XX PA Chadwick BP, Frischauf A;
XX WPI; 2004-515395/49.
XX New CD-39-like polypeptides and polynucleotides, useful in chromosome and
XX gene mapping, as molecular weight markers, as food supplements, or as
XX anti-thrombotic or anti-tissue graft rejection agents.
XX Example; Fig 8; 104pp; English.
XX The invention relates to novel CD39-like polypeptides (CD39-like
XX nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
XX such polypeptides. CD39-like polynucleotides may be used as hybridisation
XX probes, PCR primers and in chromosome and gene mapping. Polypeptides of
XX the invention may be used as molecular weight markers, as food
XX supplements, in generating an antibody that specifically binds the
XX polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or
XX for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
XX or brain. Sequences of the invention are useful in modulating ecto-ATPase
XX activity and for identifying compounds that modulate ecto-ATPase
XX activity. The present sequence is human CD39 protein, a member of the
XX CD39-like protein family. Note: This sequence is stated to be the same as
XX that shown as SEQ ID NO:13 in the sequence listing of the specification.
XX However this sequence has additional residues at its ends.
SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVF 60
DB 36 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVF 95

Qy	61	QKWEIGIYLTDCMERAREVTPRSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS	120
Db	96	QKWEIGIYLTDCMERAREVTPRSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS	155
Qy	121	LSNYPDFQAGARIITGQEEGAYGMITNYLLGKFSQKTRWFSIVPVETNNOETFGALDUG	180
Db	156	LSNYPDFQAGARIITGQEEGAYGMITNYLLGKFSQKTRWFSIVPVETNNOETFGALDUG	215
Qy	181	GASTQVTVFPQNOTTIESPDNALQFLRYGKGVNVTYHSFLCYGKDQALWQKLAKDIQVASN	240
Db	216	GASTQVTVFPQNOTTIESPDNALQFLRYGKGVNVTYHSFLCYGKDQALWQKLAKDIQVASN	275
Qy	241	EILRDPCHPGYKVKVNVSDLYKTPCTKRPENTLPPQOPEIQIGIGNVQOCHOSILELFT	300
Db	276	EILRDPCHPGYKVKVNVSDLYKTPCTKRPENTLPPQOPEIQIGIGNVQOCHOSILELFT	335
Qy	301	SYCPYSQCAFNGIFUPLPQGFQAFSAFYFVWKFLNLTSEKVSOEKVTEMMKFKCAQPWE	360
Db	336	SYCPYSQCAFNGIFUPLPQGFQAFSAFYFVWKFLNLTSEKVSOEKVTEMMKFKCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLQGYHTFADSWEHIFPGIKIQCSDAGWTLGVM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLQGYHTFADSWEHIFPGIKIQCSDAGWTLGVM	455
Qy	421	LNLTNMIPAEQPLSTPLSHSTYV	443
Db	456	LNLTNMIPAEQPLSTPLSHSTYV	478

RESULT 9
ADR69210

ID ADR69210 standard; protein; 510 AA.

AC ADR69210;

DT 04-NOV-2004: (first entry)

Human CD39 protein #3.

CD39-like protein; autoimmune deficiency disorder;
connective tissue disease; multiple sclerosis;
systemic lupus erythematosus; rheumatoid arthritis;
autoimmune pulmonary inflammation; Guillain-Barre syndrome;
autoimmune thyroiditis; insulin dependent diabetes mellitus;
myaesthenia gravis; graft-versus-host disease;
autoimmune inflammatory eye disease; allergic disorder; asthma;
respiratory disorder; myeloid or lymphoid cell deficiency;
periodontal disease; tooth repair process; inflammatory bowel disease;
Crohn's disease; leukaemia; nervous system disorder; anticoagulant;
food supplement; anti-tissue graft rejection; ATP neurotransmission;
gene therapy; human.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	47. .68
FT Region	/note= "Apryse region (ACR) I "
FT Region	124. .142
FT Region	/note= "Apryse region (ACR) II "
FT Region	169. .191
FT Region	/note= "Apryse region (ACR) III "
FT Region	207. .228
FT Region	/note= "Apryse region (ACR) IV "

PN US6780410-B1.

24-AUG-2004.

13-JUL-2001: 2001US-00905744.

XX 29-JAN-1999: 99US-00240639

XX PA (NIVE-) NUVELO INC.

Chadwick BP, Frischauf A;

WPI: 2004-613270/59.

New isolated CD39LA polypeptide and polynucleotide, useful for preventing, treating, or ameliorating multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-host disease.

Example; Fig 8; 103pp; English.

The present invention relates to CD39-like polypeptide and its encoding polynucleotide. The invention is useful for preventing, treating or ameliorating autoimmune deficiency disorders including connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease or autoimmune inflammatory eye disease, allergic disorders including asthma and other respiratory problems, myeloid or lymphoid cell deficiencies, periodontal diseases and other tooth repair processes, inflammatory conditions including inflammatory bowel disease and Crohn's disease, leukaemias and nervous system disorders. The invention is also useful as an anticoagulant for inhibiting platelet aggregation, food supplement, anti-tissue graft rejection agents, for regulating neurotransmission by ATP in smooth muscle, peripheral ganglia or brain and in gene therapy. The present sequence is a human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these sequences differ.

Sequence 510 AA;

100.0%: Score 2369: DB 8: Length 510:

Local Similarity 100.0%, Fied: NO: 2.3E-233,
Matches 443: Conservative 0: Mismatches 0:

1 GLTONKALPENVKYGI VLPAGSSHTSLYTYKWPAEKENDTGWVHOVEECRVKGPGISKFV 60

Db	36	GLTQNKALPENVKYGIYVLDAGSSHTSYIYKWPBAEKENDTVGVHQVECRVKGPGLSKFV	95
Qy	61	QKWEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMBESELADRVLDVVERS	120
Db	96	QKWEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLLRMBESELADRVLDVVERS	155
Qy	121	LSNYPFPQGARIIITGQEBGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDVG	180
Db	156	LSNYPFPQGARIIITGQEBGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDVG	215
Qy	181	GASTQTVTFVQONQTIESP DNALQRLXGKDYNVYTHSPCLYCGKQOALWQKLAKDIQVASN	240
Db	216	GASTQTVTFVQONQTIESP DNALQRLXGKDYNVYTHSPCLYCGKQOALWQKLAKDIQVASN	275
Qy	241	EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFMT	300
Db	276	EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFMT	335
Qy	301	SYCPYSQCAFNGIFLPLQGDGFAGSAFYFVWKFLNLTSEKVSQBKVTEMKKFCAQPWE	360
Db	336	SYCPYSQCAFNGIFLPLQGDGFAGSAFYFVWKFLNLTSEKVSQBKVTEMKKFCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGSTYILSLLQGYHFTADSWEHHPFTGKIQGSDAGWTLGYM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGSTYILSLLQGYHFTADSWEHHPFTGKIQGSDAGWTLGYM	455
Qy	421	LNLTNMTPAEOPPLSTPLSHSTYV	443
Db	456	LNLTNMTPAEOPPLSTPLSHSTYV	478

RESULTS

RESULI I
ADR69042

ID ADR69042 standard; protein; 510 AA.

XX ADR69042;
 XX 04-NOV-2004 (first entry)
 XX Human CD39 protein #3.
 XX
 KW CD39-like protein; CD39-like nucleotide triphosphatase; NTPase; cancer;
 KW leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia;
 KW chronic leukaemia; autoimmune disorder; multiple sclerosis;
 KW rheumatoid arthritis; Guillain-Barre syndrome;
 KW insulin dependent diabetes mellitus; myasthenia gravis;
 KW graft-versus-host disease; GVHD; allergic disorder; asthma;
 KW respiratory disorder; inflammatory disorder; septic shock;
 KW systemic inflammatory response syndrome; SIRS; Crohn's disease;
 KW central nervous system disorder; peripheral nervous system disorder;
 KW ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea;
 KW systemic lupus erythematosus;
 KW human immunodeficiency virus-associated myelopathy;
 KW transverse myelopathy; nutritional disorder; vitamin B12 deficiency;
 KW folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;
 KW Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;
 KW nutritional supplement; ecto-ATPase activity; cytosstatic; immunotherapy;
 KW human; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 47..68
 FT /note= "Apyrase (ACR) I"
 FT Region 124..142
 FT /note= "Apyrase (ACR) II"
 FT Region 169..191
 FT /note= "Apyrase (ACR) III"
 FT Region 202..228
 FT /note= "Apyrase (ACR) IV"
 XX
 XX US6780977-B1.
 XX
 XX 24-AUG-2004.
 XX
 XX 27-MAR-2002; 2002US-00107660.
 XX
 XX 29-JAN-1999; 99US-00240639.
 XX 13-JUL-2001; 2001US-00905589.
 XX
 XX (NUVE-) NUVELO INC.
 XX
 XX Chadwick BP, Frischauf A;
 XX
 XX WPI; 2004-613273/59.
 XX GENBANK; S73813.
 XX
 XX New antibody or its fragment that specifically binds to CD39L3
 XX polypeptide, useful for detecting and purifying CD39L3 polypeptide, for
 XX treating leukemia, and for detecting and preventing metastatic spread of
 XX cancerous cells.
 XX
 XX Example; Fig 8; 102pp; English.
 XX
 XX The present invention provides novel CD39-like polypeptides (CD39-like
 XX nucleotide triphosphatase; NTPase) and their encoding polynucleotides.
 XX The invention is useful in treating cancer, leukaemia and related
 XX disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia
 XX and chronic leukaemia, autoimmune disorders such as multiple sclerosis,
 XX rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes
 XX mellitus, myasthenia gravis and graft-versus-host disease, allergic
 XX disorders such as asthma, respiratory disorders, inflammatory disorders
 XX such as septic shock, systemic inflammatory response syndrome (SIRS) and
 XX Crohn's disease, central and peripheral nervous system disorders such as
 XX ischaemia, Parkinson's disease, Alzheimer's disease, Huntington's chorea,
 XX systemic lupus erythematosus, human immunodeficiency virus-associated
 XX myelopathy and transverse myelopathy and nutritional disorders such as

CC vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-
 CC alcohol amblyopia and Marchiafava-Bignami disease. The invention also has
 CC haemostatic and thrombolytic activity, serve as nutritional supplements
 CC and modulates ecto-ATPase activity. The invention acts as a cytosstatic
 CC agent and is useful in immunotherapy. The present sequence is human CD39
 CC protein. Note: This sequence is described in the specification as being
 CC the same as the human CD39 protein represented in SEQ ID NO: 13 of the
 CC sequence listing, however the two sequences are different.
 XX
 SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 8; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.5e-233;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLTNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKPGISKFV 60
 DB 36 GLTNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKPGISKFV 95
 QY 61 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESELDRLVDVVRS 120
 DB 96 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESELDRLVDVVRS 155
 QY 121 LSNYPDFQGARITITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 180
 DB 156 LSNYPDFQGARITITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 215
 QY 181 GASTQVTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDALWQKLADIQVSN 240
 DB 216 GASTQVTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDALWQKLADIQVSN 275
 QY 241 EILRDCPFHPCYKKNVNSDLYKTPCTKRPEMTLPQOFIEIGIGNYQOCHQSTLELFT 300
 DB 276 EILRDCPFHPCYKKNVNSDLYKTPCTKRPEMTLPQOFIEIGIGNYQOCHQSTLELFT 335
 QY 301 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWE 360
 DB 336 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWE 395
 QY 361 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 420
 DB 396 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 455
 QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
 DB 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 11
 ADS17924
 ID ADS17924 standard; protein; 510 AA.
 XX
 AC ADS17924;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 XX Human CD39 protein #3.
 XX
 KW CD39-like protein; gene mapping; food supplement; ecto-ATPase activity;
 KW gene therapy; multiple sclerosis; rheumatoid arthritis;
 KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
 KW autoimmune inflammatory eye disease; osteoporosis; osteoarthritis;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW leukaemia; nervous system disorder; neuroprotective; antiarthritic;
 KW antirheumatic; antithyroid; immunosuppressive; antidiabetic;
 KW muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian;
 KW cytosstatic; human; CD39 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 47..68
 FT /note= "Apyrase region (ACR) I"

FT	Region	124. .142	
FT	/note= "Apyrase region (ACR) II"		
FT	Region	169. .191	
FT	/note= "Apyrase region (ACR) III"		
FT	Region	207. .228	
FT	/note= "Apyrase region (ACR) IV"		
XX			
PN	US6787328-B1.		
XX			
PD	07-SEP-2004.		
XX			
XX	13-JUL-2001; 2001US-00905732.		
XX			
PR	29-JAN-1999; 99US-00240639.		
XX			
PA	(NUVE-) NUVELO INC.		
XX			
PI	Chadwick BP, Frischauf A;		
XX			
DR	WPI; 2004-632929/61.		
XX			
PT	New isolated CD39L4 polynucleotide, useful for preventing, treating, or		
PT	ameliorating multiple sclerosis, rheumatoid arthritis, diabetes, or		
PT	osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or		
PT	leukemia.		
XX			
PS	Example; Fig 8; 103pp; English.		
XX			
CC	The present invention relates to a CD39-like polypeptides and the		
CC	encoding polynucleotides. The CD39L4 polynucleotide is useful as		
CC	hybridisation probes, as primers for PCR, for chromosome or gene mapping,		
CC	in the recombinant production of protein, and in generation of antisense		
CC	DNA or RNA. The protein of the invention is used as molecular weight		
CC	markers, and as food supplements and for modulating ecto-ATPase activity		
CC	and for identifying compounds that can be utilised for modulating ecto-		
CC	ATPase activity. The invention is useful for preventing, treating or		
CC	ameliorating a medical condition, e.g. multiple sclerosis, rheumatoid		
CC	arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,		
CC	autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,		
CC	Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,		
CC	leukaemia or nervous system disorders and in gene therapy. The present		
CC	sequence is the human CD39 protein. Note: This sequence is stated to be		
CC	the same as that shown as SEQ ID 13 in sequence listing, however these		
CC	sequences differ.		
XX			
SQ	Sequence 510 AA;		
Query Match 100.0%; Score 2369; DB 8; Length 510;			
Best Local Similarity 100.0%; Pred. No. 2.5e-233;			
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GLTONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVMHVECRVKGPGISKFV	60
Db	36	GLTONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVMHVECRVKGPGISKFV	95
Qy	61	QKVNIEGILYTDCEMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS	120
Db	96	QKVNIEGILYTDCEMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS	155
Qy	121	LSNYPDFQGARITIQBEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG	180
Db	156	LSNYPDFQGARITIQBEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG	215
Qy	181	GASTQVTFVPONOTTESPDNALQPLRYGKDVNVYTHSLFCYGKQOALWQKLAKDIOVASN	240
Db	216	GASTQVTFVPONOTTESPDNALQPLRYGKDVNVYTHSLFCYGKQOALWQKLAKDIOVASN	275
Qy	241	EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLFPQCFEIQGIGNYQQCHQSILELFPNT	300
Db	276	EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLFPQCFEIQGIGNYQQCHQSILELFPNT	335
Qy	301	SYCPYSQCAFNGIFLPPIQGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE	360

Db	336	SYCPYSQCAFNGIFLPPIQGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE	395
Qy	361	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGTKIQSDAGWTLGYM	420
Db	396	EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGTKIQSDAGWTLGYM	455
Qy	421	LNLTNMIPAEQPLSTPLSHSTYV	443
Db	456	LNLTNMIPAEQPLSTPLSHSTYV	478
RESULT 12.			
ABO84674			
ID	ABO84674	standard; protein; 510 AA.	
XX			
AC	ABO84674;		
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Human cancer-associated protein HP20-011.5.		
XX			
KW	Human; cancer-associated protein; cytostatic; cancer; leukaemia;		
KW	lymphoma; CAP.		
XX			
OS	Homo sapiens.		
XX			
FN	WO2004074320-A2.		
XX			
PD	02-SEP-2004.		
XX			
PF	17-FEB-2004; 2004WO-US004730.		
XX			
PR	14-FEB-2003; 2003US-00367094.		
PR	14-MAR-2003; 2003US-00388838.		
PR	15-APR-2003; 2003US-00417375.		
PR	13-JUN-2003; 2003US-00461862.		
PR	15-SEP-2003; 2003US-00663431.		
PR	15-DEC-2003; 2003US-00737318.		
XX	(SAGR-) SAGRES DISCOVERY INC.		
XX			
PI	Morris DW, Morris DW, Malandro MS;		
XX			
DR	WPI; 2004-652914/63.		
DR	N-PSDB; ABD32958.		
XX			
PT	New isolated cancer-associated polynucleotides and polypeptides useful		
PT	for diagnosing, preventing or treating cancers, especially lymphoma and		
PT	leukemia, or in screening for agents that modulate cancer.		
XX			
PS	claim 18; seqid 698; 310pp; English.		
XX			
CC	The invention relates to an isolated nucleic acid comprising at least 10		
CC	contiguous nucleotides of any of the 233 polynucleotide sequences given		
CC	in the specification, or its complement. The nucleic acids encode cancer-		
CC	associated proteins. Also included are an expression vector comprising		
CC	the isolated nucleic acid cited above, a host cell comprising the above		
CC	recombinant nucleic acid or expression vector, a microarray for detecting		
CC	a cancer-associated (CA) nucleic acid comprising at least one probe		
CC	comprising at least 10 contiguous nucleotides of any of the above-		
CC	mentioned nucleotide sequences, an isolated polypeptide (encoded within		
CC	an open reading frame of a CA sequence selected from any of the 95		
CC	polynucleotide sequences as mentioned in the specification, or its		
CC	complement), an isolated antibody, (or its antigen binding fragment) that		
CC	binds to the above polypeptide, a hybridoma that produces the above		
CC	monoclonal antibody, a pharmaceutical composition comprising the above		
CC	cells (comprising the antibody cited above, methods for diagnosing cancer		
CC	antibody and a pharmaceutical excipient, a kit for detecting cancer		
CC	or for detecting the presence or absence of cancer cells in an		
CC	individual, a method for inhibiting growth of cancer cells in an		
CC	individual, a method for delivering a therapeutic agent to cancer cells		
CC	in an individual, an electronic library comprising the above		
CC	polynucleotide or polypeptide (or their fragments), methods of screening		

CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGPISKFV 60
Db |||||
36 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGPISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVERS 120
Db |||||
96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVERS 155
QY 121 LSNYPDFQGARITGOEGAGYMTINYLKFSQKTRWFSIVPYETNNQETFGALDLG 180
Db |||||
156 LSNYPDFQGARITGOEGAGYMTINYLKFSQKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVQNOTIESPDNALQFLYKGDYNNVTHSFLCYGKQALWOKLAKDIQVASN 240
Db |||||
216 GASTQVTFVQNOTIESPDNALQFLYKGDYNNVTHSFLCYGKQALWOKLAKDIQVASN 275
QY 241 EILRDCPHGPGYKVVNSDLYKTPCTKRPFMTLPFQOFEIIGIGNYQCHQSILELFT 300
Db |||||
276 EILRDCPHGPGYKVVNSDLYKTPCTKRPFMTLPFQOFEIIGIGNYQCHQSILELFT 335
QY 301 SYCPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 360
Db |||||
336 SYCPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 420
Db |||||
396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 455
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db |||||
456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 13

AD87821
ID AD87821 standard; protein; 510 AA.

XX AC

AD87821;

XX DT 18-NOV-2004 (first entry)

XX DE Human CD39 protein #3.

XX KW CD39-like protein; CD39-like nucleotide-triphosphatase; NTPase;
XX KW HIV infection; hepatitis; multiple sclerosis;
XX KW systemic lupus erythematosus; rheumatoid arthritis;XX KW Guillain-Barre syndrome; thyroiditis; diabetes; myasthenia gravis;
XX KW Graft-versus-host disease; GHVD; asthma; human; human; enzyme; CD39.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FH 47..68
XX FT RegionXX FT /note= "Apyrase region (ACR) I"
XX FT 125..142FT Region /note= "Apyrase region (ACR) II"
FT 169..191FT Region /note= "Apyrase region (ACR) III"
FT 207..228

XX Region /note= "Apyrase region (ACR) IV"

XX US6783959-B1.

XX 31-AUG-2004.

XX 27-MAR-2002; 2002US-00107576.

XX 29-JAN-1999; 99US-00240639.

XX 13-JUL-2001; 2001US-00908510.

XX (NUVE-) NUVELO INC.

XX Chadwick BP, Frischauf A;

XX WPI; 2004-623544/60.

XX GENBANK; S73813.

XX New isolated CD39L3 polypeptide and polynucleotide, useful for
XX diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis,
XX systemic lupus erythematosus, arthritis, diabetes and asthma.

XX Example; Fig 8; 102pp; English.

XX The invention relates to CD39-like polypeptides (CD39-like nucleotide-
XX triphosphatase; NTPase) and their corresponding polynucleotides. The
XX invention also relates to a method for making CD39L proteins. The methods
XX and compositions of the invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the CD39-like polypeptide, such as HIV
XX infection, hepatitis, multiple sclerosis, systemic lupus erythematosus,
XX rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes,
XX myasthenia gravis, graft-versus-host disease (GHVD) and asthma. The
XX present sequence is the human CD39 protein. Note: This sequence is
XX described in the specification as being the same as the human CD39
XX protein represented in SEQ ID NO: 13 of the sequence listing, however the
XX two sequences are different.

SQ Sequence 510 AA;

Query Match 100.0%; Score 2369; DB 8; Length 510;

Best Local Similarity 100.0%; Pred. No. 2.5e-233;

Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGPISKFV 60

Db |||||

36 GLTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGPISKFV 95

QY 61 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVERS 120

Db |||||

96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVERS 155

QY 121 LSNYPDFQGARITGOEGAGYMTINYLKFSQKTRWFSIVPYETNNQETFGALDLG 180

Db |||||

156 LSNYPDFQGARITGOEGAGYMTINYLKFSQKTRWFSIVPYETNNQETFGALDLG 215

QY 181 GASTQVTFVQNOTIESPDNALQFLYKGDYNNVTHSFLCYGKQALWOKLAKDIQVASN 240

Db |||||

216 GASTQVTFVQNOTIESPDNALQFLYKGDYNNVTHSFLCYGKQALWOKLAKDIQVASN 275

QY 241 EILRDCPHGPGYKVVNSDLYKTPCTKRPFMTLPFQOFEIIGIGNYQCHQSILELFT 300

Db |||||

276 EILRDCPHGPGYKVVNSDLYKTPCTKRPFMTLPFQOFEIIGIGNYQCHQSILELFT 335

QY 301 SYCPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 360

Db |||||

336 SYCPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395

QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 420

||||| 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLGYM 455
Db ADK60421
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db 456 LNLTNMIPAEQPLSTPLSHSTYV 478

RESULT 14
ID ADK60421 standard; protein; 511 AA.
XX AC ADK60421;
XX DT 06-MAY-2004 (first entry)
XX DE Angiogenesis differentially expressed protein #61.
XX KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;
XX KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;
XX KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
XX KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
XX KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
XX KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
XX KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
XX KW ischemia; angina; myocardial infarction; chronic heart disease;
XX KW cardiac congestion; macular degeneration; osteoporosis.
XX OS Homo sapiens.
XX FN FR2836687-A1.
XX PD 05-SEP-2003.
XX PF 11-APR-2002; 2002FR-00004546.
XX PR 04-MAR-2002; 2002FR-00002717.
XX PA (GENE-) GENE SIGNAL.
XX PA (ALMA/) AL MAHMOOD S.
XX FI Colin S, Schneider C, Al Mahmood S;
XX DR WPI; 2004-013912/02.
XX DR N-PSDB; ADK60414.
XX PT Compositions for diagnosing, prognosing and treating angiogenic disorders
XX PT including tumor vascularization and heart disease, comprise nucleic acid
XX PT or polypeptide differentially expressed in angiogenesis.
XX PS Claim 7; SEQ ID NO 297; 424pp; French.
XX CC The invention relates to a novel pharmaceutical composition active on
XX CC angiogenesis comprising an endothelial cell nucleic acid whose expression
XX CC is induced by an angiogenic factor and inhibited by an angiostatic agent
XX CC or its complement or fragment, a polypeptide sequence encoded by the
XX CC nucleic acid or its fragment, a molecule capable of inhibiting expression
XX CC of the nucleic acid or a molecule which binds to the polypeptide
XX CC sequence. The invention is used to diagnose, prognose or treat an
XX CC angiogenic disorder in a mammal, particularly a human. The disorder is
XX CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,
XX CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,
XX CC endometriosis associated with neovascularization, restenosis due to
XX CC angioplasty, overproduction of tissue due to cicatrization, a peripheral
XX CC vascular disease, hypertension, vascular inflammation, Raynaud disease,
XX CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,
XX CC myocardial infarction, chronic heart disease, cardiac congestion or
XX CC macular degeneration due to age or osteoporosis. This sequence
XX CC corresponds to a protein encoded by a differentially expressed DNA used
XX CC in the composition of the invention.
XX SQ Sequence 511 AA;

Query Match 100.0%; Score 2369; DB 8; Length 511;
Best Local Similarity 100.0%; Pred. No. 2.5e-233;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYGI VLDAGSSHTSLYIYKWPAAKENDTG VHVQVEECRVKGPGISKFV 60
Db 37 GLTONKALPENVKYGI VLDAGSSHTSLYIYKWPAAKENDTG VHVQVEECRVKGPGISKFV 96
QY 61 QKVNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERS 120
Db 97 QKVNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERS 156
QY 121 LSNYPDFQOARIITGOEBGAYGWITINYLKGFQSKTRWFSIYPYETNNQETFGALDLG 180
Db 157 LSNYPDFQOARIITGOEBGAYGWITINYLKGFQSKTRWFSIYPYETNNQETFGALDLG 216
QY 181 GASTQVTFVQNOTIESPDNALQRLYKGDYNNVTHSFLCYGKDOALWQKLAKDIQVASN 240
Db 217 GASTQVTFVQNOTIESPDNALQRLYKGDYNNVTHSFLCYGKDOALWQKLAKDIQVASN 276
QY 241 EILRDPCHFPGYKKVNVNVDLYKTPTCTKRPEMTLPFQOFEIQIGNYQQCHQSILELFT 300
Db 277 EILRDPCHFPGYKKVNVNVDLYKTPTCTKRPEMTLPFQOFEIQIGNYQQCHQSILELFT 336
QY 301 SYCPSYOCARNGIPLPLOGDFGAFSAFYFMVKFLNLTSEKVSQEKVTEMKKFCAQPWE 360
Db 337 SYCPSYOCARNGIPLPLOGDFGAFSAFYFMVKFLNLTSEKVSQEKVTEMKKFCAQPWE 396
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLGYM 420
Db 397 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLGYM 456
QY 421 LNLTNMIPAEQPLSTPLSHSTYV 443
Db 457 LNLTNMIPAEQPLSTPLSHSTYV 479

RESULT 15
ID ADK60722 standard; protein; 511 AA.
XX AC ADK60722;
XX DT 06-MAY-2004 (first entry)
XX DE Angiogenesis differentially expressed protein #61.
XX KW vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;
XX KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;
XX KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;
XX KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;
XX KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;
XX KW angioplasty; cicatrization; peripheral vascular disease; hypertension;
XX KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;
XX KW ischemia; angina; myocardial infarction; chronic heart disease;
XX KW cardiac congestion; macular degeneration; osteoporosis.
XX OS Homo sapiens.
XX FN FR2836686-A1.
XX PD 05-SEP-2003.
XX PF 04-MAR-2002; 2002FR-00002717.
XX PR 04-MAR-2002; 2002FR-00002717.
XX PA (GENE-) GENE SIGNAL.
XX PA (ALMA/) AL MAHMOOD S.
XX FI Colin S, Schneider C, Al Mahmood S;
XX DR WPI; 2004-013911/02.

DR N-PSDB; ADK60715.

XX Compositions containing nucleic acid or polypeptide differentially

PT expressed in angiogenesis are useful to diagnose, prognosis and treat

XX angiogenic disorders including tumor vascularization and heart disease.

XX Claim 7; SEQ ID NO 297; 405pp; French.

XX The invention relates to a novel pharmaceutical composition active on

CC angiogenesis comprising an endothelial cell nucleic acid whose expression

CC is induced by an angiogenic factor and inhibited by an angiostatic agent

CC or its complement or fragment, a polypeptide sequence encoded by the

CC nucleic acid or its fragment, a molecule capable of inhibiting expression

CC of the nucleic acid or a molecule which binds to the polypeptide

CC sequence. The invention is used to diagnose, prognosis or treat an

CC angiogenic disorder in a mammal, particularly a human. The disorder is

CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,

CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,

CC endometriosis associated with neovascularization, restenosis due to

CC angioplasty, overproduction of tissue due to cicatrization, a peripheral

CC vascular disease, hypertension, vascular inflammation, Raynaud disease,

CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,

CC myocardial infarction, chronic heart disease, cardiac congestion or

CC macular degeneration due to age or osteoporosis. This sequence

CC corresponds to a protein encoded by a differentially expressed DNA used

CC in the composition of the invention.

XX SQ Sequence 511 AA;

Query Match 100.0%; Score 2369; DB 8; Length 511;

Best Local Similarity 100.0%; Pred. No. 2.5e-233;

Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTQNKALPENVKYGVILDAGSSHTSLYIYKWPAAEKENDTGVTQVQVEECRVKGFISKFV 60

DB 37 GLTQNKALPENVKYGVILDAGSSHTSLYIYKWPAAEKENDTGVTQVQVEECRVKGFISKFV 96

QY 61 QKWEIGIYLTDCMERAREVTPRSQHOETPVVLGATAGMRLRMESEELADRLVDVVRS 120

DB 97 QKWEIGIYLTDCMERAREVTPRSQHOETPVVLGATAGMRLRMESEELADRLVDVVRS 156

QY 121 LSNYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 180

DB 157 LSNYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 216

QY 181 GASTQVTFVQNOTIESPDNALQRLYCKDYNNVTHSFLCYGKQALWQKLAKDIQVASN 240

DB 217 GASTQVTFVQNOTIESPDNALQRLYCKDYNNVTHSFLCYGKQALWQKLAKDIQVASN 276

QY 241 EILRDPCHPGYKKVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQCHOSILELFT 300

DB 277 EILRDPCHPGYKKVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQCHOSILELFT 336

QY 301 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVEMMKFCAQFWE 360

DB 337 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVEMMKFCAQFWE 396

QY 361 EIKTSYAGVKEKYLSEYCFSGTYSILSLILQGYHFTADSWEHIFIGIKQSDAGWTILGYM 420

DB 397 EIKTSYAGVKEKYLSEYCFSGTYSILSLILQGYHFTADSWEHIFIGIKQSDAGWTILGYM 456

QY 421 LNLNMIPEQPLSTPLSHSTYV 443

DB 457 LNLNMIPEQPLSTPLSHSTYV 479

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 51.9709 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-2_COPY_36_478

Perfect score: 2369
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2369	100.0	502	13	US-10-092-063-38
2	2369	100.0	510	9	US-09-835-147-2
3	2369	100.0	510	9	US-09-374-586-1
4	2369	100.0	510	10	US-09-781-796B-1
5	2369	100.0	510	16	US-10-646-308-30
6	2348	99.1	439	9	US-09-374-586-2
7	2348	99.1	454	9	US-09-835-147-6
8	2348	99.1	463	9	US-09-835-147-30
9	2348	99.1	464	9	US-09-835-147-27
10	2348	99.1	473	9	US-09-835-147-29
11	2348	99.1	474	9	US-09-835-147-28
12	2348	99.1	476	9	US-09-835-147-3
13	2348	99.1	478	9	US-09-835-147-8

14	2348	99.1	487	9	US-09-835-147-26
15	2297	97.0	476	9	US-09-835-147-4
16	1009	42.6	495	9	US-09-823-356-4
17	911	38.5	529	9	US-09-923-304-4
18	906.5	38.3	458	13	US-10-052-586-496
19	906.5	38.3	458	14	US-10-174-590-496
20	906.5	38.3	458	14	US-10-176-758-496
21	906.5	38.3	458	14	US-10-175-737-496
22	906.5	38.3	458	14	US-10-174-581-496
23	906.5	38.3	458	14	US-10-176-483-496
24	906.5	38.3	458	14	US-10-176-749-496
25	906.5	38.3	458	14	US-10-176-514-496
26	906.5	38.3	458	14	US-10-176-915-496
27	906.5	38.3	458	14	US-10-173-706-496
28	906.5	38.3	458	14	US-10-175-738-496
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45	906.5	38.3	458	14	US-10-176-747-496

ALIGNMENTS

RESULT 1
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-38
Query Match 100.0%; Score 2369; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.66-211;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 60
DB 36 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 120
DB 96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 155
QY 121 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 240
DB 216 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 275
QY 241 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 300
DB 276 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 335
QY 301 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 360
DB 336 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFHFGIKQSGDAGWTLGYM 420
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFHFGIKQSGDAGWTLGYM 455
QY 421 LNLTMIPAEQPLSTPLSHSTYV 443
DB 456 LNLTMIPAEQPLSTPLSHSTYV 478

RESULT 2

US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match 100.0%; Score 2369; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.8e-211;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 60
DB 36 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 120

DB 96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 155
QY 121 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 240
DB 216 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 275
QY 241 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 300
DB 276 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 335
QY 301 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 360
DB 336 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFHFGIKQSGDAGWTLGYM 420
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFHFGIKQSGDAGWTLGYM 455
QY 421 LNLTMIPAEQPLSTPLSHSTYV 443
DB 456 LNLTMIPAEQPLSTPLSHSTYV 478

RESULT 3

US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match 100.0%; Score 2369; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.8e-211;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 60
DB 36 GLTONKALPENVKYGVILVLDAGSHTSLYIKWPAEKENDTGVVHVOVEECRVKGPISKFV 95
QY 61 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 120
DB 96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVVERS 155
QY 121 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 180
DB 156 LSNYPDFQAGARIITGOBEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 215
QY 181 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 240
DB 216 GASTQVTFVPOQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKQDQALWQKLAKDIQVASN 275
QY 241 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 300
DB 276 EILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPQFEIQGIGNYQQCHQSILELFTNT 335
QY 301 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 360
DB 336 SYCPYSQCAFNGIFLPLQDGFAGFSAFYFVKMFLNLTSEKVSQEKVTEMKKFCAQPWE 395

QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 420
Dbs 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 455
QY 421 LNLNMIAPAEQPLSTPLSHSTYV 443
Dbs 456 LNLNMIAPAEQPLSTPLSHSTYV 478

RESULT 4
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 100.0%; Score 2369; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.8e-211; Mismatches 0; Indels 0; Gaps 0;
Matches 443; Conservative 0;
QY 1 GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVVHVQVECRVKGPGISKPV 60
Dbs 36 GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVVHVQVECRVKGPGISKPV 95
QY 61 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 120
Dbs 96 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 155
QY 121 LSNYPDFQGARIIITQOBEGAGWTITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 180
Dbs 156 LSNYPDFQGARIIITQOBEGAGWTITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 215
QY 181 GASTQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 240
Dbs 216 GASTQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 275
QY 241 EILRDPCHPHGYKKVNVVSDLYKTPCTKRPFMTLPFQOFEIQGIGNYQCHQSILELFNT 300
Dbs 276 EILRDPCHPHGYKKVNVVSDLYKTPCTKRPFMTLPFQOFEIQGIGNYQCHQSILELFNT 335
QY 301 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMMKKFCAQPMW 360
Dbs 336 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMMKKFCAQPMW 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 420
Dbs 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 455
QY 421 LNLNMIAPAEQPLSTPLSHSTYV 443
Dbs 456 LNLNMIAPAEQPLSTPLSHSTYV 478

Db 456 LNLNMIAPAEQPLSTPLSHSTYV 478
RESULT 5
US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30
Query Match 100.0%; Score 2369; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.8e-211; Mismatches 0; Indels 0; Gaps 0;
Matches 443; Conservative 0;
QY 1 GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVVHVQVECRVKGPGISKPV 60
Dbs 36 GLTONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVVHVQVECRVKGPGISKPV 95
QY 61 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 120
Dbs 96 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 155
QY 121 LSNYPDFQGARIIITQOBEGAGWTITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 180
Dbs 156 LSNYPDFQGARIIITQOBEGAGWTITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 215
QY 181 GASTQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 240
Dbs 216 GASTQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 275
QY 241 EILRDPCHPHGYKKVNVVSDLYKTPCTKRPFMTLPFQOFEIQGIGNYQCHQSILELFNT 300
Dbs 276 EILRDPCHPHGYKKVNVVSDLYKTPCTKRPFMTLPFQOFEIQGIGNYQCHQSILELFNT 335
QY 301 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMMKKFCAQPMW 360
Dbs 336 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMMKKFCAQPMW 395
QY 361 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 420
Dbs 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 455
QY 421 LNLNMIAPAEQPLSTPLSHSTYV 443
Dbs 456 LNLNMIAPAEQPLSTPLSHSTYV 478

RESULT 6
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pineky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586

; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 99.1%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 7e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TQNKALPENVKYGIIVLDAGSSHTSLIYKPAEKENDTGVVHVECRVKGPGISKFKVOK 62
DB 1 TQNKALPENVKYGIIVLDAGSSHTSLIYKPAEKENDTGVVHVECRVKGPGISKFKVOK 60
QY 63 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 122
DB 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 120
QY 123 NYPPDFQGARITGOEGAGYMITINYLKGSQKTRWFSIVPYETNNQETFGALDLGGA 182
DB 121 NYPPDFQGARITGOEGAGYMITINYLKGSQKTRWFSIVPYETNNQETFGALDLGGA 180
QY 183 STQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 242
DB 181 STQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 240
QY 243 LRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHOSILELFTNSY 302
DB 241 LRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHOSILELFTNSY 300
QY 303 CPYSQCAFNGIFLPPQGDGFAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 362
DB 301 CPYSQCAFNGIFLPPQGDGFAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 360
QY 363 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWHEHHIFGKIQSDAGWTGLGYMLN 422
DB 361 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWHEHHIFGKIQSDAGWTGLGYMLN 420
QY 423 LTNMIPAEQPLSTPLSHST 441
DB 421 LTNMIPAEQPLSTPLSHST 439

RESULT 7

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 99.1%; Score 2348; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 7.4e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TQNKALPENVKYGIIVLDAGSSHTSLIYKPAEKENDTGVVHVECRVKGPGISKFKVOK 62
DB 16 TQNKALPENVKYGIIVLDAGSSHTSLIYKPAEKENDTGVVHVECRVKGPGISKFKVOK 75
QY 63 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 122
DB 76 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 135
QY 123 NYPPDFQGARITGOEGAGYMITINYLKGSQKTRWFSIVPYETNNQETFGALDLGGA 182
DB 136 NYPPDFQGARITGOEGAGYMITINYLKGSQKTRWFSIVPYETNNQETFGALDLGGA 195
QY 183 STQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 242
DB 196 STQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 255
QY 243 LRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHOSILELFTNSY 302
DB 256 LRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHOSILELFTNSY 315
QY 303 CPYSQCAFNGIFLPPQGDGFAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 362
DB 316 CPYSQCAFNGIFLPPQGDGFAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 375
QY 363 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWHEHHIFGKIQSDAGWTGLGYMLN 422
DB 376 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWHEHHIFGKIQSDAGWTGLGYMLN 435
QY 423 LTNMIPAEQPLSTPLSHST 441
DB 436 LTNMIPAEQPLSTPLSHST 454

RESULT 8

US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 99.1%; Score 2348; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 7.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TONKALPENVKYIGVLDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKGGISKFVOK 62
DB 25 TONKALPENVKYIGVLDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKGGISKFVOK 84

QY 63 VNEIGIYLTDCMERAREVTPRSHQOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 122
DB 85 VNEIGIYLTDCMERAREVTPRSHQOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 144

QY 123 NYPPDFQAGARIITGQEGAYGWITINYLKGFSSQKTRWFSIYVPYETNNQETFGALDLGGA 182
DB 145 NYPPDFQAGARIITGQEGAYGWITINYLKGFSSQKTRWFSIYVPYETNNQETFGALDLGGA 204

QY 183 STQVTFVFNQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDOALWQKLAKDIQVASNEI 242
DB 205 STQVTFVFNQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKDOALWQKLAKDIQVASNEI 264

QY 243 LRDPCFHGKYKVVNSDLYKTPCTKRFEMTLPFOQFEIQGIGNYQOCHQSILELFTNTSY 302
DB 265 LRDPCFHGKYKVVNSDLYKTPCTKRFEMTLPFOQFEIQGIGNYQOCHQSILELFTNTSY 324

QY 303 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 362
DB 325 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 384

QY 363 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTGLYMLN 422
DB 385 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTGLYMLN 444

QY 423 LTNMIPAEQPLSTPLSHST 441
DB 445 LTNMIPAEQPLSTPLSHST 463

RESULT 9
US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 99.1%; Score 2348; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 7.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TONKALPENVKYIGVLDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKGGISKFVOK 62
DB 35 TONKALPENVKYIGVLDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKGGISKFVOK 94

63	Qy	VNEIGIYITDCW	REAREVIPSQ	HOQETPVYLG	ATAGMBLLRN	MESEBELADRV	LDVVVERSL	122
95	Db	VNEIGIYITDCW	REAREVIPSQ	HOQETPVYLG	ATAGMBLLRN	MESEBELADRV	LDVVVERSL	154
123	Qy	NYPDFQGARII	TOEGEAGY	WITINYL	LKFSOKTRWF	SIVPYETNNQ	ETFGALD	182
155	Db	NYPDFQGARII	TOEGEAGY	WITINYL	LKFSOKTRWF	SIVPYETNNQ	ETFGALD	214
183	Qy	STQVTFPQNT	IESPDNAL	QFRLYGKD	YVYTHSFL	CGKDOALW	KLADIQV	242
215	Db	STQVTFPQNT	IESPDNAL	QFRLYGKD	YVYTHSFL	CGKDOALW	KLADIQV	274
243	Qy	LRDPCHFPGY	KXVNVN	SDLYKTP	CTKRREMT	LPFOQFEI	QIGIGNY	302
275	Db	LRDPCHFPGY	KXVNVN	SDLYKTP	CTKRREMT	LPFOQFEI	QIGIGNY	334
303	Qy	CPYSQCAFNG	IPLPQD	GAFSAFY	FWKFLNLT	SEKVSQEK	TEMKKFCAQ	362
335	Db	CPYSQCAFNG	IPLPQD	GAFSAFY	FWKFLNLT	SEKVSQEK	TEMKKFCAQ	394
363	Qy	KTSYAGVKE	KEYLSY	CFSGT	YILSL	LLQGYHFT	ADSWEH	422
395	Db	KTSYAGVKE	KEYLSY	CFSGT	YILSL	LLQGYHFT	ADSWEH	454
423	Qy	LTNNMIPAE	QPLST	PLSHST	441			
455	Db	LTNNMIPAE	QPLST	PLSHST	473			

Qy	183	STQTVFPQNQTIESPDNALOPRLYGKDYNVYTHSFCLVCGKDQAALWOKLAKIOIVASNEI	242
Dd	218	STQTVFPQNQTIESPDNALOFRLYGKDYNVYTHSFCLVCGKDQAALWOKLAKIOIVASNEI	277
Qy	243	L R D P C F H P G Y K K V N V S D L Y K T P C T K R E M T L P F Q O F E I Q G I G N Y Q O C H S I L E L F N T S Y	302
Dd	278	L R D P C F H P G Y K K V N V S D L Y K T P C T K R E M T L P F Q O F E I Q G I G N Y Q O C H S I L E L F N T S Y	337
Qy	303	C P Y S Q C A F N G I F L P P L Q D G A F S A F Y F V M K F L N L T S B K V S O E K Y T E M M K F C A Q P W B E I	362
Dd	338	C P Y S Q C A F N G I F L P P L Q D G A F S A F Y F V M K F L N L T S B K V S O E K Y T E M M K F C A Q P W B E I	397
Qy	363	K T S Y A G V K E K Y L S E Y C F S G T Y I L S L L Q Y H P T A D S W E H I F I G K I Q G S D A G W T L G Y M L N	422
Dd	398	K T S Y A G V K E K Y L S E Y C F S G T Y I L S L L Q Y H P T A D S W E H I F I G K I Q G S D A G W T L G Y M L N	457
Qy	423	L T N M I P A E Q P L S T P L S H S T	441
Dd	458	L T N M I P A E O P L S T P L S H S T	476

RESULT 13
US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US2002000277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ.ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match	99.1%	Score 2348;	DB 9;	Length 478;
Best Local Similarity	100.0%;	Pred.No. 7.9e-209;		
Matches 439; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	3	TONKALPENVKYGI	VLDAGSHTSLYYIKVPAEKENDTGVVHQVEECRVKPGIGISKFPVK	62
Db	40	TONKALPENVKYGI	VLDAGSHTSLYYIKVPAEKENDTGVVHQVEECRVKPGIGISKFPVK	99
Qy	63	VNEIGIYLTDCEMAR	EVI PRSQHQTFFVLGATAGMRLLRMESEELADRLVDVVRSLS	122
Db	100	VNEIGIYLTDCEMAR	EVI PRSQHQTFFVLGATAGMRLLRMESEELADRLVDVVRSLS	159
Qy	123	NYPDFOGARIITCGE	GAGVCIWITI NYLLGKFOSOKTRWFSTVPYETNNQTFFGALDGG	182
Db	160	NYPDFOGARIITCGE	GAGVCIWITI NYLLGKFOSOKTRWFSTVPYETNNQTFFGALDGG	219
Qy	183	STQVTVPQNQTIESP	NALQFRLYGKDYNVYTHSFICYGKOQALWOKLAKDIQVASNEI	242
Db	220	STQVTVPQNQTIESP	NALQFRLYGKDYNVYTHSFICYGKOQALWOKLAKDIQVASNEI	279

Qy	243	LRDPCFHPGKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFTNSY	302
Db	280	LRDPCFHPGKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFTNSY	339
Qy	303	CPYSQCAFNGIFLPLQGDGFAFVFMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	362
Db	340	CPYSQCAFNGIFLPLQGDGFAFVFMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	399
Qy	363	KTSYAGVKEKYSBFCFSGVYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYMLN	422
Db	400	KTSYAGVKEKYSBFCFSGVYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLGYMLN	459
Qy	423	LTNMIPAEQPLSTPLSHST	441
Db	460	LTNMIPAEQPLSTPLSHST	478
RESULT 14			
US-09-835-147-26			
; Sequence 26, Application US/09835147			
; Patent No. US20020002277A1			
; GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835.147			
; CURRENT FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585.			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 26			
; LENGTH: 487			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-26			

Query Match	99.1%;	Score 2348;	DB 9;	Length 487;
Best Local Similarity	100.0%;	Pred. No. 8.2e-209;		
Matches 439;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	3	TONKALPENVKYGI	VLDAGSSHTSLY	YIKKPAEKENDTGVVHQYEECRVKPGISKFKVQK 62
Db	49	TONKALPENVKYGI	VLDAGSSHTSLY	YIKKPAEKENDTGVVHQYEECRVKPGISKFKVQK 108
Qy	63	VNEIGIYLLTDCMR	AREVIPRSOHOETPV	YGATAGMRLRMESSEELADRVLDVVVERSL 122
Db	109	VNEIGIYLLTDCMR	AREVIPRSOHOETPV	YGATAGMRLRMESSEELADRVLDVVVERSL 168
Qy	123	NYPFDFOGARIIT	GQEBGAGWITINLL	GKFSOKTRWFISIVPYETNNQETFGALDLGGA 182
Db	169	NYPFDFOGARIIT	GQEBGAGWITINLL	GKFSOKTRWFISIVPYETNNQETFGALDLGGA 228
Qy	183	STQVTFVPQNTIES	PDNALQFRLYGKDY	VNYTHYSFLCYGKQALWQKLAKDIQVASNEI 242
Db	229	STQVTFVPQNTIES	PDNALQFRLYGKDY	VNYTHYSFLCYGKQALWQKLAKDIQVASNEI 288
Qy	243	LRDPCFHGKCVNV	SDLYKTPCTKGFEM	TLPPQQFEIOGIGNYQOCHQSILBLFNTSY 302
Db	289	LRDPCFHGKCVNV	SDLYKTPCTKGFEM	TLPPQQFEIOGIGNYQOCHQSILBLFNTSY 348

QY 303 CPYSQCAFNGIFLPLQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 362
Db 349 CPYSQCAFNGIFLPLQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 408
QY 363 KTSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 422
Db 409 KTSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 468
QY 423 LTNMIPAEQPLSTPLSHST 441
Db 469 LTNMIPAEQPLSTPLSHST 487

RESULT 15

US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gampel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 97.0%; Score 2297; DB 9; Length 476;
Best Local Similarity 97.1%; Pred. No. 4.3e-204;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
QY 1 GLTONKALPENVK-----YGIIVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVECRVKPGI 56
Db 32 GIPFSSMXPINVSASTLYGIIVLDAGSSHTSLIYIKWPAEKENDTGVVHVQVECRVKPGI 91
QY 57 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVVLGATAGWRLLRMESEELADRVLDV 116
Db 92 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVVLGATAGWRLLRMESEELADRVLDV 151
QY 117 VERSLSNYPDFQAGRIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 176
Db 152 VERSLSNYPDFQAGRIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 211
QY 177 LDLGASTQVTFVPQNTIESPDNALQFRLYKDNVYTHSFICYGKQALWQKLAKDTQ 236
Db 212 LDLGASTQVTFVPQNTIESPDNALQFRLYKDNVYTHSFICYGKQALWQKLAKDTQ 271
QY 237 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEWTLFPQOFEILOGIGNYQOCHOSILE 296
Db 272 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEWTLFPQOFEILOGIGNYQOCHOSILE 331

QY 297 LFNTSYCPYSQCAFNGIFLPLQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCA 356
Db 332 LFNTSYCPYSQCAFNGIFLPLQDGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCA 391
QY 357 QPWEEIKTSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFIKIQGSDAGWT 416
Db 392 QPWEEIKTSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFIKIQGSDAGWT 451
QY 417 LGYMLNLTNMIPAEQPLSTPLSHST 441
Db 452 LGYMLNLTNMIPAEQPLSTPLSHST 476

Search completed: March 7, 2005, 14:12:33
Job time : 53.9709 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 18.8788 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-30_COPY_21_463

Perfect score: 2368
Sequence: 1 APTSTONKALPENVKYIGVL.....NLTNMIPAEQLPLSHST 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	99.2	502	US-09-557-800C-55	Sequence 55, Appl
2	2348	99.2	502	US-09-370-625A-38	Sequence 38, Appl
3	2348	99.2	510	US-08-930-921-1	Sequence 1, Appl
4	2348	99.2	510	US-09-781-796C-1	Sequence 1, Appl
5	910.5	38.5	529	US-09-240-639-4	Sequence 4, Appl
6	910.5	38.5	529	US-09-908-510A-4	Sequence 4, Appl
7	910.5	38.5	529	US-09-905-744B-4	Sequence 4, Appl
8	910.5	38.5	529	US-10-107-660-4	Sequence 4, Appl
9	910.5	38.5	529	US-10-107-576-4	Sequence 4, Appl
10	910.5	38.5	529	US-09-905-732B-4	Sequence 4, Appl
11	910.5	38.5	529	US-09-923-304-4	Sequence 4, Appl
12	910.5	38.5	529	US-09-949-016-6049	Sequence 6049, Ap
13	910.5	38.5	529	US-09-905-743B-4	Sequence 4, Appl
14	910.5	38.5	556	US-09-949-016-11328	Sequence 11328, A
15	865	36.5	479	US-09-949-016-11559	Sequence 11559, A
16	847.5	35.8	282	US-09-949-016-7977	Sequence 7977, Ap
17	803	33.9	153	US-09-240-639-13	Sequence 13, Appl
18	803	33.9	153	US-09-908-510A-13	Sequence 13, Appl
19	803	33.9	153	US-09-905-744B-13	Sequence 13, Appl
20	803	33.9	153	US-10-107-660-13	Sequence 13, Appl
21	803	33.9	153	US-10-107-576-13	Sequence 13, Appl
22	803	33.9	153	US-09-905-732B-13	Sequence 13, Appl
23	803	33.9	153	US-09-905-743B-13	Sequence 13, Appl
24	604	25.5	154	US-09-240-639-14	Sequence 14, Appl
25	604	25.5	154	US-09-908-510A-14	Sequence 14, Appl
26	604	25.5	154	US-09-905-744B-14	Sequence 14, Appl
27	604	25.5	154	US-10-107-660-14	Sequence 14, Appl

28	604	25.5	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	25.5	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	25.5	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	18.7	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	18.7	153	4	US-09-908-510A-15	Sequence 15, Appl
33	442.5	18.7	153	4	US-09-905-744B-15	Sequence 15, Appl
34	442.5	18.7	153	4	US-10-107-660-15	Sequence 15, Appl
35	442.5	18.7	153	4	US-10-107-576-15	Sequence 15, Appl
36	442.5	18.7	153	4	US-09-905-732B-15	Sequence 15, Appl
37	442.5	18.7	153	4	US-09-905-743B-15	Sequence 15, Appl
38	423	17.9	462	4	US-09-129-112-2	Sequence 2, Appl
39	421.5	17.8	462	4	US-09-129-112-15	Sequence 15, Appl
40	417.5	17.6	150	3	US-09-240-639-16	Sequence 16, Appl
41	417.5	17.6	150	4	US-09-908-510A-16	Sequence 16, Appl
42	417.5	17.6	150	4	US-09-905-744B-16	Sequence 16, Appl
43	417.5	17.6	150	4	US-10-107-660-16	Sequence 16, Appl
44	417.5	17.6	150	4	US-10-107-576-16	Sequence 16, Appl
45	417.5	17.6	150	4	US-09-905-732B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 99.2%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 2e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	5	TQNKALPENVKYIGVL	DAGSSHTSLYYKWP	AEKENDTGVVHVQVEECRVKPGISKPVQK	64
Db	38	TQNKALPENVKYIGVL	DAGSSHTSLYYKWP	AEKENDTGVVHVQVEECRVKPGISKPVQK	97
Qy	65	VNEIGVLTDCMERAREV	IPRSQHQETPVYLGATAGMRLLRMESEELADRLVDVVERSL	124	
Db	98	VNEIGVLTDCMERAREV	IPRSQHQETPVYLGATAGMRLLRMESEELADRLVDVVERSL	157	
Qy	125	NYPDFQARIITQEEGAYC	GWITINVLKFKSQKTRWFSIVPVYETNNQETFGALDLGGA	184	

Db 158 NYPPDFQAGRIITGOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
QY 185 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 244
Db 218 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 277
QY 245 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 304
Db 278 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 337
QY 305 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
Db 338 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 424
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 457
QY 425 LTNMIPAEQPLSTPLSHST 443
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 2

US-09-370-625A-38
; Sequence 38, Application US/09370625A
; Patent No. 660032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-38

Query Match 99.2%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 2e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHVQVEECRVKPGISKVFQK 64
Db 38 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHVQVEECRVKPGISKVFQK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRLVDVVERSL 124
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRLVDVVERSL 157
QY 125 NYPPDFQAGRIITGOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 184
Db 158 NYPPDFQAGRIITGOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
QY 185 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 244
Db 218 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 277
QY 245 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 304
Db 278 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 337

QY 305 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
Db 338 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 424
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 457
QY 425 LTNMIPAEQPLSTPLSHST 443
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 3

US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; CURRENT FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1

Query Match 99.2%; Score 2348; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 2e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHVQVEECRVKPGISKVFQK 64
Db 38 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHVQVEECRVKPGISKVFQK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRLVDVVERSL 124
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLMESEELADRLVDVVERSL 157
QY 125 NYPPDFQAGRIITGOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 184
Db 158 NYPPDFQAGRIITGOEGAGYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
QY 185 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 244
Db 218 STQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 277
QY 245 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 304
Db 278 LRDPCHFPGYKVKVNSDLYKTPCTKRFEMTLPPQOFETQIGIGNYQOCHOSILELFTSY 337
QY 305 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
Db 338 CPYSQCAFNGIFLPPQLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 424
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTGLGYMLN 457
QY 425 LTNMIPAEQPLSTPLSHST 443
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEROPE AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781.796C
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 99.2%; Score 2348; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 2e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVQK 64
Db 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVQK 97

Qy 65 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLEMESEELADRLDVVERSLN 124
Db 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLEMESEELADRLDVVERSLN 157

Qy 125 NYPDFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 184
Db 158 NYPDFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217

Qy 185 STQVTFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALWOKLADQVASNEI 244
Db 218 STQVTFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALWOKLADQVASNEI 277

Qy 245 LRDPFCFHPGKVKVNVSDLYKTPCTKRFEMTLPFQOPEIQGNYQOCHQSILELFTSY 304
Db 278 LRDPFCFHPGKVKVNVSDLYKTPCTKRFEMTLPFQOPEIQGNYQOCHQSILELFTSY 337

Qy 305 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPPW 364
Db 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPPW 397

Qy 365 KTSYAGVKEKYLSCYCFSGTYILSLLOQHYFTADSWEHIFHFGIKQSDAGWTGLYMLN 424
Db 398 KTSYAGVKEKYLSCYCFSGTYILSLLOQHYFTADSWEHIFHFGIKQSDAGWTGLYMLN 457

Qy 425 LTNMIPAEQPLSTPLSHST 443
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischau, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240.639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 38.5%; Score 910.5; DB 3; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 6 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVQK 65
Db 47 KQEVLPPLKLYGIIVLDAGSSRTTVVYQWPAEKENNTGVVSQTEKCSVKSGSISSYGNP 106

Qy 66 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLEMESEELADRLDVVERSLN 125
Db 107 QDVPRAFECMQKVKGVQVPSHLHGSTPIHLGATAGMRLLEMESEELADRLDVVERSLN 166

Qy 126 YPDPFQAGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 185
Db 167 QPDPFRGRIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 224

Qy 186 TQVTFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALWOKLADQVASNEI 244
Db 225 TQISFVAGERKMDLNTSDIMQVSLVGYVYVYTHSFLCYGKQDQALWOKLADQVASNEI 284

Qy 245 LRDPFCFHPGKVKVNVSDLYKTPCTKRFEMTLPFQOPEIQGNYQOCHQSILELFTSY 302
Db 285 LTNMIPAEQPLSTPLSHST 344

Qy 303 SYC-PYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPPW 361
Db 345 KACHDQETCSFDGVYQPKIGPFAVAFGYTASALNL-SGSFSLDTFNSSTWFCSQNW 403

Qy 362 EBKTSYAGVKEKYLSCYCFSGTYILSLLOQHYFTADSWEHIFHFGIKQSDAGWTGLY 421
Db 404 SOLPLLLPKFDEVYARSYCFSAFYVYHFLVNGYKFTETWQIHFKEVGNSSIAWSLGY 463

Qy 422 LTNMIPAEQPL 435
Db 464 MSLTNQIPAESPL 477

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischau, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908.510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

Query Match 38.5%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 6 QNKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVHGVHVEECRVKPGISKVFQKV 65
DB 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVSTQPKSVKSGISYGNP 106

QY 66 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 125
DB 107 QDVPRAFECMKQKGVQVPSHLHGSTPIHLGATAGMRLLRQNETANEVLESIOSYFKS 166

QY 126 YPFDFOGARIITCOBEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGAS 185
DB 167 QPFDPRGAQIIISQOEEGVYGTITANYLMGNFLEKMLWMWV--HPHGVETTGALDLGGAS 224

QY 186 TQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQOALWQKLAKDIQVA-SNEI 244
DB 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLYTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284

QY 245 LRDCPFHPGKVKVNVSDLYKTPCT--KRFEMTLFQOFEIQGIGNYQOCHOSILELNT 302
DB 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGDPCLCKEKVASIFDF 344

QY 303 SYC-PYSOCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPW 361
DB 345 KACHDOETCSPDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWFCSONW 403

QY 362 BEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTIGY 421
DB 404 SOLPPLLKPFDEVYARSYCFSSANYIYHLFVNGYKFTETWPIQHFEKEVGNSSIAWSLIGY 463

QY 422 MLNLTNMTAPAOPL 435
DB 464 MSLTNQIPAESPL 477

RESULT 7
US-09-905-744B-4
; Sequence 4, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120A
; CURRENT APPLICATION NUMBER: US/09/905.744B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-744B-4

Query Match 38.5%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 6 QNKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVHGVHVEECRVKPGISKVFQKV 65
DB 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVSTQPKSVKSGISYGNP 106

QY 66 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 125
DB 107 QDVPRAFECMKQKGVQVPSHLHGSTPIHLGATAGMRLLRQNETANEVLESIOSYFKS 166

QY 126 YPFDFOGARIITCOBEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGAS 185

DB 167 QPFDPRGAQIIISQOEEGVYGTITANYLMGNFLEKMLWMWV--HPHGVETTGALDLGGAS 224
QY 186 TQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQOALWQKLAKDIQVA-SNEI 244
DB 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLYTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284
QY 245 LRDCPFHPGKVKVNVSDLYKTPCT--KRFEMTLFQOFEIQGIGNYQOCHOSILELNT 302
DB 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGDPCLCKEKVASIFDF 344
QY 303 SYC-PYSOCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPW 361
DB 345 KACHDOETCSPDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWFCSONW 403
QY 362 BEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTIGY 421
DB 404 SOLPPLLKPFDEVYARSYCFSSANYIYHLFVNGYKFTETWPIQHFEKEVGNSSIAWSLIGY 463
QY 422 MLNLTNMTAPAOPL 435
DB 464 MSLTNQIPAESPL 477

RESULT 8
US-10-107-660-4
; Sequence 4, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107.660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-660-4

Query Match 38.5%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 6 QNKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGTVHGVHVEECRVKPGISKVFQKV 65
DB 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVSTQPKSVKSGISYGNP 106

QY 66 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 125
DB 107 QDVPRAFECMKQKGVQVPSHLHGSTPIHLGATAGMRLLRQNETANEVLESIOSYFKS 166

QY 126 YPFDFOGARIITCOBEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGAS 185
DB 167 QPFDPRGAQIIISQOEEGVYGTITANYLMGNFLEKMLWMWV--HPHGVETTGALDLGGAS 224
QY 186 TQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQOALWQKLAKDIQVA-SNEI 244
DB 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLYTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284
QY 245 LRDCPFHPGKVKVNVSDLYKTPCT--KRFEMTLFQOFEIQGIGNYQOCHOSILELNT 302
DB 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGDPCLCKEKVASIFDF 344
QY 303 SYC-PYSOCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPW 361
DB 345 KACHDOETCSPDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWFCSONW 403

Qy 362 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGIKQSDAGWTIGY 421
Db 404 SOLPLLPKPFDEVARSYCFGSANYIYHLFVNGYKFTETWPIQHFEKEVGNSSIAWSLGY 463
Qy 422 MLNLTMIPAEQPL 435
Db 464 MSLTNQIPAESPL 477

RESULT 9

US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4

Query Match 38.5%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 6 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGTVHGVHVECRVKPGISKFKVQKV 65
Db 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVWSQTFKCSVKGSGISSYGNP 106
Qy 66 NEIGYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN 125
Db 107 QDVPAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYPKS 166
Qy 126 YPRDFQARITGOEAGAYGWITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 185
Db 167 QPFDERGAQIISGOEEGYGMITANYLMGNFLEKNLWMMV--HPHGVETTTGALDLGGAS 224
Qy 186 TQVTFVQNGTIESPDNALQRLYKGDYNNVTHSFLCYGKDOALWQKLAKDIOVA-SNEI 244
Db 225 TQISFVAGERKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
Qy 245 LRDPCEHPGYKKVNVSDLYKTCT--KRPEMTLPFOQFEIQGICNTQOCHQSIILEFNT 302
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPCLCKEKVASIFDF 344
Qy 303 SYC-PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSKVSQEKVTEMMKKFCQAPW 361
Db 345 KACHDQETCSFDGVYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
Qy 362 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGIKQSDAGWTIGY 421
Db 404 SOLPLLPKPFDEVARSYCFGSANYIYHLFVNGYKFTETWPIQHFEKEVGNSSIAWSLGY 463
Qy 422 MLNLTMIPAEQPL 435
Db 464 MSLTNQIPAESPL 477

RESULT 10

US-09-905-732B-4
; Sequence 4, Application US/09905732B
; Patent No. 6787328

; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-732B-4

Query Match 38.5%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 4.4e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 6 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGTVHGVHVECRVKPGISKFKVQKV 65
Db 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVWSQTFKCSVKGSGISSYGNP 106
Qy 66 NEIGYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN 125
Db 107 QDVPAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYPKS 166
Qy 126 YPRDFQARITGOEAGAYGWITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 185
Db 167 QPFDERGAQIISGOEEGYGMITANYLMGNFLEKNLWMMV--HPHGVETTTGALDLGGAS 224
Qy 186 TQVTFVQNGTIESPDNALQRLYKGDYNNVTHSFLCYGKDOALWQKLAKDIOVA-SNEI 244
Db 225 TQISFVAGERKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
Qy 245 LRDPCEHPGYKKVNVSDLYKTCT--KRPEMTLPFOQFEIQGICNTQOCHQSIILEFNT 302
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPCLCKEKVASIFDF 344
Qy 303 SYC-PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSKVSQEKVTEMMKKFCQAPW 361
Db 345 KACHDQETCSFDGVYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
Qy 362 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGIKQSDAGWTIGY 421
Db 404 SOLPLLPKPFDEVARSYCFGSANYIYHLFVNGYKFTETWPIQHFEKEVGNSSIAWSLGY 463
Qy 422 MLNLTMIPAEQPL 435
Db 464 MSLTNQIPAESPL 477

RESULT 11

US-09-923-304-4
; Sequence 4, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UTSC:658US
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-4


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Db 345 KACHDOETCSFDGVYQPKIKGPFVAFAGFYTTASALNL-SGSFSLDTFNSWTNFCSONW 403
Qy 362 BEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLY 421
Db 404 SOLPLLLPKFDEYVARSYCFSANYYIHLFVNGYKFTETWQIHFKEKEVGNSSIAWSLGY 463
Qy 422 MLNLTNMIPAEQPL 435
Db 464 MSLTNQIPAESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 38.5%; Score 910.5; DB 4; Length 556;
Best Local Similarity 41.5%; Pred. No. 4.7e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 6 QNKLALPENVKYIGVLDAAGSSHTSLYIKWPAEKENDTGTVVHQBECRVKGGISKFVQKV 65
Db 74 KOVLPLPKLYIGVLDAAGSSRTTVVYQWPAEKENNTGVSQTFKCSYKSGISYGNP 133
Qy 66 NEIGYILDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSLN 125
Db 134 QDVPAFEECKQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLIESIQSYPKS 193
Qy 126 YPFQOGARIITGOBEGAYGMITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 185
Db 194 QPFDERGAQIISGQEGYGVMITANYLGNFLEKXLMHWV--HPHGVETTTGALDLGGAS 251
Qy 186 TQVTFVQNTIESPDNALQFLRYGKYNVYTHSFLCYGKQOALWQKLAKDIOVA-SNEI 244
Db 252 TQISFVAGEKMDLNTSDIMQVSLYGVYVTLVTHSFQCYGRNEAEKFLAMLQNSPTQKH 311
Qy 245 LRDCFFHGYKKVNVVSDLYKTPTCT--KRPENTLPPQOFEIQGNYQOCHQSIILEPNT 302
Db 312 LTNPCYPRDYSISFTMGHVFSLCTVDQRPESYNPDVITFEGTGDPSLCKEKVASIPDF 371
Qy 303 SYC-PYSOCAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTEMMKFKCAQPW 361
Db 372 KACHDOETCSFDGVYQPKIKGPFVAFAGFYTTASALNL-SGSFSLDTFNSWTNFCSONW 430
Qy 362 BEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLY 421
Db 431 SOLPLLLPKFDEYVARSYCFSANYYIHLFVNGYKFTETWQIHFKEKEVGNSSIAWSLGY 490
Qy 422 MLNLTNMIPAEQPL 435
Db 491 MSLTNQIPAESPL 504
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RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 36.5%; Score 865; DB 4; Length 479;
Best Local Similarity 41.3%; Pred. No. 3e-84;
Matches 183; Conservative 69; Mismatches 137; Indels 54; Gaps 9;

Qy 5 TQNKALPENVKYIGVLDAAGSSHTSLYIKWPAEKENDTGTVVHQBECRVKGGISKFVQK 64
Db 36 TRDVREPPALKYIGVLDAAGSSHTSMFIYKWPADKENDTGVQHSQSDVPGGSISSYADN 95
Qy 65 VNEIGYILDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSLN 124
Db 96 PSGASQSLVGLQALQDVPKERRHAGTPLYLGATAGMRLNLNLTPEASTSVLMVTHTLT 155
Qy 125 NYPDFQARIITGOBEGAYGMITINLLG---KFSQKTRWFSIVPYETNNQETFGALDL 181
Db 156 QYPDFRGAAILSGQEGYGVMITANYLLENFIKYGVGRWF-----RPRKGTILGANDL 209
Qy 182 GGASTQVTFVQNTIESPDNA--LQFLRYGKYNVYTHSFLCYGKQOALWQKLAKDIOV 239
Db 210 GGASTQITF--ETTSPAEDRASEVQLHLYGQHYRVYTHSFLCYGRDQVLRLLASALQT 266
Qy 240 ASNEILRDPCEHPGYKKVNVVSDLYKTPTCTKRFENTLPPQOF-----EIQGNYQOCH 293
Db 267 HGPH-----PCWPRGFSTQVLLGDVYQSPCT----MAQRPNQFNSSARVSLSGSDPHLCR 318
Qy 294 QSILELENTSYCPYSQCAFNIGIFLPLQDGFAGFSAFYFVMKFL--NLTSEKVSQEKVTE 351
Db 319 DLVSGLSFSSCPSRCSFNGVFPQPPAGNFVAISAFYTVDFLRTSMGLPVATLQQLA 378
Qy 352 MMKFKCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQ 411
Db 379 AAVNVNQTWQAQ-----QLLSRGYGDFDERAFGCVIFQKAA 414
Qy 412 GSDAGWTGLYMLNLTNMIPAEQ 434
Db 415 DTAVGWALGYMLNLNLIPADPP 437

Search completed: March 7, 2005, 13:28:02
Job time : 20.8788 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 61.3608 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-2_COPY_39_476
Perfect score: 2343
Sequence: 1 QNKPENKYGIVLDAGSS.....NLTNMPAEQPLSTPLSHST 438

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2343	100.0	510	1 ENP1_HUMAN	P49961 homo sapien
2	1830	78.1	510	1 ENP1_MOUSE	P55772 mus musculus
3	1830	78.1	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1825	77.9	510	2 Q92106	Q921q6 mus musculus
5	1818	77.6	372	2 Q86VJ3	Q85vw3 homo sapien
6	1789.5	76.4	511	1 ENP1_RAT	P97687 rattus norv
7	1710	73.0	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1685.5	71.9	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	67.2	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1450	61.9	508	2 Q8DFJ1	Q6dfs1 xenopus tro
11	1418	60.5	508	2 Q8GP74	Q6gp74 xenopus lae
12	1306.5	55.8	492	2 Q8DC46	Q6dc46 brachydanio
13	1046	44.6	497	2 Q8UQ22	Q6uq22 mus musculus
14	1004	42.9	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	42.6	493	2 Q90X66	Q90x66 gallus gall
16	973	41.5	454	2 Q8ZM69	Q6zm69 brachydanio
17	966.5	41.3	495	1 ENP2_RAT	O35795 rattus norv
18	961	41.0	455	2 Q7T014	Q7t014 brachydanio
19	959.5	41.0	495	1 ENP2_MOUSE	O55026 mus musculus
20	959.5	41.0	495	2 Q921R1	Q921r1 mus musculus
21	953	40.7	494	1 ENP2_CHICK	P79784 gallus gall
22	937.5	40.0	502	2 Q66L64	Q66l64 brachydanio
23	936	39.9	526	2 Q6GNA4	Q6gna4 xenopus lae
24	933	39.8	500	2 Q6NVI9	Q6nv19 xenopus tro
25	913.5	39.0	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	38.9	529	1 ENP3_HUMAN	O75355 homo sapien
27	906.5	38.7	458	2 Q6UVZ0	Q6uvz0 homo sapien
28	906.5	38.7	495	1 ENP2_HUMAN	Q9y5l3 homo sapien
29	902.5	38.5	529	2 Q8BFW6	Q8bfw6 m mus muscu
30	854	36.4	453	2 Q8ZM68	Q6zm68 brachydanio
31	825.5	35.2	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	28.1	544	2 Q7YTA4	Q7yta4 schistosoma
33	620.5	26.5	300	2 Q8K0L2	Q8k0l2 mus musculus
34	596.5	25.5	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	505	21.6	483	2 Q9X162	Q9x162 arabidopsis
36	504	21.5	488	2 Q6NQ48	Q6nq48 arabidopsis
37	491	21.0	503	2 Q94AF8	Q94af8 arabidopsis
38	491	21.0	503	2 Q8H1D8	Q8h1d8 arabidopsis
39	485	20.7	537	2 Q6Z543	Q6z543 oryza sativ
40	483	20.6	634	2 Q6FRC2	Q6frc2 candida gla
41	482.5	20.6	336	2 Q8CCV2	Q8ccv2 mus musculus
42	471.5	20.1	555	2 Q94E22	Q94e22 arabidopsis
43	459.5	20.0	405	2 Q9M9T7	Q9m9t7 arabidopsis
44	466	19.9	611	2 Q6DH30	Q6dh30 brachydanio
45	465.5	19.9	555	2 Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1		ENP1_HUMAN		STANDARD;		PRT;		510 AA.	
ID	AC	P49961	OSUQO9	Q9Y3Q9					
DT	01-OCT-1996	(Rel. 34, Created)							
DT	01-OCT-1996	(Rel. 34, Last sequence update)							
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)								
DE	(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell								
DE	activation antigen) (Ecto-apyrase) (CD39 antigen).								
GN	Name=ENTPD1; Synonyms=CD39;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
[1]	SEQUENCE FROM N.A. (ISOFORM VASCULAR).								
RP	MEDLINE=95015846; PubMed=7930580;								
RX	Maliszewski C.R., Deleespesse G.J.T., Schoenborn M.A., Armitage R.J.,								
RA	Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Polindexter K.,								
RA	Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;								
RT	"The CD39 lymphoid cell activation antigen. Molecular cloning and								
RT	structural characterization.";								
J.	J. Immunol. 153:3574-3583(1994).								
[2]	SEQUENCE FROM N.A. (ISOFORM VASCULAR).								
RP	TISSUE=Umbilical vein;								
RC	MEDLINE=97149443; PubMed=8996251;								
RX	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Koziak K.,								
RA	Millan M., Hancock W.W., Bach F.H.;								
RT	"Loss of ATP diphosphohydrolase activity with endothelial cell								
RT	activation.";								
J.	J. Exp. Med. 185:153-163(1997).								
[3]	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).								
RP	TISSUE=Placenta;								
RC	MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;								
RX	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,								
RA	Titani K., Fujimura Y., Narita N.;								
RT	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I								
RT	and II.";								
F.	FEBS Lett. 453:335-340(1999).								
[4]	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.								
RP	TISSUE=Placenta;								
RX	MEDLINE=9609723; PubMed=8529670;								
RA	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;								
RT	"Purification and properties of human placental ATP								
RT	diphosphohydrolase.";								
J.	Eur. J. Biochem. 234:66-74(1995).								
[5]	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND								
RP	399-405 (ISOFORM PLACENTAL I).								
RC	TISSUE=Placenta;								

ENP1_MOUSE	STANDARD;	PRT;	510 AA.
AC	P55772;		
DT	01-NOV-1997, (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	05-JUL-2004, (Rel. 44, Last annotation update)		
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)		
DE	(NTPase), [ecto-ATP diphosphohydrolase (ATPase)] (lymphoid cell		
DE	activation antigen) (ecto-apyrase) (CD39 antigen).		
GN	Names=Entpd1; Synonyms=Cd39;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RN	MEDLINE=95035846; PubMed=7930580;		
RX	Maliszewski C.R., Delsepess G.J.T., Schoenborn M.A., Armitage R.J.,		
RA	Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,		
RA	Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;		
RA	"The CD39 lymphoid cell activation antigen. Molecular cloning and		
RT	structural characterization.";		
RL	J. Immunol. 153:3574-3583(1994).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=129/3vJ;		
RC	MEDLINE=9839871; PubMed=9730622;		
RX	Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,		
RA	Gayle R.B. III, Maliszewski C.R.;		
RA	"Gene structure and chromosome location of mouse Cd39 coding for an		
RT	ecto-apyrase.";		
RL	Cytogenet. Cell Genet. 81:287-289(1998).		
CC	-1- FUNCTION: In the nervous system, could hydrolyze ATP and other		
CC	nucleotides to regulate purinergic neurotransmission. Could also		
CC	be implicated in the prevention of platelet aggregation.		
CC	Hydrolyzes ATP and ADP equally well.		
CC	-1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.		
CC	-1- COFACTOR: Requires calcium and magnesium (By similarity).		
CC	-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC	-1- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/annouce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF037366; AAB92259.1; -		
DR	EMBL; AF041818; AAC83203.1; -		
DR	ENBL; AF041812; AAC83203.1; JOINED.		
DR	EMBL; AF041813; AAC83203.1; JOINED.		
DR	ENBL; AF041814; AAC83203.1; JOINED.		
DR	EMBL; AF041815; AAC83203.1; JOINED.		
DR	EMBL; AF041816; AAC83203.1; JOINED.		
DR	EMBL; AF041817; AAC83203.1; JOINED.		
DR	MGD; MGI:102805; Entpd1.		
DR	GO; GO:0005605; C:basal lamina; IDA.		
DR	GO; GO:0004050; F:apyrase activity; IDA.		
DR	GO; GO:0006200; P:ATP catabolism; IDA.		
DR	GO; GO:0003186; P:G-protein coupled receptor protein signalin. .; IDA.		
DR	GO; GO:0030168; P:platelet activation; IDA.		
DR	GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.		
DR	InterPro; IPR000407; GDAL_CD39_NTPase.		
DR	Pfam; PF011150; GDAL_CD39.1.		
DR	PROSITE; PS01238; GDAL_CD39_NTPASE; 1.		
KW	Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.		
FT	DOMAIN 1 16 Cytoplasmic (Potential).		
FT	TRANSMEM 17 37 Potential.		
FT	DOMAIN 38 478 Extracellular (Potential).		
FT	TRANSMEM 479 499 Potential.		
FT	DOMAIN 500 510 Cytoplasmic (Potential).		

```

RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN [4]
RP Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029512; BAC26485.1; -.
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:aprase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDA1_CD39_NTFase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 539 AA; 60590 MW; 49565788313321F4 CRC64;

Query Match 78.1%; Score 1830; DB 2; Length 539;
Best Local Similarity 76.4%; Pred. No. 7.1e-136;
Matches 336; Conservative 45; Mismatches 55; Indels 4; Gaps 3;

QY 1 QNKLPEVNVKGVILVDAGSSHTSLYIKWPAEKENDTGVHVECRVKGPGISKVFQVK 60
DB 68 QNKLPEVNVKGVILVDAGSSHTSLYIKWPAEKENDTGVHVECRVKGPGISKYQKT 127

QY 61 NEIGYITDCMERAREVTPRSHOQTPVYLGTAGMRLLRMESEBELADRVLDVVERSLN 120
DB 128 DEIGYLAECMELSTELIPTSKHQTVPVYLGTAGMRLLRMESEADEVLAAVSTSLKS 187

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QY 121 YPDPQGARITTOEGEAGYGWITINYLKFSQKTRWFSIVPVETNNQETFGALDLGGAS 180
DB 188 YPDPQGARITTOEGEAGYGWITINYLKFSQKTRWFSIVPVETNNQETFGALDLGGAS 246
QY 181 TQVTFVFNQNTIESPQNALQFRLYKDYNNVYTHFLCYGKQDQALWQKLAKDIQVANSBIL 240
DB 247 TQVTFVFNQNTIESPQNALQFRLYKDYNNVYTHFLCYGKQDQALWQKLAKDIQVANSBIL 306
QY 241 RDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPQOFIIGIGNYQQHQSHLELFTSYC 300
DB 307 KDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPQOFIIGIGNYQQHQSHLELFTSYC 366
QY 301 PYSOCANGLFLPQLQDGFASAFYFMKFLNLTSEK--VSQKVTMMKKFCAQPMEE 358
DB 367 PYSOCANGLFLPQLQDGFASAFYFMKFLNLTSEK--VSQKVTMMKKFCAQPMEE 426
QY 359 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTGLGYML 418
DB 427 TKTSYPSVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTGLGYML 485
QY 419 NLTNMIPAEQPLSPPLSHST 438
DB 486 NLTNMIPAEQPLSPPLSHST 505

RESULT 4
Q921Q6 PRELIMINARY; PRT; 510 AA.
ID AC Q921Q6;
DC 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Entpd1 protein.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011278; AAHL1278.1; -.
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:aprase activity; IDA.

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DR GO:0006400; P-ATP catabolism; IDA.
DR GO:0007186; P-G-protein coupled receptor protein signalin. ...; IDA.
DR GO:0030168; P-platelet activation; IDA.
DR GO:0009181; P-purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam: PF01150; GDA1_CD39_1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 77.9%; Score 1825; DB 2; Length 510;
Best Local Similarity 76.1%; Pred. No. 1.6e-135;
Matches 335; Conservative 45; Mismatches 56; Indels 4; Gaps 3;

QY 1 QNKALPENVKYGVILVADGSSHTSLIYKWPARKENDTGVVHGVCECRVKPGGIGSFVKV 60
Db 39 QNKALPENVKYGVILVADGSSHTSLIYKWPARKENDTGVVHGVCECRVKPGGIGSKYAQT 98

QY 61 NEIGLYLTDCHERAREVTPRSQHQSTPVYLGATAGWLLRWESEELADRVLDVVERSLN 120
Db 99 DEIGAYLAECMELSTELIPTSXHQTPVYLGATAGWLLRWESEELADRVLDVVERSLN 158

QY 121 YPFDQAGARIITQEGAGYGMTINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAS 180
Db 159 YPFDQAGARIITQEGAGYGMTINYLGRFTQEQSWLSLTS-DSQKQETFGALDLGGAS 217

QY 181 TQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVANSIL 240
Db 218 TQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVANSIL 277

QY 241 RDCPHRGYKVVVSDLYKTPCTKRFEMTLPPQFQFEGYGGYQCHQSILELNTSYC 300
Db 278 KDCPCNPGYKVVVSDLYKTPCTKRFEMTLPPQFQFEGYGGYQCHQSILELNTSYC 337

QY 301 PYSCAFNGIPLPQLOGDFGAFSAFYVFMKFLNLTSEK--VSOEKVTEMMKKFCAOPWEE 358
Db 338 PYSCAFNGIPLPQLOGDFGAFSAFYVFMKFLNLTSEK--VSOEKVTEMMKKFCAOPWEE 397

QY 359 IKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIFIKIQGSDAGWTLGYML 418
Db 398 IKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIFIKIQGSDAGWTLGYML 456

QY 419 NLTNMIPAEQPLSTPLSHST 438
Db 457 NLTNMIPAEQPLSTPLSHST 476

RESULT 5
Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TREMREL. 24, Created)
DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshynki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1;
DR GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000407; GDA1_CD39_NTPASE.
DR Pfam: PF01150; GDA1_CD39_1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; AB81DE136635EE3 CRC64;

Query Match 77.6%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.9e-135;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 MESEELADRVLDVVERSLSNYPDFQAGARIITQEGAGYGMTINYLKGFQSKTRWFSI 160
Db 1 MESEELADRVLDVVERSLSNYPDFQAGARIITQEGAGYGMTINYLKGFQSKTRWFSI 60

QY 161 VPYETNNQETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGK 220
Db 61 VPYETNNQETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGK 120

QY 221 DQALWQKLAKDIQVANSILRDCPHRGYKVVVSDLYKTPCTKRFEMTLPPQFQFEGYGG 280
Db 121 DQALWQKLAKDIQVANSILRDCPHRGYKVVVSDLYKTPCTKRFEMTLPPQFQFEGYGG 180

QY 281 IGNYQQCHQSILELNTSYCFYSCAFNGIPLPQLOGDFGAFSAFYVFMKFLNLTSEKVS 340
Db 181 IGNYQQCHQSILELNTSYCFYSCAFNGIPLPQLOGDFGAFSAFYVFMKFLNLTSEKVS 240

QY 341 QEKVTEMMKKFCAOPWEEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIF 400
Db 241 QEKVTEMMKKFCAOPWEEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIF 300

QY 401 FIGIKQSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 438
Db 301 FIGIKQSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 338

RESULT 6
ENP1_RAT STANDARD; PRT; 511 AA.
ID ENP1_RAT
AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase) (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
EX PubMed=9221928;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
RL apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302 (1997).
RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Cochlea; DOI=10.1016/S0169-328X(99)00244-2;
 RX MEDLINE=20050856; PubMed=10581401;
 RA Vlasjkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 termination of purinergic transmission.";
 RL Brain Res. Mol. Brain Res. 73:85-92(1999).
 RN [3]
 RP SEQUENCE OF 432-511 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
 RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 rat brain.";
 RL Neuropharmacology 36:1189-1200(1997).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
 kidney, liver, muscle, thymus, lung and spleen.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U81295; AAC53195.1; -;
 DR EMBL; Y15685; CAA75730.1; -;
 DR RGD; 69265; Entpd1.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 FT DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 511 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 332 332 P > L (in Ref. 2).
 SQ SEQUENCE 511 AA; 57408 MW; 4CC12D3B8644C193 CRC64;
 Query Match 76.4%; Score 1789.5; DB 1; Length 511;
 Best Local Similarity 74.5%; Pred. No. 1e-132;
 Matches 327; Conservative 51; Mismatches 58; Indels 3; Gaps 3;
 QY 2 NKALPENVKYGVILDAGSSHTSLYIKWPAKENDTGVVHVECRVKGPGISKVQKVN 61
 DB 40 NKPLPENVKYGVILDAGSSHTSLYIKWPAKENDTGVVHVECRVKGPGISKVQKTD 99
 QY 62 EIGIYLTDCMERAREVPRSQHQTTPVYLGTAGMRLRMESEELADRVLDVRSLSNY 121
 DB 100 EIAAYLAECMKMSTERIPASKQHQTTPVYLGTAGMRLRMESEELADRVLDVRSLSKY 159
 QY 122 PPDFOGARIITGOEBGAGWITINYLKGFQSKTRFISVIVETNNQTFPGALDGGAST 181
 DB 160 PPDFOGAKIITGOEBGAGWITINYLKGFQSKTRFIS-DSQKATFGALDGGST 218

182 QVTFVPOQTIESPDNALOPRLYKGDYVYTHSFLCYGKQDQALWQKLAKDIOVASNLR 241
 DB 219 QVTFVPLNQTLAPETISLQRLYGTDTVYTHSFLCYGKQDQALWQKLAKDIOVSSGGILK 278
 QY 242 DPCFHPGYKKVNVSDLYKTPCTKCFPMFTLPFOQFEIQGNYOQCHQSILLELFTSYCP 301
 DB 279 DPCFYPGYKKVNVSELYGTCTKCFEKLFPNQFQVQGTGDEYQCHQSILKFFNNSHCP 338
 QY 302 YSOCAFNGIELPLQDGFAGSAFYFWMKFL-NLTSEKV-SOEKVTEMMKKFCAQPWEI 359
 DB 339 YSOCAFNGVFLPLQSGFAGSAFYFVMDFFKQWANDSVSSQEKWTBITNFCSKPWEV 398
 QY 360 KTSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFGIKIOGSDAGTWLGYMLN 419
 DB 399 KASYPTVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFGIKIOGSDAGTWLGYMLN 458
 QY 420 LTNMIPAEQPLSTPLSHST 438
 DB 459 LTNMIPAEQPLSPPLPHST 477
 RESULT 7
 ID ENPI_PIG STANDARD; PRT; 510 AA.
 AC Q9MYU4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase)
 DE activation antigen) (Ecto-apyrase) (CD39 antigen).
 GN Name=ENTPD1; Synonyms=CD39;
 OS Sus scrofa (Pig);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9923;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic endothelium;
 RX MEDLINE=20325090; PubMed=1086813;
 RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O.,
 RA Sevigny J.;
 RT "Distribution, cloning, and characterization of porcine nucleoside
 triphosphate diphosphohydrolase-1.";
 RL Eur. J. Biochem. 267:4106-4114(2000).
 RN [2]
 RP SEQUENCE OF 202-220.
 RC TISSUE=Pancreas;
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Highest expression found in vascular
 endothelium, smooth muscle, spleen and lung.
 CC -1- PTM: Cleaved into two polypeptides that seem to stay together by
 noncovalent interactions.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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EMBL; AJ133746; CAB95871.1; -
InterPro: IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Magnesium; Transmembrane.
CHAIN 1 510
Ectonucleoside triphosphate
diphosphohydrolase 1.
FT CHAIN 1 201
Ectonucleoside triphosphate
diphosphohydrolase 1 27 kDa subunit.
FT CHAIN 202 510
Ectonucleoside triphosphate
diphosphohydrolase 1 54 kDa subunit.
FT CHAIN 1 16
Cytoplasmic (Potential).
FT DOMAIN 17 37
Potential.
FT DOMAIN 38 477
Extracellular (Potential).
FT TRANSMEM 478 498
Potential.
FT DOMAIN 499 510
Cytoplasmic (Potential).
FT CARBOHYD 73 73
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 245 245
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 274 274
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 291 291
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 333 333
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 370 370
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 457 457
N-linked (GlcNAc. .) (Potential).
FT CONFLICT 203 203
G -> S (in Ref. 2).
SQ SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;

Query Match 73.0%; Score 1710; DB 1; Length 510;
Best Local Similarity 70.6%; Pred. No. 2e-126;
Matches 310; Conservative 63; Mismatches 64; Indels 2; Gaps 2;

QY 1 QNKALPENVKGVILVDAGSSHTSLIYKWPAAKENDTGTVHQBECRVKGGISKFQKV 60
DB 39 QNKPLPENVKGVILVDAGSSHTSLIYKWPAAKENDTGTVHQBECRVKGGISKFQKV 98
QY 61 NEIGYLTDCMERAREVTPRSQHOETPVVLGATAGMRLRMESEBELADRVLDVVERSLN 120
DB 99 GEIDYLEACMERARTVVKQHAETPVVLGATAGMRLRMESEBELADRVLDVVERSLN 158
QY 121 YPFDQAGRIITQEGAGYMITINYLKFSQKTRWFSIYPIETNNQETFGALDLGAS 180
DB 159 YPFDQAGRIITQEGAGYMITINYLKFSQKTRWFSIYPIETNNQETFGALDLGAS 218
QY 181 TQVTFVPOQIESPDNALQRLYKDYNTVTHSPFLCYGKQOALMOKLAKIOVASNEIL 240
DB 219 TQITFPVQNVLESPEPTLHFLRYGKNSVYTHSPFLCYGKQOALMOKLAKIOVASNEIL 277
QY 241 RDCPHGKVKVNVSDLYKTPCTKREBMTLPFQOFEIQQIGNVOOCHQSILEFNTSYC 300
DB 278 HEPCHSGYQRMNVSHYEAFTKRLTSLPFPPELEIQTGDPKQOOSIRLPFNFSYC 337
QY 301 PYSQAFNGIIFLPLQGGFGAFSAFYVMKFLNLTSEKVS-QEKVTENMKKFCQAPWBEI 359
DB 338 PYSRCSFGVFLPLPQGGFAFSAFYVMKFLNLTSEKVSFQSKVTSLFAFCSPRAEL 397
QY 360 KTSVAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWBHHPIGKIQSDAGWTLYMLN 419
DB 398 QMYGDKVKEKYLSEYCFSGTIVLSLLQGYHFTADSWBHHPIGKIQSDAGWTLYMLN 457
QY 420 LTNMIPASQPLSTPLSHST 438
DB 458 LTNMIPSEPSSTRUSHST 476

RESULT 8
ENP1_BOVIN STANDARD; PRT; 513 AA.

ID ENP1_BOVIN
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPD1; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RT Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RL diphosphohydrolase";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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EMBL; AF005940; AAB62382.1; -
InterPro: IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Magnesium; Transmembrane.
DOMAIN 1 16
CYTOPLASMIC (Potential).
FT TRANSMEM 17 37
Potential.
FT DOMAIN 38 481
Extracellular (Potential).
FT TRANSMEM 482 502
Potential.
FT DOMAIN 503 513
CYTOPLASMIC (Potential).
FT CARBOHYD 73 73
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 227 227
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 245 245
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 307 307
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 336 336
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 373 373
N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 460 460
N-linked (GlcNAc. .) (Potential).
FT CONFLICT 97 97
K -> N (in Ref. 2).
FT CONFLICT 101 103
INV -> CGF (in Ref. 2).
FT CONFLICT 464 464
K -> V (in Ref. 2).
SQ SEQUENCE 513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;

Query Match 71.9%; Score 1685.5; DB 1; Length 513;
Best Local Similarity 69.7%; Pred. No. 1.7e-124;
Matches 308; Conservative 64; Mismatches 65; Indels 5; Gaps 3;

QY 1 QNKALPENVKGVILVDAGSSHTSLIYKWPAAKENDTGTVHQBECRVKGGISKFQKV 60
DB 39 QNKALPENVKGVILVDAGSSHTSLIYKWPAAKENDTGTVHQBECRVKGGISKFQKV 98


```

Qy 61 NEIGYLTDCMERAREVTPRSHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN 120
Db 99 NEINVLTFACMERAKVLPSTQHMETPVYLGATAGMRLRMESEELADRVLDVVERSLN 158
Qy 121 YPFQFQAGRIITQOEGAGYATTINYLKGFQKTRWFSIVPYETNNQETFGALDGGAS 180
Db 159 YPFQFQAGRIITQOEGAGYATTINYLKGFQKTRWFSIVPYETNNQETFGALDGGAS 218
Qy 181 TQVTFVPOQNTIESPDNALQPRLYGKYNVYTHFLCYGKQDQALWQKLAKDIQVASEIL 240
Db 219 TQVTFVPOQNTIESPDNALQPRLYGKYNVYTHFLCYGKQDQALWQKLAKDIQVASEIL 277
Qy 241 RDPCHFGYKVVNVSDLYKTPCTKREMT---LPQOFEILOGIYGVYQCHOSITLLEPNT 297
Db 278 HEPCHFGYKVVNVSDLYKTPCTKREMT---LPQOFEILOGIYGVYQCHOSITLLEPNT 337
Qy 298 SYCPYSCAFNGIIFLPPLOQDFGAFSAFYVMKFLNLTSEK-VSOEKVTENMKKFCQAPW 356
Db 338 SYCPYSCAFNGIIFLPPLOQDFGAFSAFYVMKFLNLTSEK-VSOEKVTENMKKFCQAPW 397
Qy 357 EEIKTSYAGVKEKYLSEYCFSGTGYLSSLLQGYHFTADSWHIIHFIQKIQSDAGWTIGY 416
Db 398 EEIKTSYAGVKEKYLSEYCFSGTGYLSSLLQGYHFTADSWHIIHFIQKIQSDAGWTIGY 457
Qy 417 MLNLTNNIPAEQPLSTPLSHST 438
Db 458 MLNLTNNIPAEQPLSTPLSHST 479

RESULT 9
Q8CEB1 PRELIMINARY; PRT; 420 AA.
ID Q8CEB1
AC Q8CEB1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732419M16 product:ectonucleoside triphosphate
DE diaphosphorylase 1, full insert sequence. (fragment).
GN Name=Entpd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN PANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tgami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1;
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:apyrase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
Query Match 67.2%; Score 1574; DB 2; Length 420;
Best Local Similarity 74.5%; Pred. No. 8.5e-116;
Matches 289; Conservative 42; Mismatches 53; Indels 4; Gaps 3;
Qy 53 ISKPVQKNEIGIYLTDCMERAREVTPRSHOETPVYLGATAGMRLRMESEELADRVLD 112
Db 1 ISKPVQKNEIGIYLTDCMERAREVTPRSHOETPVYLGATAGMRLRMESEELADRVLD 60
Qy 113 VVERSLNYPDFOGARIITQOEGAGYATTINYLKGFQKTRWFSIVPYETNNQETFG 172
Db 61 AVSTLSKSYFPDFOGAKIITQOEGAGYATTINYLKGFQKTRWFSIVPYETNNQETFG 119
Qy 173 ALDILGGASTQVTFVPOQNTIESPDNALQPRLYGKYNVYTHFLCYGKQDQALWQKLAKDI 232
Db 120 ALDILGGASTQVTFVPOQNTIESPDNALQPRLYGKYNVYTHFLCYGKQDQALWQKLAKDI 179
Qy 233 QVASENLRDPCFHPGKVVNVSDLYKTPCTKREMTLPQOFEILOGIYGVYQCHOSIL 292
Db 180 QVSSGGVLKDCPCFNPGEYKVVNVSELYGTPCTKREMTLPQOFEILOGIYGVYQCHOSIL 239
Qy 293 ELFNITSYCPYSCAFNGIIFLPPLOQDFGAFSAFYVMKFLNLTSEK-VSOEKVTENMKK 350
Db 240 ELFNITSYCPYSCAFNGIIFLPPLOQDFGAFSAFYVMKFLNLTSEK-VSOEKVTENMKK 299
Qy 351 FCAQFWEEIKTSYAGVKEKYLSEYCFSGTGYLSSLLQGYHFTADSWHIIHFIQKIQSDA 410

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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073267; AAH73267.1; -.
DR GO; 0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; 1.
SQ SEQUENCE 508 AA; 57049 MW; BD205818A0C523B CRC64;

Query Match 60.5%; Score 1418; DB 2; Length 508;
Best Local Similarity 59.1%; Pred. No. 2.3e-103;
Matches 259; Conservative 72; Mismatches 105; Indels 2; Gaps 2;

Qy 1 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVQKV 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 39 QNKLPKNIKYGVLDAGSSHTSVIYEWPEKENDTGVVQVQINDCKVEGNGISYQHEP 98
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 99 TKAGLSLQKCNKARQVPEMQOKETPVYLGATAGMRLLRNNATMAEVLSSVENMLRS 158
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 YPDPQAGARIITQEGAGYGMITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGAS 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 159 YPDPQAGARIITQEGAGYGMITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGAS 217
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 TQVTFVPCNQTIESPDNALQFRLYGKDVNYVTHSFLCYGKQDALWQKLAKDIQVASNEIL 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 218 TQITFESKKE-IESQENSLHFLYKSDVYVTHSFLCYGKQDALWQKLAKDIQVASNEIL 276
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 RDPCEPHGPKYKVVNSDYLYKTPCTKRFEMTLFPQOFEIIGIGNYQCHQSILELFTSYC 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 277 MDPCFNSGYYRNTSTSDLYSSPCISNLRAISTAPSLDVKGTGNYQLCKRNVEAIFDRTRC 336
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 PYSQCAFNGIFLPPLOGDFGAFSAFYFWMKFLNLTSEKVSQEKVTEMKFKCAOPWEEK 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 337 TYSKCSFNGIFQFTLDGTGFCGAFSAFYFWMKFLNLTSEKVSQEKVTEMKFKCAOPWEEK 396
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 TSVAGVKELSEYCFSGTYILSLLOQVHFTADSWEHIFTKIQSDAGWTGLGYMLNL 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 397 KEFKPKIKELSEYCFSGTYILSLLOQVHFTADSWEHIFTKIQSDAGWTGLGYMLNL 456
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 TNMIPAEQPLSTPLSH 438
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 457 TNMIPAEQPLSTPLSH 474
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q6DC46 PRELIMINARY; PRT; 492 AA.
AC Q6DC46;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:100819 protein.
GN Names:zgc:100819;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,
```

diphosphohydrolase.";

J. Biol. Chem. 273:16043-16049(1998).

[2]

SEQUENCE OF 1-17.

TISSUE=Stomach;

MEDLINE#97442428; PubMed#9295305; DOI#10.1074/jbc.272.38.23645;

Lewis-Carl S., Kitley T.L.;

"Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken gizzard and stomach. Purification and N-terminal sequence of the stomach ecto-apyrase."

J. Biol. Chem. 272:23645-23652(1997).

-I- FUNCTION: In the nervous system, could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation.

Hydrolyzes ATP and ADP equally well [By similarity].

-I- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.

-I- COFACTOR: Requires calcium and magnesium (By similarity).

-I- SUBUNIT: Homodimer; disulfide-linked (Probable).

-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-I- PTM: N-glycosylated.

-I- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

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EMBL; AF041355; AAC26491.1; --

InterPro; IPR000407; GDA1_CD39_NTPase.

Pfam; PF01150; GDA1_CD39_1.

DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.

KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase; Magnesium; Transmembrane.

KW DOMAIN 1 7 Cytoplasmic (Potential).

FT TRANSMEM 8 28 Potential.

FT DOMAIN 29 463 Extracellular (Potential).

FT TRANSMEM 464 486 Potential.

FT DOMAIN 487 493 Potential.

FT CARBOHYD 65 65 Cytoplasmic (Potential).

N-linked (GlcNAc..) (Potential).

FT CARBOHYD 79 79 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 133 133 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 223 223 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 234 234 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 267 267 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 324 324 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 330 330 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 361 361 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 372 372 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 382 382 N-linked (GlcNAc..) (Potential).

FT CARBOHYD 445 445 N-linked (GlcNAc..) (Potential).

C -> W (in Ref. 2).

FT CONFLICT 16 16

FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).

SQ SEQUENCE 493 AA; 54034 MW; F14FF4C3AA2F3603 CRC64;

Query Match 42.9%; Score 1004; DB 1; Length 493;

Best Local Similarity 45.7%; Pred.No. 1.1e-70;

Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

QY 5 LPENVKYGVLVDAGSSHTSLYIKVPAEKENDTGVVHVEECRVKGPGISKVKVNEIG 64
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 35 LPPGTGIKGLVFDDGSTHTALYVTQWPADKENGTVISQVESCTVNGSGISSYADDPAGAG 94
|||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

QY 65 IVLTDCMERAREVIPRSQHQTPTPYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFD 124
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 95 ASLKPCLDKRAMAIVPEQQWQFTYLGAAGMRLLREQNSTKAEQVFAEVSKAIRFPVD 154
|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

QY 125 FGARIITCGERAGYWITINILLG---KFOSKTRWFSTVPVETNNQETFGALDLGGAST 191
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 155 FRQAQILTNEGSGFWITVNTLLETFLIFSPAGKW-----BHPQNTEVLGALLDGAST 209
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

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Qy 182 QVTFVPCQNTIESPDNALQRLYKGYNNVYTHSFLCYGKDOA---LWOKLAKDIOVASNE 238
Db 210 QITFQP-GVTIEDKNTSVLFRLYGTNYSLYTHSLCYGQIQASKRLMAALHQDGSYVQN- 267
Qy 239 ILRDCPFHFGYKVVNVDLYKTCTKRFEMTLPPFQQFEIQGIGNYQQCHQSILELFNTS 298
Db 268 -ISHPCYKPGYRRITIAEIVDSPCVTPPSMLSPAQILTVTGTGNPAACPTAILKLEFNT 326
Qy 299 YCPYSQCAFNGIFLPPLOQDGFASAFYFVWKFLNLTSEKVSQEKVTEMKFKCAQPWEE 358
Db 327 CGANRTCGFDGVYPPVRGQFFAFGYTTFSLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
Qy 359 IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGTKIOGSDAGWTGLYML 418
Db 386 LVETFPQNK-ELHTYCVWGLYILTLVDGKFDHTWSNIHFSQKAGNADIGWTGLFML 444
Qy 419 NLTNMIPAE 427
Db 445 NLTNMIPTE 453

RESULT 15
Q90X66
ID Q90X66 PRELIMINARY; PRT; 493 AA.
AC Q90X66;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21982040; PubMed=11985621;
RA Knowles A.F., Negy A.K., Strobel R.S., Wu-Weis M.;
RT "Purification, characterization, cloning, and expression of the
RT chicken liver ecto-ATP-diphosphohydrolase.";
RL Eur. J. Biochem. 269:2373-2382(2002).
DR EMBL; AF426405; AAL25086.1; -
DR GO; GO:0004050; F:apyrase activity; IEA.
DR GO; GO:0016787; E:hydrolase activity; IEA.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;

Query Match 42.6%; Score 997; DB 2; Length 493;
Best Local Similarity 45.7%; Pred. No. 3.9e-70;
Matches 196; Conservative 72; Mismatches 145; Indels 16; Gaps 7;

Qy 5 LPENVKYGILVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGIGSKFVKVNEIG 64
Db 35 LPPGTGYGLVFDAGSTHTALVYQWPAKENGTVGVSQVESCIVNGSGISSYADDPAG 94
Qy 65 IYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLVDVRSISNYPFD 124
Db 95 ASLKPCLDKAMAVIPEQWOTPTVYLGATAGMRLRMESEELADRLVDVRSISNYPFD 154
Qy 125 FQGAIIITQOEGAGYGTINVLG---KFSQKTFWFSIVPYETNNQETFGALDILGGAST 181
Db 155 FRGAQLTNGERGSFGVITVNYLLETLLKFSFAGKW-----EHPQNTFVLGALDILGGAST 209
Qy 182 QVTFVPCQNTIESPDNALQRLYKGYNNVYTHSFLCYGKDOA---LWOKLAKDIOVASNE 238
Db 210 QITFQP-GVTIEDKNTSVLFRLYGTNYSLYTHSLCYGQIQASKRLMAALHQDGSYVQN- 267
Qy 239 ILRDCPFHFGYKVVNVDLYKTCTKRFEMTLPPFQQFEIQGIGNYQQCHQSILELFNTS 298
Db 268 -ISHPCYKPGYRRITIAEIVDSPCVTPPSMLSPAQILTVTGTGNPAACPTAILKLEFNT 326
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Qy 299 YCPYSQCAFNGIFLPPLOQDGFASAFYFVWKFLNLTSEKVSQEKVTEMKFKCAQPWEE 358
Db 327 CGANRTCGFDGVYPPVRGQFFAFGYTTFSLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
Qy 359 IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGTKIOGSDAGWTGLYML 418
Db 386 LVETFPQNK-ELHTYCVWGLYILTLVDGKFDHTWSNIHFSQKAGNADIGWTGLFML 444
Qy 419 NLTNMIPAE 427
Db 445 NLTNMIPTE 453
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Search completed: March 7, 2005, 13:22:41
Job time : 62.3608 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 71.5518 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147A-2_COPY_39_476
Perfect score: 2343
Sequence: 1_QNKALPENVKYIVLDAGSS.....NLTNMPABQPLSTPLSHST 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2343	100.0	439	4	Aab71918 Soluble h
2	2343	100.0	454	3	Aay70913 Human sol
3	2343	100.0	454	3	Aay70890 Protein e
4	2343	100.0	463	3	Aay70925 Human sol
5	2343	100.0	463	3	Aay70902 Protein e
6	2343	100.0	464	3	Aay70922 Human sol
7	2343	100.0	464	3	Aay70899 Protein e
8	2343	100.0	473	3	Aay70924 Human sol
9	2343	100.0	473	3	Aay70901 Protein e
10	2343	100.0	474	3	Aay70923 Human sol
11	2343	100.0	474	3	Aay70900 Protein e
12	2343	100.0	476	3	Aay70911 Human CD3
13	2343	100.0	476	3	Aay70888 Protein e
14	2343	100.0	478	3	Aay70914 Human sol
15	2343	100.0	478	3	Aay70891 Protein e
16	2343	100.0	487	3	Aay70921 Human sol
17	2343	100.0	487	3	Aay70898 Protein e
18	2343	100.0	510	2	Aaw04334 Human lym
19	2343	100.0	510	2	Aaw04264 Human CD3
20	2343	100.0	510	3	Aay70910 Human sol
21	2343	100.0	510	3	Aay70887 Human sol
22	2343	100.0	510	4	Aab71917 Human CD3
23	2343	100.0	510	7	Adj57262 Human CD3
24	2343	100.0	510	8	Adl24295 Human CD3
25	2343	100.0	510	8	Adq99453 Human CD3

26	2343	100.0	510	8	ADR69210 Human CD3
27	2343	100.0	510	8	ADR69042 Human CD3
28	2343	100.0	510	8	ADR17924 Human CD3
29	2343	100.0	510	8	ABO84674 Human can
30	2343	100.0	510	8	ADR87821 Human CD3
31	2343	100.0	511	8	Adk60421 Angiogene
32	2343	100.0	511	8	Adk60722 Angiogene
33	2343	100.0	511	8	Adp73345 CD39 lym
34	2343	100.0	517	7	Adn95839 Human BEC
35	2343	100.0	517	8	Adk60221 Angiogene
36	2343	100.0	517	8	Adk60522 Angiogene
37	2343	100.0	517	8	Adp73145 Angiogene
38	2343	100.0	522	8	ABO84672 Human can
39	2294	97.9	476	3	Aay70912 Human CD3
40	2294	97.9	476	3	Aay70889 Protein e
41	2294	97.9	529	8	ABM83376 Human dia
42	2136	91.2	503	8	ABM83377 Human dia
43	1969	84.0	402	8	ABO84671 Human can
44	1841	78.6	377	7	Adl62735 Human apo
45	1118	47.7	311	8	ABO84673 Human can

ALIGNMENTS

RESULT 1
AAB71918
ID AAB71918 standard; protein; 439 AA.
XX
AC AAB71918;
XX
DT 09-MAY-2001 (first entry)
XX
DE Soluble human CD39 polypeptide.
XX
KW Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
KW stroke; thrombotic disorder; ischaemic disorder.
XX
OS Homo sapiens.
XX
PN WO2000111949-A1.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022060.
XX
PR 13-AUG-1999; 99US-00374586.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Pinsky DJ;
XX
DR WPI; 2001-202805/20.
XX
PT Treating stroke in a subject susceptible to intracranial hemorrhaging and
PT an ischemic disorder, involves administering a CD39 polypeptide which
PT inhibits ADP-mediated platelet aggregation or leukocyte accumulation.
XX
PS Claim 3; Page 14; 118pp; English.
XX
CC The present sequence is the active fragment of human CD39. CD39 or its
CC active fragment may be administered to treat or prevent stroke in a
CC subject susceptible to intracranial haemorrhaging or an ischaemic
CC disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
CC or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
CC subject. CD39 or its active fragment is useful for treating or preventing
CC stroke, thrombotic disorders and ischaemic disorders such as peripheral
CC vascular disorder, pulmonary embolus, venous thrombosis, myocardial
CC infarction, transient ischaemic attack, unstable angina, reversible
CC ischaemic neurological deficit and sickle cell anaemia. It is also useful
CC for treating or preventing a stroke disorder in a subject undergoing
CC heart surgery, lung surgery, spinal surgery, brain surgery, vascular
CC surgery, abdominal surgery, or organ transplantation surgery

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XX SQ Sequence 439 AA;
Query Match 100.0%; Score 2343; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGWHQVEECRVKPGISKFKVQKV 60
DB 2 QNKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGWHQVEECRVKPGISKFKVQKV 61
QY 61 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESSELDADRVLDVVERSLN 120
DB 62 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESSELDADRVLDVVERSLN 121
QY 121 YPFPDQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 180
DB 122 YPFPDQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 181
QY 181 TQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIOVASNEIL 240
DB 182 TQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIOVASNEIL 241
QY 241 RDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFIEIQIGNYQQCHQSILELFTNSYC 300
DB 242 RDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFIEIQIGNYQQCHQSILELFTNSYC 301
QY 301 PYSQCAFNGIFLPLQDGFAGSAPFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIK 360
DB 302 PYSQCAFNGIFLPLQDGFAGSAPFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIK 361
QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIGIKIQGSDAGWTLYMLNL 420
DB 362 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIGIKIQGSDAGWTLYMLNL 421
QY 421 TNMIPAEQPLSTPLSHST 438
DB 422 TNMIPAEQPLSTPLSHST 439

RESULT 2
AAV70913
ID AAV70913 standard; protein; 454 AA.
XX AC AAV70913;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.
XX KW Soluble CD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiatic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Protein 1..15
FT /label= Mature human interleukin_2
FT /note= "N-terminal region"
FT Protein 16..454
FT /note= "Human soluble CD39 protein"
XX WO200023459-A1.
XX PD 27-APR-2000.
XX
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PF 13-OCT-1999; 99WO-US022955.
XX 16-OCT-1998; 98US-0104585P.
PR 08-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX (IMMV ) IMMUNEX CORP.
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
DR N-PSDB; AAD00206.
XX New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
FT infarction, stroke, coronary artery disease or injury.
XX Claim 6a; Page 95-97; 122pp; English.
XX The present sequence is a fusion construct, comprising the N-terminal
CC amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
CC region, that has apyrase activity. This results in high levels of solCD39
CC expression and activity in the transfected cells. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations
CC and the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
CC embolism, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX SQ Sequence 454 AA;
Query Match 100.0%; Score 2343; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGWHQVEECRVKPGISKFKVQKV 60
DB 17 QNKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGWHQVEECRVKPGISKFKVQKV 76
QY 61 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESSELDADRVLDVVERSLN 120
DB 77 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESSELDADRVLDVVERSLN 136
QY 121 YPFPDQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 180
DB 137 YPFPDQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 196
QY 181 TQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIOVASNEIL 240
DB 197 TQVTFVQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDIOVASNEIL 256
QY 241 RDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFIEIQIGNYQQCHQSILELFTNSYC 300
DB 257 RDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFIEIQIGNYQQCHQSILELFTNSYC 316
QY 301 PYSQCAFNGIFLPLQDGFAGSAPFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIK 360
DB 317 PYSQCAFNGIFLPLQDGFAGSAPFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWBEIK 376
QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIGIKIQGSDAGWTLYMLNL 420
DB 377 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIGIKIQGSDAGWTLYMLNL 436
QY 421 TNMIPAEQPLSTPLSHST 438
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Db 437 TNMIPAEQPLSTPLSHST 454
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RESULT 3
AAV70890
ID AAV70890 standard; protein; 454 AA.
XX AC AAV70890;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by fusion construct of human soluble CD39 cDNA-1.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
XX KW unstable angina; myocardial infarction; stroke; coronary artery disease;
XX KW atherosclerosis; peripheral vascular occlusion; preecclampsia; embolism;
XX KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
XX KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
XX KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
XX KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
XX KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
XX KW occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiant;
XX KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
XX KW coronary ischaemia; vascular occlusion.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key : Location/Qualifiers
XX FT Protein 1..15
XX FT /label= Mature human interleukin_2
XX FT /note= "N-terminal region"
XX FT Protein 16..454
XX FT /note= "Human soluble CD39 protein"
XX FT
XX FT WO200023094-A2.
XX PN
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US023641.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX XX (IMMUNEX CORP.
XX XX (CORR ) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX DR WPI; 2000-339518/29.
XX DR N-PSDB; AAD00201.
XX XX
XX PT Inhibiting platelet activation and recruitment, useful for treating a
XX PT mammal suffering from unstable angina, myocardial infarction, stroke,
XX PT coronary artery disease or injury, comprises administering soluble CD39
XX PT polypeptides.
XX XX
XX PS Claim 6; Page 95-97; 118pp; English.
XX XX
CC CC The present sequence is the protein encoded by a fusion construct of
CC CC sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from
CC CC the N-terminus of mature human IL2 to the solCD39 coding region results
CC CC in high levels of both expression and activity in the supernatants of
CC CC transfected cells. This is used in the treatment of unstable angina,
CC CC myocardial infarction, stroke, coronary artery disease or injury,
CC CC atherosclerosis, peripheral vascular occlusion, preecclampsia, embolism,
CC CC platelet-associated ischaemic disorder including lung ischaemia, coronary
CC CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
CC CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC CC
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CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX SQ Sequence 454 AA;
Query Match 100.0%; Score 2343; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFKVKV 60
DB 17 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFKVKV 76
QY 61 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLN 120
DB 77 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLN 136
QY 121 YPFDFOGARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAS 180
DB 137 YPFDFOGARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAS 196
QY 181 TQVTFVFNQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIQVANSNEIL 240
DB 197 TQVTFVFNQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDALWQKLAKDIQVANSNEIL 256
QY 241 RDPCHFPGYKVVNVNVDLYKTPCTKRFEMTLPFQOFEIQIGIGNYQQCHQSILEFNTSYC 300
DB 257 RDPCHFPGYKVVNVNVDLYKTPCTKRFEMTLPFQOFEIQIGIGNYQQCHQSILEFNTSYC 316
QY 301 PYSQCAFNGIFLPPLOQDFGAFSAFYFMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEK 360
DB 317 PYSQCAFNGIFLPPLOQDFGAFSAFYFMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEK 376
QY 361 TSYAGVKEKYLSEYCSFGTILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYMLNL 420
DB 377 TSYAGVKEKYLSEYCSFGTILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYMLNL 436
QY 421 TNMIPAEQPLSTPLSHST 438
DB 437 TNMIPAEQPLSTPLSHST 454
RESULT 4
AAV70925
ID AAV70925 standard; protein; 463 AA.
XX AC AAV70925;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 fusion protein construct, IgkappaLsolCD39.
XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
XX KW unstable angina; myocardial infarction; stroke; coronary artery disease;
XX KW atherosclerosis; peripheral vascular occlusion; preecclampsia; embolism;
XX KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
XX KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
XX KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
XX KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
XX KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig;
XX KW immunoglobulin kappa.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key : Location/Qualifiers
XX FT Peptide 1..20
XX FT /label= Leader peptide
XX FT /note= "Derived from human immunoglobulin Ig kappa"
XX FT Cleavage-site 20..21
XX FT /note= "Cleavage site of leader sequence"
XX FT Region 21..24
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FT	Protein	/note= "Residues derived from human interleukin 2 (IL2)"	
FT		25. .463	
FT		/note= "Human soluble CD39 protein"	
XX	WO200023459-A1.		
XX	27-APR-2000.		
XX	13-OCT-1999;	99WO-US0222955.	
XX	16-OCT-1998;	98US-0104585P.	
PR	06-NOV-1998;	98US-0107466P.	
PR	13-AUG-1999;	99US-0149010P.	
XX	(IMMV) IMMUNEX CORP.		
XX	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;		
XX	WPI; 2000-339644/29.		
XX	New soluble CD39 polypeptides having apyrase activity, useful for		
FT	inhibiting angiogenesis and treating unstable angina, myocardial		
PT	infarction, stroke, coronary artery disease or injury.		
XX	Claim 6; Page 116-118; 122pp; English.		
XX	The present sequence is the fusion protein construct, IgpappaSolCD39.		
CC	This construct comprises of the leader peptide from human immunoglobulin		
CC	Ig kappa, linked to the soluble CD39 (solCD39) protein region by few		
CC	residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase		
CC	activity and is constructed by removing the N- and C-terminal		
CC	transmembrane domains. It retains the capacity to metabolise ATP and ADP		
CC	at relevant concentrations and the ability to block and reverse ADP-		
CC	induced platelet activation and recruitment, including platelet		
CC	aggregation. Soluble CD39 polypeptides are useful for inhibiting		
CC	angiogenesis. It is useful for the treatment of unstable angina, stroke,		
CC	myocardial infarction, coronary artery disease or injury, embolism,		
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-		
CC	associated ischaemic disorders including lung, coronary and cerebral		
CC	ischaemia, thrombotic disorders including coronary, peripheral and		
CC	cerebral artery thrombosis, intracardiac and venous thrombosis,		
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and		
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing		
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or		
CC	restenosis of blood vessels or stroke		
XX			
SQ	Sequence 463 AA;		
	Query Match	100.0%; Score 2343; DB 3; Length 463;	
	Best Local Similarity	100.0%; Pred. No. 1.2e-230;	
	Matches 438; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QNKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTG VHQVECRVKGPGISKFTQKV 60		
Db	26 QNKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTG VHQVECRVKGPGISKFTQKV 85		
QY	61 NEIGYILTDCMERAREVTPRSQHQETPVYLGATAGMRLLRMESELADRLDVVRSLSN 120		
Db	86 NEIGYILTDCMERAREVTPRSQHQETPVYLGATAGMRLLRMESELADRLDVVRSLSN 145		
QY	121 YPFDFQGARITITQEGAYGWTITNLLGKFSQKTRWFISIVPYETNNQETFGALDLGGAS 180		
Db	146 YPFDFQGARITITQEGAYGWTITNLLGKFSQKTRWFISIVPYETNNQETFGALDLGGAS 205		
QY	181 TQVTFVPPQNQTIESPDNALQFLRYGKDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSN 240		
Db	206 TQVTFVPPQNQTIESPDNALQFLRYGKDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSN 265		
QY	241 RDCPFHGGYKVVNYSYLYKTPCTKRFWTLPFQOFELQIGNYQOCHQSILELFTSYC 300		
Db	266 RDCPFHGGYKVVNYSYLYKTPCTKRFWTLPFQOFELQIGNYQOCHQSILELFTSYC 325		
QY	301 PYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEK 360		

Db	326 PYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEEK 385		
QY	361 TSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFGIKIOGSDAGWTGLGYMLNL 420		
Db	386 TSYAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHFGIKIOGSDAGWTGLGYMLNL 445		
QY	421 TNMIPAEQPLSTPLSHST 438		
Db	446 TNMIPAEQPLSTPLSHST 463		
RESULT 5			
AAAY70902			
ID	AAAY70902 standard; protein; 463 AA.		
XX	AAAY70902;		
XX	17-AUG-2000 (first entry)		
XX	Protein encoded by IgpappaSolCD39 construct.		
XX	Soluble CD39; ADP-induced platelet activation; platelet aggregation;		
KW	unstable angina; myocardial infarction; stroke; coronary artery disease;		
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;		
KW	platelet-associated ischaemic disorder; lung ischaemia; thrombotic;		
KW	cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;		
KW	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;		
KW	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;		
KW	PE; pulmonary embolism; transient ischaemic attack; thrombus formation;		
KW	occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiac;		
KW	cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;		
KW	coronary ischaemia; vascular occlusion; IgpappaSolCD39 construct.		
XX	Homo sapiens.		
OS	Synthetic.		
XX			
XX	Key	Location/Qualifiers	
FT	Peptide	1. .20	
FT		/note= "Igpappa leader sequence"	
FT	Cleavage-site	20. .21	
FT	Region	21. .24	
FT		/note= "Derived from IL-2"	
FT	Region	25. .463	
FT		/note= "Soluble portion of CD39"	
FT	Region	25. .32	
FT		/note= "Derived from solCD39"	
XX	WO200023094-A2.		
XX	27-APR-2000.		
XX	13-OCT-1999;	99WO-US023641.	
XX	16-OCT-1998;	98US-0104585P.	
PR	06-NOV-1998;	98US-0107466P.	
PR	13-AUG-1999;	99US-0149010P.	
XX	(IMMV) IMMUNEX CORP.		
FA	(CORR) CORNELL RES FOUND INC.		
XX	Maliszewski CR, Gayle RB, Marcus AJ;		
XX	WPI; 2000-339518/29.		
XX	Inhibiting platelet activation and recruitment, useful for treating a		
PT	mammal suffering from unstable angina, myocardial infarction, stroke,		
PT	coronary artery disease or injury, comprises administering soluble CD39		
PT	polypeptides.		
XX	Claim 6; Page 116-118; 118pp; English.		
XX	The present sequence is the protein encoded by IgpappaSolCD39 construct.		
CC			

CC This is used for transient expression of soluble(sol)CD39 in recombinant
CC cells for determining enzymatic activity and platelet inhibitory activity
CC for each protein product. SolCD39 is used in the treatment of unstable
CC angina, myocardial infarction, stroke, coronary artery disease or injury,
CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
CC platelet-associated ischaemic disorder including lung ischaemia, coronary
CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke

XX SQ Sequence 463 AA;

Query Match 100.0%; Score 2343; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.2e-230; Indels 0; Gaps 0;
Matches 438; Conservative 0; Mismatches 0;
QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKFVKV 60
Db 26 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKFVKV 85
QY 61 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEBELADRVLDVVERSLN 120
Db 86 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEBELADRVLDVVERSLN 145
QY 121 YPFDQAGARIITGOEGAGWITINYLKGFQSKTRWFESIVPYETNNQETFGALDLGAS 180
Db 146 YPFDQAGARIITGOEGAGWITINYLKGFQSKTRWFESIVPYETNNQETFGALDLGAS 205
QY 181 TQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIOVASNEIL 240
Db 206 TQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIOVASNEIL 265
QY 241 RDPCHPGYKVVNVDLYKTPCTKRFEMTLPPQFQFEIGIGNYQOCHOSILELPNTSYC 300
Db 266 RDPCHPGYKVVNVDLYKTPCTKRFEMTLPPQFQFEIGIGNYQOCHOSILELPNTSYC 325
QY 301 PYSQAFNGIFLPPQGGPAGFSAFYVWKFNLNTSEKVSQKVTMMKKKCAQPWEEK 360
Db 326 PYSQAFNGIFLPPQGGPAGFSAFYVWKFNLNTSEKVSQKVTMMKKKCAQPWEEK 385
QY 361 TSYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSDAGWTLGYMLNL 420
Db 386 TSYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGSDAGWTLGYMLNL 445
QY 421 TNMIPAEQPLSTPLSHST 438
Db 446 TNMIPAEQPLSTPLSHST 463

RESULT 6

AAAY70922
ID AAAY70922 standard; protein; 464 AA.

AC AAAY70922;

XX 17-AUG-2000 (first entry)

DE Human soluble CD39 fusion protein construct, pIL2LTrim1.

KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers
Peptide 1..24

FT /label= Leader peptide
FT /note= "Derived from human interleukin 2 (hIL2)"

FT Cleavage-site 24..25

FT /note= "Cleavage site of leader sequence"

FT Protein 26..464

FT /note= "Human soluble CD39 protein"

PN WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

PT New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.

PS Claim 6; Page 111-112; 122pp; English.

CC The present sequence is the fusion protein construct, pIL2LTrim1. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity. The
CC two regions are joined by an intervening Ala residue. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations
CC and the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, stroke, myocardial infarction, coronary artery disease
CC or injury, embolism, atherosclerosis, peripheral vascular occlusion,
CC preclampsia, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke

SQ Sequence 464 AA;

Query Match 100.0%; Score 2343; DB 3; Length 464;

Best Local Similarity 100.0%; Pred. No. 1.2e-230;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKFVKV 60

Db 27 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKFVKV 86

QY 61 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEBELADRVLDVVERSLN 120

Db 87 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEBELADRVLDVVERSLN 146

QY 121 YPFDQAGARIITGOEGAGWITINYLKGFQSKTRWFESIVPYETNNQETFGALDLGAS 180

Db 147 YPFDQAGARIITGOEGAGWITINYLKGFQSKTRWFESIVPYETNNQETFGALDLGAS 206

QY 181 TQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIOVASNEIL 240

Db 207 TQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIOVASNEIL 266

QY 241 RDPCHFGYKVVNVDLYKTPCTKRFEMTLFQQFEIQGIGNYQQCHQSILELFTSYC 300
 DB 267 RDPCHFGYKVVNVDLYKTPCTKRFEMTLFQQFEIQGIGNYQQCHQSILELFTSYC 326
 QY 301 PYSQAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 360
 DB 327 PYSQAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 386
 QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMNL 420
 DB 387 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMNL 446
 QY 421 TNMIPAEQPLSTPLSHST 438
 DB 447 TNMIPAEQPLSTPLSHST 464

RESULT 7
 AAY70899
 ID AAY70899 standard; protein; 464 AA.
 XX
 AC AAY70899;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by Trim 1 construct.
 XX
 KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion; pIL2Trim1 variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 24..25
 FT Protein 26..464
 FT /note= "Soluble portion of CD39"
 XX
 WO2000023094-A2.
 XX
 PD 27-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US023641.
 XX
 PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX
 XX (IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.
 XX
 XX Example 11; Page 111-112; 118pp; English.
 PS
 XX The present sequence is the protein encoded by Trim1 construct. pIL2Trim1

CC variant was constructed by removing the human IL2 residues from solCD39
 CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
 CC human IL2 to the solCD39 coding region results in high levels of both
 CC expression and activity in the supernatants of transfected cells. SolCD39
 CC is used in the treatment of unstable angina, myocardial infarction,
 CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
 CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
 CC disorder including lung ischaemia, coronary ischaemia and cerebral
 CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
 CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
 CC Soluble CD39 is also useful for preventing thrombus formation or
 CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
 CC vessels or stroke
 XX
 SQ Sequence 464 AA;

Query Match 100.0%; Score 2343; DB 3; Length 464;
 Best Local Similarity 100.0%; Pred. No. 1.2e-230;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSHTSLYIKWPAEKENDTGVVHVQVECKRVKPGISKVFQKV 60
 DB 27 QNKALPENVKYGIIVLDAGSHTSLYIKWPAEKENDTGVVHVQVECKRVKPGISKVFQKV 86
 QY 61 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERLSN 120
 DB 87 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERLSN 146
 QY 121 YPFDFOGARIITQEGAGYCMITINVLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 180
 DB 147 YPFDFOGARIITQEGAGYCMITINVLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 206
 QY 181 TQVTFVQNGTIESPDNALQFRLYKDYNYTTHSFLCYGKQALWQKLAKDIQVASNEIL 240
 DB 207 TQVTFVQNGTIESPDNALQFRLYKDYNYTTHSFLCYGKQALWQKLAKDIQVASNEIL 266
 QY 241 RDPCHFGYKVVNVDLYKTPCTKRFEMTLFQQFEIQGIGNYQQCHQSILELFTSYC 300
 DB 267 RDPCHFGYKVVNVDLYKTPCTKRFEMTLFQQFEIQGIGNYQQCHQSILELFTSYC 326
 QY 301 PYSQAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 360
 DB 327 PYSQAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 386
 QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMNL 420
 DB 387 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMNL 446
 QY 421 TNMIPAEQPLSTPLSHST 438
 DB 447 TNMIPAEQPLSTPLSHST 464

RESULT 8
 AAY70924
 ID AAY70924 standard; protein; 473 AA.
 XX
 AC AAY70924;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Human soluble CD39 fusion protein construct, pIL2Trim4.
 XX
 KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

[illegible]

QY 181 TQVTFVFNQTTIESPDNALQFLYKGVNYYTHSFLCYGKQDALWOKLAKDIQVASNEIL 240
Db |||||
217 TQVTFVFNQTTIESPDNALQFLYKGVNYYTHSFLCYGKQDALWOKLAKDIQVASNEIL 276
QY 241 RDPCHFGYKXVNVSDLYKTPCTKRFEWTLPPQOFEIQGIGNYQOCHQSILELNTSYC 300
Db |||||
277 RDPCHFGYKXVNVSDLYKTPCTKRFEWTLPPQOFEIQGIGNYQOCHQSILELNTSYC 336
QY 301 PYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 360
Db |||||
337 PYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 396
QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNL 420
Db |||||
397 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNL 456
QY 421 TNMIPAEQPLSTPLSHST 438
Db |||||
457 TNMIPAEQPLSTPLSHST 474

RESULT 11
AA70900
ID AAY70900 standard; protein; 474 AA.

AC AAY70900;
XX |||||
DT 17-AUG-2000 (first entry)
XX |||||
DE Protein encoded by Trim 3 construct.
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarrhythmic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pIL2Trim3 variant.

OS Homo sapiens.
OS Synthetic.
XX |||||
FH Key Location/Qualifiers
FT Cleavage-site 24..25
FT Protein 36..474
FT /note= "Soluble portion of CD39"

XX WO200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

XX (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

XX Inhibiting platelet activation and recruitment, useful for treating a

XX mammal suffering from unstable angina, myocardial infarction, stroke,

XX coronary artery disease or injury, comprises administering soluble CD39

XX polypeptides.

XX Example 11; Page 113-114; 118pp; English.

XX The present sequence is the protein encoded by Trim3 construct. pIL2Trim3
XX variant was constructed by removing the human IL2 residues from solCD39
XX fusion construct. Fusion of 12 amino acids from the N-terminus of mature
XX human IL2 to the solCD39 coding region results in high levels of both
XX expression and activity in the supernatants of transfected cells. SolCD39
XX is used in the treatment of unstable angina, myocardial infarction,
XX stroke, coronary artery disease or injury, atherosclerosis, peripheral
XX vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
XX disorder including lung ischaemia, coronary ischaemia and cerebral
XX ischaemia, a thrombotic disorder including coronary artery thrombosis,
XX cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
XX thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
XX thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
XX Soluble CD39 is also useful for preventing thrombus formation or
XX reformation, occlusion, reocclusion, stenosis or restenosis of blood
XX vessels or stroke

XX Sequence 474 AA;

Query Match 100.0%; Score 2343; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRVKPGISKPVOKV 60
Db |||||
37 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRVKPGISKPVOKV 96
QY 61 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELAORVLDVVERSLN 120
Db |||||
97 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELAORVLDVVERSLN 156
QY 121 YPPDFQGARITTGSEGAIGHITINLLGKFSQKTRWFSIVPYETNNQETFGALDGGAS 180
Db |||||
157 YPPDFQGARITTGSEGAIGHITINLLGKFSQKTRWFSIVPYETNNQETFGALDGGAS 216
QY 181 TQVTFVFNQTTIESPDNALQFLYKGVNYYTHSFLCYGKQDALWOKLAKDIQVASNEIL 240
Db |||||
217 TQVTFVFNQTTIESPDNALQFLYKGVNYYTHSFLCYGKQDALWOKLAKDIQVASNEIL 276
QY 241 RDPCHFGYKXVNVSDLYKTPCTKRFEWTLPPQOFEIQGIGNYQOCHQSILELNTSYC 300
Db |||||
277 RDPCHFGYKXVNVSDLYKTPCTKRFEWTLPPQOFEIQGIGNYQOCHQSILELNTSYC 336
QY 301 PYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 360
Db |||||
337 PYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 396
QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNL 420
Db |||||
397 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQGS DAGWTLYMLNL 456
QY 421 TNMIPAEQPLSTPLSHST 438
Db |||||
457 TNMIPAEQPLSTPLSHST 474

RESULT 12
AA70911
ID AAY70911 standard; protein; 476 AA.

XX AC AAY70911;

XX 17-AUG-2000 (first entry)

XX Human CD39-L4-1 protein construct.

KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;

KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antidiagonal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic.
 XX
 OS Homo sapiens.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..37
 FT /note= "Human CD39-L4 protein N-terminal end"
 FT Cleavage-site 20..21
 FT /note= "Cleavage site of leader sequence"
 FT Region 38..476
 FT /note= "Human soluble CD39 protein"
 XX
 PN WO200023459-A1.
 XX
 XX 27-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US022955.
 XX
 PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX WPI; 2000-339644/29.
 XX
 XX New soluble CD39 polypeptides having apyrase activity, useful for
 PT inhibiting angiogenesis and treating unstable angina, myocardial
 PT infarction, stroke, coronary artery disease or injury.
 XX
 PS Claim 6; Page 89-91; 122pp; English.
 XX
 CC The present sequence is a fusion protein construct CD39-L4-1, comprising
 CC the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is
 CC a secreted apyrase, belonging to the CD39 family. Soluble CD39 is
 CC constructed by removing the N- and C-terminal transmembrane domains. It
 CC retains the capacity to metabolise ATP and ADP at relevant concentrations
 CC and the ability to block and reverse ADP-induced platelet activation and
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC are useful for inhibiting angiogenesis. It is useful for the treatment of
 CC unstable angina, myocardial infarction, stroke, coronary artery disease
 CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
 CC embolism, platelet-associated ischaemic disorders including lung,
 CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
 CC peripheral and cerebral artery thrombosis, intracardiac and venous
 CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
 CC for preventing thrombus formation or reformation, occlusion, reocclusion,
 CC stenosis or restenosis of blood vessels or stroke
 XX
 SQ Sequence 476 AA;

Query Match 100.0%; Score 2343; DB 3; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.3e-230;
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENYKGIIVLDAGSSHTSLYIKWPAKENDTGVVHVECRVKGPGISKFVQKV 60
 DB 39 QNKALPENYKGIIVLDAGSSHTSLYIKWPAKENDTGVVHVECRVKGPGISKFVQKV 98
 QY 61 NEIGIYLTDCMERAREVIFRSQHQETPVYLGATAGMRLRMESEELADRLVDVRSLSN 120
 DB 99 NEIGIYLTDCMERAREVIFRSQHQETPVYLGATAGMRLRMESEELADRLVDVRSLSN 158
 QY 121 YPFDFOGARIITQEEGAYGWITINYLKFGQKTRWFSIVPYETNNQETFGALDGGAS 180
 DB 159 YPFDFOGARIITQEEGAYGWITINYLKFGQKTRWFSIVPYETNNQETFGALDGGAS 218

QY 181 TQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALMOKLAKDIQVASNEIL 240
 DB 219 TQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALMOKLAKDIQVASNEIL 278
 QY 241 RDPFPHGYKVVNSDLYKTPCTKRFEMTLPPQOPEIQIGIGNYQOCHOSILELFTSYC 300
 DB 279 RDPFPHGYKVVNSDLYKTPCTKRFEMTLPPQOPEIQIGIGNYQOCHOSILELFTSYC 338
 QY 301 PYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEEK 360
 DB 339 PYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEEK 398
 QY 361 TSVAGVKEKYLSEYCFSGTVILSLILQGYHFTADSWEHIFHIGIKIOGSDAGMTLGYMLNL 420
 DB 399 TSVAGVKEKYLSEYCFSGTVILSLILQGYHFTADSWEHIFHIGIKIOGSDAGMTLGYMLNL 458
 QY 421 TNMIPAEQPLSTPLSHST 438
 DB 459 TNMIPAEQPLSTPLSHST 476
 XX
 XX AAY70888 standard; protein; 476 AA.
 AC AAY70888;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by CD39-L4-1 construct.
 XX
 KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral artery thrombosis; intracardiac thrombosis; coronary artery thrombosis;
 KW cerebral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..37
 FT /note= "Derived from CD39-L4"
 FT Cleavage-site 20..21
 FT Region 38..476
 FT /note= "Soluble portion of CD39"
 FT
 XX WO200023094-A2.
 XX
 XX 27-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US023641.
 XX
 PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX
 PA (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,

PT coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
PS Claim 6; Page 89-91; 118pp; English.
XX
CC The present sequence is a fusion construct of human soluble CD39 encoded
CC by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the
CC CD39 family. The fusion construct is used for the expression and activity
CC of soluble CD39 in CHO (Chinese hamster ovary) cells. Soluble CD39
CC retains the capacity of wildtype CD39 to metabolise ATP and ADP at
CC physiologically relevant concentrations as well as the ability to block
CC and reverse ADP-induced platelet activation and recruitment including
CC platelet aggregation. This is used in the treatment of unstable angina,
CC myocardial infarction, stroke, coronary artery disease or injury,
CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,
CC platelet-associated ischaemic disorder including lung ischaemia, coronary
CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
SQ Sequence 476 AA;

Query Match 100.0%; Score 2343; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSSHTSLIYKWPAREKENDTGVVHQVEECRVKPGISKFKVQK 60
DB 39 QNKALPENVKYGIIVLDAGSSHTSLIYKWPAREKENDTGVVHQVEECRVKPGISKFKVQK 98

QY 61 NEIGIYLTDCMERAREVTPRSQHOETPVYLGATGMRLLRMESEELADRVLDVVERSLN 120
DB 99 NEIGIYLTDCMERAREVTPRSQHOETPVYLGATGMRLLRMESEELADRVLDVVERSLN 158

QY 121 YPFDQGARITQEGEGAYGWTITINYLKGFQKTRFWSIVPYETNNQETFGALDLGAS 180
DB 159 YPFDQGARITQEGEGAYGWTITINYLKGFQKTRFWSIVPYETNNQETFGALDLGAS 218

QY 181 TQVTFVQNTQIESPDNALQFLYKQDYNVYTHSLFCYKQDQALWOKLAKIQVASNEIL 240
DB 219 TQVTFVQNTQIESPDNALQFLYKQDYNVYTHSLFCYKQDQALWOKLAKIQVASNEIL 278

QY 241 RDCPHPGYKVVNYSILYKTPCTKRFEMTLPPQOFETQIGINYQQCHQSILEFNTSYC 300
DB 279 RDCPHPGYKVVNYSILYKTPCTKRFEMTLPPQOFETQIGINYQQCHQSILEFNTSYC 338

QY 301 PYSQCAFNGIFLPPQDGFAPSAFYFVNMKFLNLTSEKVSQSKVTEMKKFCAQPWEIK 360
DB 339 PYSQCAFNGIFLPPQDGFAPSAFYFVNMKFLNLTSEKVSQSKVTEMKKFCAQPWEIK 398

QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGHVHTFADSWEHIFGKIQGSDAGWTGLYMLNL 420
DB 399 TSYAGVKEKYLSEYCFSGTYILSLLLQGHVHTFADSWEHIFGKIQGSDAGWTGLYMLNL 458

QY 421 TNMIPAEQPLTSLSHST 438
DB 459 TNMIPAEQPLTSLSHST 476

RESULT 14
AAAY70914
ID AAAY70914 standard; protein; 478 AA.
XX AAAY70914;
XX
DT 17-AUG-2000 (first entry)
XX
XX Human soluble CD39 fusion protein construct, pIL2LsolCD39.
DE
XX

KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= Leader peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT Protein 25..36
FT /label= Mature human interleukin_2
FT /note= "Derived from N-terminal end of human IL2"
FT Region 37..39
FT /note= "Linker"
FT Protein 40..478
FT /note= "Human soluble CD39 protein"
XX
XX WO200023459-A1.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMV) IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX
XX WPI; 2000-339644/29.
XX N-PSDB; AAD00207.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Disclosure; Page 99-101; 122pp; English.
XX
XX The present sequence is a fusion construct pIL2LsolCD39, comprising the
XX leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
XX mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,
XX having apyrase activity. This produces high levels of solCD39 expression
XX and activity in the transfected cells. Soluble CD39 is constructed by
XX removing the N- and C-terminal transmembrane domains. It retains the
XX capacity to metabolise ATP and ADP at relevant concentrations and the
XX ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,
XX embolism, platelet-associated ischaemic disorders including lung,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis, intracardiac and venous
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 478 AA;

Query Match 100.0%; Score 2343; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 421 TNMIPAEQPLSTPLSHST 438
Db 461 TNMIPAEQPLSTPLSHST 478
RESULT 15
AAV70891
ID AAY70891 standard; protein; 478 AA.
XX AC AAY70891;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by p1L2Lsol CD39.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion.
XX OS Homo sapiens.
OS Synthetic.
XX FH Key
XX FT Peptide
FT /note= "hull2 leader sequence"
FT Protein
FT /note= "Mature human IL2"
FT Region
FT /note= "Linker"
FT Protein
FT /note= "SolCD39 protein"
XX WO200023094-A2.
XX 27-APR-2000.
XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX PA (IMV) IMMUNEX CORP.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
DR N-PSDB; AAD00202.
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39
PT polypeptides.
XX Disclosure; Page 99-101; 118pp; English.
XX The present sequence is protein encoded by the coding region of
CC p1L2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase
CC activity. Fusion of 12 amino acids from the N-terminus of mature human
CC IL2 to the solCD39 coding region results in high levels of both
CC expression and activity in the supernatants of transfected cells. This is
CC used in the treatment of unstable angina, myocardial infarction, stroke,
CC coronary artery disease or injury, atherosclerosis, peripheral vascular
CC occlusion, preclampsia, embolism, platelet-associated ischaemic disorder
CC including lung ischaemia, coronary ischaemia and cerebral ischaemia, a
CC thrombotic disorder including coronary artery thrombosis, cerebral artery
CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
CC thrombosis, reocclusion, stenosis, restenosis, antidiagonal, cardiac,
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
CC useful for preventing thrombus formation or reformation, occlusion,
CC reocclusion, stenosis or restenosis of blood vessels or stroke
XX SQ Sequence 478 AA;
Query Match 100.0%; Score 2343; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKFKVQV 60
Db 41 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKFKVQV 100
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Db 161 YPFDFOGARIITGOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAS 220
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Db 221 TQVTFVFPQNTIESPDNALQRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIQVANSNEIL 280
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Db 281 RDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQFQFQIGNYQQCHQSILELFTNTSYC 340
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Db 341 PYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIK 400
QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYMLNL 420
Db 401 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTILGYMLNL 460
QY 421 TNMIPAEQPLSTPLSHST 438
Db 461 TNMIPAEQPLSTPLSHST 478

Search completed: March 7, 2005, 13:13:02
Job time : 72.6629 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 51.3843 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-2_COPY_39_476

Perfect score: 2343
Sequence: 1 QNKALPENVKYIGVLDAGSS.....NLTMIPABQPLSTPLSHST 438

Scoring table: BLOSUM62

dapop 10.0 , Gapext 0.5

Searched: 1391452 segs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2343	100.0	439	9	US-09-374-586-2
2	2343	100.0	454	9	US-09-835-147-6
3	2343	100.0	463	9	US-09-835-147-30
4	2343	100.0	464	9	US-09-835-147-27
5	2343	100.0	473	9	US-09-835-147-29
6	2343	100.0	474	9	US-09-835-147-28
7	2343	100.0	476	9	US-09-835-147-8
8	2343	100.0	478	9	US-09-835-147-3
9	2343	100.0	487	9	US-09-835-147-26
10	2343	100.0	502	13	US-10-092-063-38
11	2343	100.0	510	9	US-09-835-147-2
12	2343	100.0	510	9	US-09-374-586-1
13	2343	100.0	510	10	US-09-781-796B-1

14	2343	100.0	510	16	US-10-646-308-30	Sequence 30, Appli
15	2294	97.9	476	9	US-09-835-147-4	Sequence 4, Appli
16	1009	43.1	495	9	US-09-823-356-4	Sequence 4, Appli
17	910.5	38.9	529	9	US-09-923-304-4	Sequence 4, Appli
18	906.5	38.7	458	13	US-10-052-586-496	Sequence 496, App
19	906.5	38.7	458	14	US-10-174-590-496	Sequence 496, App
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26	906.5	38.7	458	14	US-10-176-915-496	Sequence 496, App
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41	906.5	38.7	458	14	US-10-175-740-496	Sequence 496, App
42	906.5	38.7	458	14	US-10-175-743-496	Sequence 496, App
43	906.5	38.7	458	14	US-10-176-488-496	Sequence 496, App
44	906.5	38.7	458	14	US-10-176-492-496	Sequence 496, App
45	906.5	38.7	458	14	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1

US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 100.0%; Score 2343; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.2e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	122	YPPDFOGARIITQCEGAGVGTITVYLLGKFSOKTWFSITVPVETNNQETFGALDGGAS	181
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Db 242 RDCPFHPGKVVVNSDLYKTPCTKRFEMTLFPQOFEIOGIGNYQOCHOSILELFNTSYC 301
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QY 421 TNMIPAEQPLSTPLSHST 438
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RESULT 2

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 100.0%; Score 2343; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.3e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVQKV 60
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Db 437 TNMIPAEQPLSTPLSHST 454

RESULT 3

US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 100.0%; Score 2343; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 2.3e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 26 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVQKV 85
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Db 86 NEIGVILTCMERAREVIPSQHOETPVVLGATAGMRLLRMESEELADRVLDVVERSLN 145
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Db 146 YPFDGAGRIITQOEGAGYGMITINYLKGFQSKTRWFSIVPYETNNQTFGALDGGAS 205
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Db 446 TNMIPAEQPLSTPLSHST 463

RESULT 4
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; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 100.0%; Score 2343; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 2.3e-209; Indels 0; Gaps 0;
Matches 438; Conservative 0; Mismatches 0

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQKV 60
Db 27 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQKV 86
QY 61 NEIGIYLTDCMERAREVIPSQHQETPPVILGATAGMRLLRMESEELADRVLDVVERSLN 120
Db 87 NEIGIYLTDCMERAREVIPSQHQETPPVILGATAGMRLLRMESEELADRVLDVVERSLN 146
QY 121 YPFDQFARIIITQCEGAGYMTINYLKGFQSKTWFISIVPYETNNQETFGALDGGAS 180
Db 147 YPFDQFARIIITQCEGAGYMTINYLKGFQSKTWFISIVPYETNNQETFGALDGGAS 206
QY 181 TQVTFVQNTIESPNALQFRLYKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEIL 240
Db 207 TQVTFVQNTIESPNALQFRLYKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEIL 266
QY 241 RDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQFQEIQIGNYQOCHOSILELFNTSYC 300
Db 267 RDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQFQEIQIGNYQOCHOSILELFNTSYC 326
QY 301 PYSQAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIK 360
Db 327 PYSQAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIK 386
QY 361 TSVAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNL 420

Db 387 TSVAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNL 446
QY 421 TNMIPAEQPLSTPLSHST 438
Db 447 TNMIPAEQPLSTPLSHST 464

RESULT 5
US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 100.0%; Score 2343; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.4e-209; Indels 0; Gaps 0;
Matches 438; Conservative 0; Mismatches 0

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQKV 60
Db 36 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQKV 95
QY 61 NEIGIYLTDCMERAREVIPSQHQETPPVILGATAGMRLLRMESEELADRVLDVVERSLN 120
Db 96 NEIGIYLTDCMERAREVIPSQHQETPPVILGATAGMRLLRMESEELADRVLDVVERSLN 155
QY 121 YPFDQFARIIITQCEGAGYMTINYLKGFQSKTWFISIVPYETNNQETFGALDGGAS 180
Db 156 YPFDQFARIIITQCEGAGYMTINYLKGFQSKTWFISIVPYETNNQETFGALDGGAS 215
QY 181 TQVTFVQNTIESPNALQFRLYKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEIL 240
Db 216 TQVTFVQNTIESPNALQFRLYKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEIL 275
QY 241 RDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQFQEIQIGNYQOCHOSILELFNTSYC 300
Db 276 RDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQFQEIQIGNYQOCHOSILELFNTSYC 335
QY 301 PYSQAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIK 360
Db 336 PYSQAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWEEIK 395
QY 361 TSVAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNL 420
Db 396 TSVAGVKEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNL 455
QY 421 TNMIPAEQPLSTPLSHST 438

Db 456 TNNMPAEQPLSTPLSHST 473
|||||

RESULT 6

US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 28

; LENGTH: 474

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: Construct of human CD39

US-09-835-147-28

Query Match 100.0%; Score 2343; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPQKV 60

Db 37 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPQKV 96

QY 61 NEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 120

Db 97 NEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 156

QY 121 YPFDFOGARIITGOEAGYCWITINYLKGFQKTRFWSIVPYETNNQSTFGALDVGAS 180

Db 157 YPFDFOGARIITGOEAGYCWITINYLKGFQKTRFWSIVPYETNNQSTFGALDVGAS 216

QY 181 TQVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEIL 240

Db 217 TQVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEIL 276

QY 241 RDCPHGPKYKVVNVDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILELFTNSYC 300

Db 277 RDCPHGPKYKVVNVDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILELFTNSYC 336

QY 301 PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 360

Db 337 PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 396

QY 361 TSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHTGKIQGSDAGWTLYGMLNL 420

Db 397 TSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHTGKIQGSDAGWTLYGMLNL 456

QY 421 TNNMPAEQPLSTPLSHST 438

Db 457 TNNMPAEQPLSTPLSHST 474

RESULT 7

US-09-835-147-3

; Sequence 3, Application US/09835147

; Patent No. US20020002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 3

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: Construct of human CD39

US-09-835-147-3

Query Match 100.0%; Score 2343; DB 9; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.4e-209;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPQKV 60

Db 39 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPQKV 98

QY 61 NEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 120

Db 99 NEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 158

QY 121 YPFDFOGARIITGOEAGYCWITINYLKGFQKTRFWSIVPYETNNQSTFGALDVGAS 180

Db 159 YPFDFOGARIITGOEAGYCWITINYLKGFQKTRFWSIVPYETNNQSTFGALDVGAS 218

QY 181 TQVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEIL 240

Db 219 TQVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEIL 278

QY 241 RDCPHGPKYKVVNVDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILELFTNSYC 300

Db 279 RDCPHGPKYKVVNVDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILELFTNSYC 338

QY 301 PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 360

Db 339 PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 398

QY 361 TSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHTGKIQGSDAGWTLYGMLNL 420

Db 399 TSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHTGKIQGSDAGWTLYGMLNL 458

QY 421 TNNMPAEQPLSTPLSHST 438

Db 459 TNNMPAEQPLSTPLSHST 476

RESULT 8

US-09-835-147-8

; Sequence 8, Application US/09835147

; Patent No. US20020002277A1

GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR FILING DATE: 1998-10-16
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match 100.0%; Score 2343; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVFQKV 60
DB 41 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVFQKV 100

QY 61 NEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 120
DB 101 NEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 160

QY 121 YPFDFOGARITQCEGAYGWIITINLLGKFSQKTRWFSIVPVYETNNQETFGALDLGGAS 180
DB 161 YPFDFOGARITQCEGAYGWIITINLLGKFSQKTRWFSIVPVYETNNQETFGALDLGGAS 220

QY 181 TQVTFVQNTIESPNALQFRLYGKDYNYTHSFLCYGKQDALWQKLAKDIOVASNEIL 240
DB 221 TQVTFVQNTIESPNALQFRLYGKDYNYTHSFLCYGKQDALWQKLAKDIOVASNEIL 280

QY 241 RDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFTNSYC 300
DB 281 RDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFTNSYC 340

QY 301 PYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIK 360
DB 341 PYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIK 400

QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGHYFTADSWEHIFHFGIKIQGSDAGWTGLGYMLNL 420
DB 401 TSYAGVKEKYLSEYCFSGTYILSLLLQGHYFTADSWEHIFHFGIKIQGSDAGWTGLGYMLNL 460

QY 421 TNMIPAEQPLSTPLSHST 438
DB 461 TNMIPAEQPLSTPLSHST 478

RESULT 9
US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.

APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US 09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 100.0%; Score 2343; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 2.5e-209;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVFQKV 60
DB 50 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVFQKV 109

QY 61 NEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 120
DB 110 NEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 169

QY 121 YPFDFOGARITQCEGAYGWIITINLLGKFSQKTRWFSIVPVYETNNQETFGALDLGGAS 180
DB 170 YPFDFOGARITQCEGAYGWIITINLLGKFSQKTRWFSIVPVYETNNQETFGALDLGGAS 229

QY 181 TQVTFVQNTIESPNALQFRLYGKDYNYTHSFLCYGKQDALWQKLAKDIOVASNEIL 240
DB 230 TQVTFVQNTIESPNALQFRLYGKDYNYTHSFLCYGKQDALWQKLAKDIOVASNEIL 289

QY 241 RDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFTNSYC 300
DB 290 RDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFTNSYC 349

QY 301 PYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIK 360
DB 350 PYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIK 409

QY 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGHYFTADSWEHIFHFGIKIQGSDAGWTGLGYMLNL 420
DB 410 TSYAGVKEKYLSEYCFSGTYILSLLLQGHYFTADSWEHIFHFGIKIQGSDAGWTGLGYMLNL 469

QY 421 TNMIPAEQPLSTPLSHST 438
DB 470 TNMIPAEQPLSTPLSHST 487

RESULT 10
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265

Qy 302 YSOCAFNGIPLPPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 361
Db 340 YSOCAFNGIPLPPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 399
Qy 362 SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGSADAGWTILGYMLNLT 421
Db 400 SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGSADAGWTILGYMLNLT 459
Qy 422 NMIPAEQPLSTPLSHST 438
Db 460 NMIPAEQPLSTPLSHST 476

Search completed: March 7, 2005, 14:12:34
Job time : 52.3843 secs

Qy 301 PYSQAFNGIFLPPPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 360
Db 339 PYSQAFNGIFLPPPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIK 398
Qy 361 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGSADAGWTILGYMLNLT 420
Db 399 TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGSADAGWTILGYMLNLT 458
Qy 421 TNMIPAEQPLSTPLSHST 438
Db 459 TNMIPAEQPLSTPLSHST 476

RESULT 15
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patehtin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 97.9%; Score 2294; DB 9; Length 476;
Best Local Similarity 98.6%; Pred. No. 8.9e-205;
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 6 PENVK-----YGIVLDAAGSSHTSLYIKWPAEKENDTGTVHQBECRVKVGPGISKFKVQKVN 61
Db 40 PINVSASTLYGIVLDAAGSSHTSLYIKWPAEKENDTGTVHQBECRVKVGPGISKFKVQKVN 99
Qy 62 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDLDVVERSLSNY 121
Db 100 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDLDVVERSLSNY 159
Qy 122 PFDFOGARIITGOEGAGYMTITNVLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 181
Db 160 PFDFOGARIITGOEGAGYMTITNVLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 219
Qy 182 QVTFVPQNTTIESPDNALQFRLYKGVNVTYTHSFCLCYKQDALWQKLAKDIQVANSNELLR 241
Db 220 QVTFVPQNTTIESPDNALQFRLYKGVNVTYTHSFCLCYKQDALWQKLAKDIQVANSNELLR 279
Qy 242 DPCFHPGKVKVNVSDLYKTPCTKRFEMILPFPQFEIQGIGNYQOCHOSILELFTSYCP 301
Db 280 DPCFHPGKVKVNVSDLYKTPCTKRFEMILPFPQFEIQGIGNYQOCHOSILELFTSYCP 339

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 14.072 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147a-3_COPY_21_476
Perfect score: 2440
Sequence: 1 VSHRNQQTWFEIGFLSTQN.....NLTNMIPAEQPLSTPLSHST 456

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	96.2	510	2 I56242	lymphoid cell acti
2	505	20.7	483	2 D86276	hypothetical prote
3	469.5	19.2	405	2 E86276	hypothetical prote
4	453	18.6	630	2 S50463	hypothetical prote
5	416	17.0	572	2 T40856	probable nucleotid
6	406.5	16.7	516	2 G84442	probable nucleosid
7	402.5	16.5	485	2 T34147	hypothetical prote
8	397.5	16.3	508	2 C86276	7A19.33 protein -
9	383.5	15.7	557	2 T16696	hypothetical prote
10	381.5	15.6	556	2 T39109	probable guanosine
11	374	15.3	455	2 S48859	nucleoside triphos
12	339	13.9	454	2 J4616	aprase (EC 3.6.1.
13	332	13.6	1052	2 T04339	hypothetical prote
14	328.5	13.5	479	2 T23508	hypothetical prote
15	323.5	13.3	518	2 A40732	guanosine-diphosph
16	167	6.8	628	2 A55421	nucleoside-triphos
17	105.5	4.3	1509	2 B99985	hypothetical prote
18	103	4.2	369	2 S77299	C4-dicarboxylase-b
19	101.5	4.2	716	2 T21516	hypothetical prote
20	100	4.1	307	2 T27332	hypothetical prote
21	100	4.1	1951	2 B43963	RNA viral polymera
22	98.5	4.0	590	2 AB1411	autolysin, N-acety
23	98.5	4.0	797	2 D86247	hypothetical prote
24	98.5	4.0	883	2 B85725	probable fibrial
25	98.5	4.0	989	2 B84532	hypothetical prote
26	98.5	4.0	3848	2 T17414	hypothetical prote
27	98	4.0	371	2 T05213	TipC protein - sli
28	98	4.0	665	2 T18979	hypothetical prote
29	98	4.0	2354	2 T13288	mei-41 protein - f

30	97.5	4.0	392	2 A96738	hypothetical prote
31	97.5	4.0	1013	2 JC2314	chitin synthase (E
32	97	4.0	494	2 T03774	probable histidine
33	97	4.0	735	2 A33369	glycogen(starch) s
34	96	3.9	1028	2 I51173	myosin I beta - bu
35	96	3.9	1415	2 A72369	(R)-2-hydroxygluta
36	96	3.9	2151	1 S16449	genome polyprotein
37	95.5	3.9	591	2 F89770	hypothetical prote
38	95.5	3.9	1900	2 AG2391	serine/threonine k
39	95	3.9	256	2 G97031	TPR-repeat contain
40	95	3.9	288	1 B48583	spore germination
41	95	3.9	451	2 G69859	Mg2+ transporter h
42	95	3.9	461	2 G91288	probable permease
43	95	3.9	461	2 F86075	probable permease
44	95	3.9	564	2 S15962	hypothetical prote
45	95	3.9	927	2 T43110	lactacin 481/lacto

ALIGNMENTS

RESULT 1

I56242

lymphoid cell activation antigen - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: I56242

R/Maliszewski, C.R.; Dellespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;

J. Immunol. 153, 3574-3583, 1994

A/Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha

A/Reference number: I56242; MUID:95015846; PMID:7930580

A/Accession: I56242

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-510 <RES>

A/Cross-references: UNIPROT:P49961; GB:S73813; NID:g765255; PIDN:AB32152.1; PID:g765255

C/Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 96.2%; Score 2348; DB 2; Length 510;

Best Local Similarity 100.0%; Pred. No. 5.6e-183;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKENDTGVVHQVECRVKGPGISKFVQK 77

Db 38 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKENDTGVVHQVECRVKGPGISKFVQK 97

Qy 78 VNEIGIYLTDCMERAREVIPSQHOETPPVYLGTAGNRLRMESEELADRVLDVVERSL 137

Db 98 VNEIGIYLTDCMERAREVIPSQHOETPPVYLGTAGNRLRMESEELADRVLDVVERSL 157

Qy 138 NYPPDFQGARIITGOEBGAGVITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 197

Db 158 NYPPDFQGARIITGOEBGAGVITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217

Qy 198 STQVTFVPQNTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEI 257

Db 218 STQVTFVPQNTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEI 277

Qy 258 LRDPCHPHGKVKVNVNVDLKYTPCTKRFEMTLFPQPEIQIGIGNYQQCHOSILELFTSY 317

Db 278 LRDPCHPHGKVKVNVNVDLKYTPCTKRFEMTLFPQPEIQIGIGNYQQCHOSILELFTSY 337

Qy 318 CPYSQCAFNGIFLPPQGDGFSAFYVMKFNLTSEKVSQEKVTMMKKFCAQPWEI 377

Db 338 CPYSQCAFNGIFLPPQGDGFSAFYVMKFNLTSEKVSQEKVTMMKKFCAQPWEI 397

Qy 378 KTSYAGVKEKYLSEYCFSGFYIISLLIQGYHFTADSMHEIHFIQKIQSDAGWTGLGYMLN 437

Db 398 KTSYAGVKEKYLSEYCFSGFYIISLLIQGYHFTADSMHEIHFIQKIQSDAGWTGLGYMLN 457

Qy 438 LTNMIPAEQPLSTPLSHST 456

Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 2

D86276
hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9XI62; GB:AE005172; NID:95080801; PIDN:AAD39311.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 20.7%; Score 505; DB 2; Length 483;
Best Local Similarity 31.3%; Pred. No. 4.5e-33;
Matches 135; Conservative 70; Mismatches 164; Indels 62; Gaps 18;
QY 27 VKYGVLDAGSSHTLYIKWPAKEN---DTGVVHVQVESCVRK-GPGISKFKVQKNEIG 82
DB 68 LRYSVLLDAGSSGRVHVFGWFFSGKPVDFGKHY---ANLKLTPGLSSYADNPGEAS 124
QY 83 IYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESBELADRLDVVVERSL--SNYP 140
DB 125 VSVTKLVEFAKQRIPKMFRSRDIRLMATAGMRLLEVPVQE---QILEVTRVLRSSGFM 181
QY 141 PDFGARIITQOEGAYGWITINYLKFKSQKTRWFSIVPYETNNQETFGALDGGASTQ 200
DB 182 FRDEWANVISGDEGIYSWITANYALGSLG-----TDPLETTGIVELGASAQ 229
QY 201 VTFVPQNTIESDNALQFLRYGK-DYNNVTHSFLCYGKQOALWQKLAKDIQVANSNE--- 256
DB 230 VTFVSSSHV---PPEYSGRTIAYGNISYTIYSHSFLDYGKQOAL-KKLEKLQNSANTVD 285
QY 257 -ILRDPCHFPGYKKVNVVDLYKTPCTKRFEMTLFPQFETQG---IGNYQOCHQSILE 311
DB 286 GVVEDPCTPKGY-----IYDTN-SKVYSSGFLADESKLQSLQAAGNFSKRSATFA 336
QY 312 LF--NTSYCPYSQCAFNGIFLPPIQGFPGAFSAFYFVNMKLFNLTSEKVSQEKVTEMKKF 369
DB 337 LLKSGKCNLYEHCSIGSTFTPDQGSFLATASFYTTAKFPFL--EERGWLSSELIPAGKRY 395
QY 370 CAQPFWEIKTSYAGVKEKLYSEYCFSTGYILSLILQGVHFTADSWEHIHFGIKQGSAG 429
DB 396 CGEWSKLIILEYPTTDEYLLRGYCFSAAYTIISMLHDSLGIALDD-ESITVASK-----AG 449
QY 430 -----WTLG 433
DB 450 EKHPLDVALG 460

RESULT 3

D86276
hypothetical protein F14L17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86276

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <STO>

A:Cross-references: UNIPROT:Q9W9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN

C:Genetics:

A:Map position: 1

Query Match 19.2%; Score 469.5; DB 2; Length 405;

Best Local Similarity 31.2%; Pred. No. 2.7e-30;

Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

QY 69 PGISKFKVQKNEIGVLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESBELADRLDV 128
DB 29 PGLSSYADNPGEASVSVTKLVEFAKGRIPKGLKKSDIRLMATAGMRLLDVVPVQE---QI 85

QY 129 LDVVERSLSNYPDFQFQ---ARIITQOEGAYGWITINYLKFKSQKTRWFSIVPYETNNQ 186
DB 86 LDVTRVLRSSGFKQDEWATVISGTDGIIYANVANHAGLSLG-----GDPL 133

QY 187 ETFGALDGGASTQVTFVPQNTIESDNALQFLRYGK-DYNNVTHSFLCYGKQOALWQKLAK 242
DB 134 KTTGIVELGASAQVTFVPSEHV---PPEFSRTISYGNVSYTIYSHSFLDYGQDAEDKL 190

QY 243 WQKLAKDIQVANSNE-ILRDPCHFPGYKKVNVVDLYKTPCTK-----RFEWTLPF 291
DB 191 LESLQNSAASTGDGVDEDPCTPKGY-----IYDTHSQKSSGFLSESKFKASL-- 240

QY 292 QQPEIIOGIGNYQOCHQSILELF--NTSYCPYSQCAFNGIFLPPIQGFPGAFSAFYFVNMK 349
DB 241 ---QVQAAGDFTKRSATLAMLQEGKENCAYKHCISGISTFTPIQGSFLATENFHTSKF 297

QY 350 LNTSEKVSQEKVTEM---KKFCAQPFWEIKTSYAGVKEKLYSEYCFSTGYILSLILQ 406
DB 298 FGL-GEK---EWLSEMLAKGRFCGEWSKLEKYPPTKDKYLHRYCFSSAYTIISMLHDS 353

QY 407 YHFTADSWEHIHFGIKI--QGS DAGWTLG-YMLN 437

DB 354 LGVALDD-ERIKYASKAGKENIPLDVALGAFILN 386

RESULT 4

S50463

hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C:Accession: S50463

R:Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda

A:Reference number: S50433

A:Accession: S50463

A:Molecule type: DNA

A:Residues: 1-630 <DIE>

A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005,

C:Genetics:

A:Gene: SGD:YND1; MIPS:YER005W

A:Cross-references: SGD:S0000807

A:Map position: 5R

Query Match 18.6%; Score 453; DB 2; Length 630;

Best Local Similarity 27.2%; Pred. No. 1.1e-28;

Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

QY 26 NVKYGIVLDAGSHTSLYIKWP-----AKENDTGV-----VHQVECRVK-GRGI 71
DB 7 NDRFGIVDAGSGSRIHFVKWQTESLHATNQDSQSILOSVPRIHQEKDWTFKLNPL 66
QY 72 SKFVQKVN-IGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRLVD 130
DB 67 SSFEKKPODAYKSHIKPLDPAKNIIPESHWSCEPVFIQATAGMKLL-----PQDIQSSILD 123
QY 131 VVERSLSNYPDF-----QGARIITGOEGAGYGTITINLLGKFSQKTRWFSIVPYETN 184
DB 124 GLCQGL-KHPAEFLVEDCSAQIQVDTGETGLGWLGLNYLGHENDYNP-----EVS 175
QY 185 NQETFGALDGGASTQVTFVQNO-----TIESPDNALQRLYKGVKYNVYTH 231
DB 176 DHFTFGMDMGASTQIAFAPHSDEIARHRRDIATIFLRSVNGDLQ-----KWDVFEVS 229
QY 232 SFLCYGKQALWOKLAKIQVA-----SNEILRDPCHPGYKVVNVSDLYKT 279
DB 230 TWLGFAGANRRYLAQLINTLPENTYENDDFSTRNLNDPCMPRG-----SSTDF--- 281
QY 280 PCTKRFEMTLPPQOFIEQIGNYQCHOSILE-LFNTSYCPSYSCAFNGIFLPPLOGDF- 337
DB 282 ---EFKDTI---PHIAGSGNYEQTKSIYPLLLKNMPCDDEPCLFNGVHAPRI--DFA 331
QY 338 ---GAFSAFYFVWKFLNLTSEKVSQKVTMMKKFCAQWEEI-----KTSYAGVKEK 387
DB 332 NDRFTGTSEYWTANDVFKLAGE-YNPKFKSKLREFCNSNWTQILANSRDKGVNSIPEN 390
QY 388 YLSEYCFSGTYSLLSQY---HFTADSWEHIIHFIKIQGSDAGWTGLYML 436
DB 391 FLKDCFGNWNVLHFGFDMPRIDVDA-ENVNDRPLFQSVKEVERELSWTLGRIL 447

RESULT 5
T40856
probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: 221952
A:Accession: T40856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-572 <RAM>
A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN000068; SPDB:
A:Experimental source: strain 972h-; cosmid cille10
C:Genetics:
A:Gene: SPDB:SPCC11E10.05c
A:Map position: 3

Query Match 17.0%; Score 416; DB 2; Length 572;
Best Local Similarity 27.3%; Pred. No. 1e-25;
Matches 131; Conservative 69; Mismatches 156; Indels 124; Gaps 19;
QY 28 KYGVLDAGSHTSLYIKWPAEKEN-----DTGVHQBVECRVKGPGIKFV 75
DB 4 KYGIFIDAGSGSRLLIYSWDYDTSLSLSDVKVKKLPLIETIGIGGKWSLKVQGISFA 63
QY 76 QKVNIEG-IYITDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRLVDVVER 134
DB 64 NNPKHVGGKHLKELLDFAAHPKDVHKTETPVFLSATAGMRLGVDAQ---NKLISHACR 120
QY 135 SL-SNYPDF---QGARIITGOEGAGYGTITINLLGKFSQKTRWFSIVPYETNQETP 189
DB 121 YIKKNYDFDIPNCNSIRVIDGKAGMGYGLATNYLLKTLLEK-----DTSTV 168
QY 190 CALDLGGASTQVTF-VPNQNTIESPD-----NALQRLYKGVKYNVYTHSFLCVGK 238
DB 169 GFLMDGGSVQIAELPPSQLKNYKDSISTVHIGLQNCQL-----EYPLFVTTWLFGA 223
QY 239 DQALWQKLAKDIQVASEI---LRDPCFHPGYKVVNVSDLYKTCTKRFEMTLPPQOFE 295

DB 224 NEARYRYLGLLIESENGKVGNTLSDDPCSLRG-----RTYDIDGIE 263
QY 296 IQGIGNYQCHOSILELFTNTSY-CPSYSCAFNGIFLPPLOGDFGAFSAFYFVWKFLNLT 354
DB 264 PAGTGDLKQCLUTYNLLNKDKPCMDPCPDGSIIPV--DF-ANTEFVGVSSEFWYTTN 320
QY 355 EKVSQ-----EKVTMMKKFCAQWEEI-----KTSYAGVKEKYLSEYCFSGTY 398
DB 321 DVPDMGGSYHFPNFKVDE---YCGTEWETMLSRNLKELTPTSTDENKLEKLCFKASW 376
QY 399 ILSLLQ-----YHFTADSWEHIIHFIKIQGSDAGWTGLYML 436
DB 377 ALNVLHGFDPKSTSSNAKOGSLVIPAYHSPFTSLE-----KIERTVSWTLGQVL 430

RESULT 6
G84442
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84442
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, D.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: UNIPROT:O80612; GB:A8020293; NID:G3461821; PIDN:AAC32915.1; GSPDB:GN
C:Genetics:
A:Gene: At2g02970
A:Map position: 2
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.7%; Score 406.5; DB 2; Length 516;
Best Local Similarity 27.5%; Pred. No. 5.1e-25;
Matches 117; Conservative 68; Mismatches 187; Indels 53; Gaps 13;
QY 26 NVKYGIVLDAGSHTSLYIKWPAEKENDTGVHQBVECRVK-GPGISKFVQKVEIGIY 84
DB 65 SLRYSVVVDGGSTGTRIHFVGRIESGKPVPEFRGANVASLKLHPGLSAPADDDPGASVS 124
QY 85 LTDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRLVDVVERSL--SNYPFD 142
DB 125 LTLEVEFAKGRVPKGMWIEVEVRLMATAGMRLLELPVQE---KILGVARRVLKSSGFLFR 181
QY 143 FOGARIITGOEGAGYGTITINLLGKFSQKTRWFSIVPYETNQETFGALDGGASTQVT 202
DB 182 DEWASVLSGSDGEGYAWVANFALGSLG-----GDPLKTTGIVELGASQAQT 229
QY 203 FVPQNTIESPDNALQRLYKGVKYNVYTHSFLCVGKQDA---LW-QKLAKD-----IQVAS 254
DB 230 FVSSEPM--PPEFSRTISFGNVTYVYSHGFLHFGQNAADHKLWGLSLSDHNSAVEPTR 287
QY 255 NEILRDPCHPGYKVVNVSDLYKTCTKRFEMTLPPQOFIEQIGNYQCHOSILELFN 314
DB 288 EKIFTDFCAPKGYNDANTOKHLSGLABESRLSDSF-----QAGGNSYQCRSAALTILQ 342
QY 315 TSYCPYSCAFNGIFLPPLOGDFGAFSAFYFVWKFLNLTSEKVSQKVTMMKKFCAQWP 374
DB 343 DG-----NRIILIIAG---FSFLFGL-----GEKAWLSNMSINGERFCCEWD 383
QY 375 EBINTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIIHFIKIQGSDAGWTGLY 434
DB 384 SKLRVKDPSLHEBDLLRYCFSSAYIVSLHDTLIGIPLDD-ERIGYANQAGDIPLDWALGA 442
QY 435 MLNLT 439
DB 443 FIOQT 447

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: C86276
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-508 <STO>
 A;Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN(C)
 C;Genetics:
 A;Map position: 1
 C;Superfamily: nucleoside triphosphatase chromatin-associated
 Query Match 16.3%; Score 397.5; DB 2; Length 508;
 Best Local Similarity 28.2%; Pred. No. 2.7e-24;
 Matches 126; Conservative 74; Mismatches 174; Indels 73; Gaps 21;
 QY 15 LSSTONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISK 73
 DB 54 LRSGRNRV--SLHYSVLIIDGGSGTRVHVGVRVIESGKPVDFGSENVASLKLSPGLSA 111
 QY 74 FVQKNEIGIYLTDCMERAREVTPRSOHOETPVYLGATAGMRLRMSESELADRVLDVVE 133
 DB 112 YADNPEGVSESVTELVEFAKRVHKGKLLKSDIRLMATAGMRLLELPVQE--QILDVTR 168
 QY 134 RSLSNYPFPOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNN-QETFGAL 192
 DB 169 RVLRSSGDFE-----RDEMASVISEILLENFQDLMKVY 200
 QY 193 DLG-----GASTQVTFVPOQNTIESPDNALQRLVKG-DYNYVTHSFLCYGKQDALWQK 245
 DB 201 MGLLLIMRSVRLEVFV---STELVSEFSRTPLAYGNVSYNLYSHSFLDFGQD-AAQEK 256
 QY 246 LAKDI-QVASNE-----ILRDPCHPGVKVKNV-SLYKTPCTK-RFEMTLPFQOPEIQ 298
 DB 257 LSLSLYNSAANSSTGEGIVDPDPCIPKGYILETNQKDLPGFLADKGFATL-----QA 309
 QY 299 IGNYQOCHOSILELF--NTSYCPYQCAFNGIFLPLQDQFGAFSAFYFVMKFLNLTSEK 356
 DB 310 AGNFSECRSAFAMLOEKGKCTYKCSIGSIFTPNLQGSFLATENFFHTSKFFGL-GEK 368
 QY 357 VSOEKVTEM---KFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYSILSLLOGYHTADS 413
 DB 369 ---EWLSEMILAGKRFGEWSKLVKYPFTKDNLLRYCFSSAYIISMLHSLGLVALDD 425
 QY 414 WEHIFGKIQGSD--AGWTIG-YMLN 437
 DB 426 -ERIKYASKAGEEDIPLDWALGAFILN 451
 RESULT 9
 T16696
 hypothetical protein R07E4.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: T16696
 R;Miller, N.
 submitted to the EMBL Data Library, October 1995
 A;Description: The sequence of C. elegans cosmid R07E4.
 A;Reference number: T18561
 A;Accession: T16696
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-557 <MTL>
 A;Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4.4
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESP:R07E4.4
 A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
 Query Match 15.7%; Score 383.5; DB 2; Length 557;
 Best Local Similarity 25.9%; Pred. No. 4.2e-23;
 Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: C86276
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-508 <STO>
 A;Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN(C)
 C;Genetics:
 A;Map position: 1
 C;Superfamily: nucleoside triphosphatase chromatin-associated
 Query Match 16.3%; Score 397.5; DB 2; Length 508;
 Best Local Similarity 28.2%; Pred. No. 2.7e-24;
 Matches 126; Conservative 74; Mismatches 174; Indels 73; Gaps 21;
 QY 15 LSSTONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISK 73
 DB 54 LRSGRNRV--SLHYSVLIIDGGSGTRVHVGVRVIESGKPVDFGSENVASLKLSPGLSA 111
 QY 74 FVQKNEIGIYLTDCMERAREVTPRSOHOETPVYLGATAGMRLRMSESELADRVLDVVE 133
 DB 112 YADNPEGVSESVTELVEFAKRVHKGKLLKSDIRLMATAGMRLLELPVQE--QILDVTR 168
 QY 134 RSLSNYPFPOGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNN-QETFGAL 192
 DB 169 RVLRSSGDFE-----RDEMASVISEILLENFQDLMKVY 200
 QY 193 DLG-----GASTQVTFVPOQNTIESPDNALQRLVKG-DYNYVTHSFLCYGKQDALWQK 245
 DB 201 MGLLLIMRSVRLEVFV---STELVSEFSRTPLAYGNVSYNLYSHSFLDFGQD-AAQEK 256
 QY 246 LAKDI-QVASNE-----ILRDPCHPGVKVKNV-SLYKTPCTK-RFEMTLPFQOPEIQ 298
 DB 257 LSLSLYNSAANSSTGEGIVDPDPCIPKGYILETNQKDLPGFLADKGFATL-----QA 309
 QY 299 IGNYQOCHOSILELF--NTSYCPYQCAFNGIFLPLQDQFGAFSAFYFVMKFLNLTSEK 356
 DB 310 AGNFSECRSAFAMLOEKGKCTYKCSIGSIFTPNLQGSFLATENFFHTSKFFGL-GEK 368
 QY 357 VSOEKVTEM---KFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYSILSLLOGYHTADS 413
 DB 369 ---EWLSEMILAGKRFGEWSKLVKYPFTKDNLLRYCFSSAYIISMLHSLGLVALDD 425
 QY 414 WEHIFGKIQGSD--AGWTIG-YMLN 437
 DB 426 -ERIKYASKAGEEDIPLDWALGAFILN 451
 RESULT 9
 T16696
 hypothetical protein R07E4.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: T16696
 R;Miller, N.
 submitted to the EMBL Data Library, October 1995
 A;Description: The sequence of C. elegans cosmid R07E4.
 A;Reference number: T18561
 A;Accession: T16696
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-557 <MTL>
 A;Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4.4
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESP:R07E4.4
 A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
 Query Match 15.7%; Score 383.5; DB 2; Length 557;
 Best Local Similarity 25.9%; Pred. No. 4.2e-23;
 Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;

Best Local Similarity 27.0%; Pred. No. 1e-18;
Matches 121; Conservative 71; Mismatches 191; Indels 65; Gaps 19;
QY 29 YGIVLDAGSSHTSYLYIKW---PAEKENDTGVVHQBVE---CRVKGPGISKFVQKWEIG 82
DB 43 FTVIDAGSTGTRHLHYFIHDPALASH--GMPKVEKEIQQVK-PQLSFAKSPSAA 99
QY 83 IYLDTCMERAREVIPSQHQTPVYLGATAGMRLLRMESEELADRLVDVRSLSNYPP- 141
DB 100 DLSLEPLLQARKEVPHEWKEKTPITLKATAGRLLL---PGMDADILLESVEERIFNSGFF 156
QY 142 -DFOGA-RITTCQEGAGWITINYLCK-PSQKTRWFSIYPYETNNQETFGALDLGAS 198
DB 157 AAFPDVAVNMGPSDEGVYSWFTMLILLETFTDE-----PTVGHKPAARHSVAAPDLGGG 212
QY 199 TQVTFVPOQNTIEGP---DNALQFLYKGDYNNVYTHSFLCYGKQDALWQ--KLAKDIQV 252
DB 213 TQLYWPNNEAVFSEHVGYERDIF--FGHIRLFTHSFLNGLIARLNILQLETNEI 270
QY 253 ASNEILRDPCHPGYKVKVNVSDLYKTCTKRFEMTLPPQOFIEIGIGNYQQCHSILEL 312
DB 271 ESTHQLITSCMPEGVQ-----LTEWEVALKFWNINGSSHSFSCYGTTKNF 317
QY 313 FNTSYCPYSQCAFNGIFLPPLOQDFGAPSAFYVWKFLNL-----TSEKVSQKVTMM 366
DB 318 VESSEI-----MHLRELKGS--PVYLFYSFFDRALNSGLVKGNEGKIELRQFKEA 367
QY 367 KKFCACQAPWEEIKTSVAGVKEKYLSEYCFSGFYLLSLQGVHFTADSWEHIFHTGKIQS 426
DB 368 EIACREKTEIDDG-----SHWMPQCLDLYIYSLRDGQF--EDNQPLVLAKKIKGM 420
QY 427 DAGWTGLYMLNLTMNP-AEQPLSTPLS 453
DB 421 EVSWGQGLAFATANEFQLTEGAIKTALS 448
RESULT 15
A40732
guanosine-diphosphate (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YEL042w
C:Species: Saccharomyces cerevisiae
C>Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
R:Accession: A40732; B40732; S30837; S50502
R:Abeljon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.;
J. Cell Biol. 122, 307-323, 1993
A:Title: Guanosine diphosphate is required for protein and sphingolipid glycosylation
A:Reference number: A40732; MUID:93308137; PMID:8391537
A:Accession: A40732
A:Molecule type: DNA
A:Residues: 1-518 <ABE>
A:Cross-references: UNIPROT:P32621; EMBL:L19560; NID:G349392; PIDN:AAA34656.1; PID:G3493
A:Note: sequence extracted from NCBI backbone (NCBI:134708, NCBI:P134711)
A:Accession: B40732
A:Molecule type: protein
A:Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>
R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor,
submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30812
A:Molecule type: DNA
A:Residues: 1-518 <MDL>
A:Cross-references: GB:U18779; EMBL:L10830; NID:G603625; PIDN:AAB65000.1; PID:G603637
R:Dietrich, F.S.
A:Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50502
A:Molecule type: DNA
A:Residues: 1-518 <DIE>
A:Cross-references: EMBL:U18779; NID:G603625; PIDN:AAB65000.1; PID:G603637; MIPS:YEL042w
C:Genetics:
A:Gene: SGD:GDAL
A:Cross-references: SGD:S0000769; MIPS:YEL042w

A:Map position: 5L
C:Function:
A:Description: hydrolase
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F:10-24/Domain: transmembrane #status predicted <TM>
F:41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 13.3%; Score 323.5; DB 2; Length 518;
Best Local Similarity 26.4%; Pred. No. 2.9e-18;
Matches 122; Conservative 73; Mismatches 194; Indels 73; Gaps 20;
QY 15 LSSTQNKALPENVKYIGVLIDAGSSHTSYLYIKWPAEKENDTGVVHQBVECRVKGPGISKF 74
DB 79 VKSQTSCSEHKYVIMIDAGSTGSRVHYIKFVDCVTSPTLL---DEKFDMLPEGLSSF 135
QY 75 VQKNEIGI--YLTDCMERAREVIPSQHQTPVYLGATAGMRLLRMESEELADRLVDV 131
DB 136 --DTDSVGAANSIDPLLVKAVNNVYPIKARCTPVAVKATAGRLRLGDAKSKILSAVRDH 193
QY 132 VERSLSNYPP---DFQGARITQEGAGWITINYLKGFQSKTRWFSIYPYETNNQ- 187
DB 194 LEK---DYPPVVEGDCVIMGGDEGCVFAWITNYLLGNIG-----ANGPKL 238
QY 188 -TFGALDLGASTQVTFVPO---NQTTIESPDNALQFLYKGVNYYTHSFLCYG----- 237
DB 239 PTAAVFDLGGSTQIVPEPTPIKEMVDEGHEKFDLKFQDENVYLYQFSLHLYGLKEGRN 298
QY 238 -KQALWQKLAKDIOVASNE-----ILRDCPFHGYKVKVNVSDLYKTCTKRFEMTLPP 291
DB 299 KNSVLVENALKDGLKDKNTKTHQLSSPLCP-----KVNATNEKVTLESK----- 346
QY 292 QQEIQIGI---NYQQHQSILEFN--TSYCPYSQCAFNGIFLPP-----QGDFGAF 340
DB 347 ETVTIDFIDPEPSGAQCRFLTDEILNKDAQCCSPCSFNGVHQPSSLVRFKESNDIYIF 406
QY 341 SAFFVNMKFLNLSEKVSQKVTMMKKFC--AQPWEEIKTSYAGVKEKYLSE--YCFSG 396
DB 407 SYPYDTRPLGMPISFTLINE-LNDLARIVCKBETWNSVFSGIAGSLDELESDFHCLIDL 465
QY 397 TYILSLILQGVHFTADSWEHIFHTGKIQGSADAGWTGLCYMLNL 438
DB 466 SFQVSLHTGYDIPLO--RELRTGKKIANKEIGWCLGASLPL 505
Search completed: March 7, 2005, 13:24:56
Job time : 16.072 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 63.8824 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147a-3_COPY_21_476

Perfect score: 2440

Sequence: 1 VSHRNQQTWFGIFLSSTQN.....NLTNMIPAEQLPLSHST 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	96.2	510	1 ENP1_HUMAN	P49961 homo sapien
2	1836	75.2	510	1 ENP1_MOUSE	P55772 mus musculus
3	1836	75.2	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1831	75.0	510	2 Q921Q6	Q921q6 mus musculus
5	1818	74.5	372	2 Q86VW3	Q86vw3 homo sapien
6	1795.5	73.6	511	1 ENP1_RAT	P97687 rattus norv
7	1717	70.4	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1692.5	69.4	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	64.5	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1455	59.6	508	2 Q8DPS1	Q6dfsl xenopus tro
11	1420	58.2	508	2 Q8GP74	Q6gp74 xenopus lae
12	1311.5	53.8	492	2 Q8DC46	Q6dc46 brachydanio
13	1048	43.0	497	2 Q8VQ22	Q6uq22 mus musculus
14	1004	41.1	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	40.9	493	2 Q90X66	Q90x66 gallus gall
16	980.5	40.2	454	2 Q8ZM69	Q6zm69 brachydanio
17	971.5	39.8	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	39.5	495	1 ENP2_MOUSE	Q55026 mus musculus
19	964.5	39.5	495	2 Q921R1	Q921r1 mus musculus
20	961	39.1	494	1 ENP2_CHICK	Q7t014 brachydanio
21	953	39.1	494	1 ENP2_CHICK	P79784 gallus gall
22	943	38.6	500	2 Q8NV19	Q6nv19 xenopus tro
23	937.5	38.4	502	2 Q66L64	Q66l64 brachydanio
24	936	38.4	526	2 Q6GNA4	Q6gna4 xenopus lae
25	913.5	37.4	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	37.3	529	1 ENP3_HUMAN	O75355 homo sapien
27	907.5	37.2	458	2 Q6UVZ0	Q6uvz0 homo sapien
28	907.5	37.2	495	1 ENP2_HUMAN	Q9y5l3 homo sapien
29	902.5	37.0	529	2 Q8BFW6	Q8bfw6 m mus muscu
30	854	35.0	453	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	33.8	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	27.0	544	2 Q7YTA4	Q7yta4 schistosoma
33	620.5	25.4	300	2 Q8K0L2	Q8k0l2 mus musculus
34	596.5	24.4	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	505	20.7	483	2 Q9XI62	Q9xi62 arabidopsis
36	504	20.7	488	2 Q6NQ48	Q6nq48 arabidopsis
37	494	20.2	503	2 Q94AF8	Q94af8 arabidopsis
38	494	20.2	503	2 Q6H1D8	Q6h1d8 arabidopsis
39	485	19.9	537	2 Q6Z543	Q6z543 oryza sativ
40	483	19.8	634	2 Q6FCR2	Q6frc2 candida gla
41	482.5	19.8	336	2 Q8CCV2	Q8ccv2 mus musculus
42	471.5	19.3	555	2 Q94E22	Q94e22 arabidopsis
43	469.5	19.2	405	2 Q9M9T7	Q9m9t7 arabidopsis
44	468.5	19.2	611	2 Q6DH30	Q6dh30 brachydanio
45	465.5	19.1	555	2 Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1

ID	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
AC	P49961; Q9UQ09; Q9Y3Q9;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)			
DE	(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).			
GN	Name=ENTPD1; Synonyms=CD39;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J., Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;			
RA	"The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization."			
RT	J. Immunol. 153:3574-3583(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RP	TISSUE=Umbilical vein;			
RX	MEDLINE=97149443; PubMed=8996251;			
RA	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K., Millan M., Hancock W.W., Bach F.H.;			
RA	"Loss of ATP diphosphohydrolase activity with endothelial cell activation."			
RT	J. Exp. Med. 185:153-163(1997).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).			
RP	TISSUE=Placenta;			
RX	MEDLINE=99332082; PubMed=104051171; DOI=10.1016/S0014-5793(99)00751-6;			
RA	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T., Titani K., Fujimura Y., Narita N.;			
RA	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II."			
RT	FEBS Lett. 453:335-340(1999).			
RL	[4]			
RN	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.			
RP	TISSUE=Placenta;			
RX	MEDLINE=9609723; PubMed=8529670;			
RA	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;			
RT	"Purification and properties of human placental ATP diphosphohydrolase."			
RL	Eur. J. Biochem. 234:66-74(1995).			
RN	[5]			
RP	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND 399-405 (ISOFORM PLACENTAL I).			
RC	TISSUE=Placenta;			

RA RX MEDLINE=99062444; PubMed=9846014;
RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.,
RT "Placental ecto-ATP diphosphohydrolase: its structural feature
RT distinct from CD39, localization and inhibition on shear-induced
RT platelet aggregation.";
RL Inc. J. Hematol. 68:297-310(1998).
RN [6]
RP FUNCTION.
RP MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase.";
RL J. Biol. Chem. 271:33116-33122(1996).
RN [7]
RP CHARACTERIZATION.
RP MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;
RA Wang T.F., Guidotti G.;
RT "CD39 is an ecto-(Ca2+, Mg2+)-ATPase.";
RL J. Biol. Chem. 271:9898-9901(1996).
RN [8]
RP PALMITOYLATION.
RP MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
RA Kozlak K., Kaczmarek E., Kittel A., Sevigny J., Blustajn J.K.,
RA Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Gawi I.,
RA Robson S.C.;
RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
RT caveolae.";
RL J. Biol. Chem. 275:2057-2062(2000).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC
CC -!- HYDROLYZES ATP AND ADP EQUALLY WELL.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H2O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Vascular;
CC IsoId=P49961-1; Sequence=Displayed;
CC Name=Placental I;
CC IsoId=P49961-2; Sequence=VSP_003607;
CC Name=Placental II;
CC IsoId=P49961-3; Sequence=VSP_003608, VSP_003609;
CC -!- TISSUE SPECIFICITY: Expressed primarily on activated lymphoid
CC cells. Also expressed in endothelial tissues. The vascular isoform
CC and the placental isoform II are present in both placenta and
CC umbilical vein, whereas placental isoform I is present in placenta
CC only.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and
CC 7.5-8.0 with ADP.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S73813; AAB32152.1; -;
CC EMBL; U87967; AAB47572.1; -;
CC EMBL; AJ133133; CAB41886.1; -;
CC EMBL; AJ133134; CAB41887.1; -;
CC PIR; I56242; I56242.
CC Genew; HGNC:3363; ENTPD1.
CC MIM; 601752; -;
DR RX GO:0005887; C:integral to plasma membrane; TAS.
DR GO:0007596; P:blood coagulation; TAS.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;
KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
KW Transmembrane.
FT DOMAIN 1 16 Cytoplasmic (Potential).
FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 478 Extracellular (Potential).
FT TRANSMEM 479 499 Potential.
FT DOMAIN 500 510 Cytoplasmic (Potential).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 4 MEDT -> MKGYKDLTSQQ (in isoform Placental
FT I and isoform Placental II).
FT FTId=VSP_003607.
FT VARSPLIC 272 299 VASNEILRDFCFHFGKVKVNVSDLYKT -> ASITQSRPA
FT PFTSAPPAPTSCCFLEFIQ (in isoform Placental
FT II).
FT FTId=VSP_003608.
FT VARSPLIC 300 510 Missing (in isoform Placental II).
FT CONFLICT 57 58 SS -> G (in Ref. 5).
FT CONFLICT 162 162 D -> K (in Ref. 4).
FT CONFLICT 208 208 T -> TGET (in Ref. 5).
FT CONFLICT 248 248 V -> Y (in Ref. 5).
SQ SEQUENCE 510 AA; 57964 MW; BAD87D249649159 CRC64;
Query Match 96.2%; Score 2348; DB 1; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.8e-174;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFVQK 77
DB 38 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFVQK 97
QY 78 VNEIGYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 137
DB 98 VNEIGYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
QY 138 NYDPDFQGARIIITQEGAGYGVITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 197
DB 158 NYDPDFQGARIIITQEGAGYGVITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
QY 198 STQVTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALMOKLAKDIOVASNEI 257
DB 218 STQVTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALMOKLAKDIOVASNEI 277
QY 258 LRDPCHPHGKVVNVSDLYKTKTRFEMTLFPQFEIOGIGNYQCHOSILELFTSY 317
DB 278 LRDPCHPHGKVVNVSDLYKTKTRFEMTLFPQFEIOGIGNYQCHOSILELFTSY 337
QY 318 CPYSQCAFNGIIFLPPLQGDGFASAFVFMKFLNLTSKYSQKVTMMKKFCAQPWEEI 377
DB 338 CPYSQCAFNGIIFLPPLQGDGFASAFVFMKFLNLTSKYSQKVTMMKKFCAQPWEEI 397
QY 378 KTSYAGVKYKLSYCFSGTYIISLLQGYHFTADSWEHHTFTKIQGSDAGWTGLYMLN 437
DB 398 KTSYAGVKYKLSYCFSGTYIISLLQGYHFTADSWEHHTFTKIQGSDAGWTGLYMLN 457
QY 438 LTNNIPAEQLSTPLSHST 456
DB 458 LTNNIPAEQLSTPLSHST 476
RESULT 2
ENPI_MOUSE

FT	CARBOHYD	73	73	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	226	226	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	291	291	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	428	428	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	457	457	N-linked (GlcNAc. . .)	(Potential).
SQ	SEQUENCE	510 AA;	5720S MW; 8BGA61I13D2EI3930 CRC64;		

Query Match		75.2%;	Score 1836;	DB 1;	Length 510;
Best Local Similarity		75.8%;	Pred. No. 2.7e-134;		
Matches	338;	Conservative	46;	Mismatches	58;
				Indels	4;
				Gaps	3;

QY	13	I FLSSTQNKALPENVKYGIVLDAGSSHTSLYYIKWPAEKENDTGVVHVVECKVGPGIS	72
Db	33	I A VGLTKNQPLPENVKYGIVLDAGSSHTNLYIKWPAEKENDTGVVQQLEECQVKGPGIS	92
QY	73	KPVQKNKEIGYLTDOMEAREVIPSQHQTTPVYLGTAGMRLLRMESEELADRVLDVV	132
Db	93	KYAQKTDETGAYLAECMELSTLIPTSKHQTFVYLGATAGMRLLRMESEQSADVLAAV	152
QY	133	ERLSNSYPDFOGARIITGOEGAGYCWITINVLLGKFOSKTRWFSTVPVTNNQETFGAL	192
Db	153	STSLKSYPDFOGAKIITGOEGAGYCWITINVLLGRFTEQSWLSLI--DSQKETFGAL	211
QY	193	D LGGASTQTVTFPQNOTIESPDNALQFRUYLGYKDYNVYTHSFCLCYGHQDALWKLANDIQV	252
Db	212	D LGGASTQITVFQPNSTIBSPNSLQFRUYGEDYTVYTHSFCLCYGHQDALWKLANDIQV	271
QY	253	ASNEILRDCFPHPGYKKVNVSDLYKTCTKPFEMTLPPQOEIIGIGNVQQCHQSI LEL	312
Db	272	SSGGVLKDCFPNPGYEKVNVSELVGTCTKPFEEKLPDQFRIQGTGDYEQCHQSI LEL	331
QY	313	FNTSYCPYSQCAPNGIFLPPLOQDFGARSAFYVMKFLNLTSBK--VSQEKVTMMKKFC	370
Db	332	FNNSHCPYSQCAPNGVFLPPLHGSGFARSAFYFMVDFFKVAKNSVISEKMTETITKNPC	391
QY	371	AQFWBEIKTSYAGVKEKYLSYCFSGTYTILSLLOGYHFTADSWEHIHFIGTIQSGDAGW	430
Db	392	SKSWEEKTSYSPVKEKYLSYCFSGAYILS--LLQGYNFTDSSWEQHFMWGKIDSNAGW	450
QY	431	TILGYMLNLTNMIPAEOPLSTPLSHST	456
Db	451	TILGYMLNLTNMIPAEOPLSPPLPHST	476

RESULT 3

Q8CDV7

ID	Q8CDV7	PRELIMINARY;	PRT;	539 AA.
AC	Q8CDV7;			
DT	01-NAR-2003 (TrEMBLrel. 23, Created)			
DT	01-WAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:492511C05 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.			
DE	Name=Entpdl;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelesostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=C57BL/6J; TISSUE=Testis;			
RX	MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carrincci P., Hayashizaki Y.,			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			

Full-length mouse cDNA collection.

DR GO; GO:0006200; P-ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 75.0%; Score 1831; DB 2; Length 510;
Best Local Similarity 75.6%; Pred. No. 6.7e-134;
Matches 337; Conservative 46; Mismatches 59; Indels 4; Gaps 3;

QY 13 IFLSTQNKALPENVKYGIIVLDAGSSHTSLIYKWPBAKENDTGVVHVQVSCRVKPGGIS 72
DB 33 IAVGLTQNKLPENVKYGIIVLDAGSSHTSLIYKWPBAKENDTGVVQVQLEECQVKGPGIS 92
QY 73 KPVQKVNIEGIVLTDCEMRAREVTPRSQHQETPVYLGATAGMRLLRSEBELADRLVDV 132
DB 93 KYAKTDEIGAYLAECMELSTELIPTSXHHQTPVYLGATAGMRLLRSEBELADRLVDV 152
QY 133 ERSLSNYPDFQGARIIITQBEAGYGVITINLLGKFSQKTRWFSIVPYETNNQETFGAL 192
DB 153 STSLKGYFPDFQGARIIITQBEAGYGVITINLLGFRFTQEQSWLSLIS-DSQKQETFGAL 211
QY 193 DLGGASTQVTPVQNTTIESPDNALQFLYKGVNVTYTHSLCYGKQDALWOKLAKIOV 252
DB 212 DLGGASTQITVFPQNTTIESPENSLOFLRYGEDYTVYTHSLCYGKQDALWOKLAKIOV 271
QY 253 ASNEILRDPCHFGYKGVNVTYTHSLCYGKQDALWOKLAKIOV 312
DB 272 SSGVGLKDPCHFGYKGVNVTYTHSLCYGKQDALWOKLAKIOV 331
QY 313 FNTSCYPSQCAFNGIFLPPQDGFAGPSAFYFVNMKFLNLTSEK--VSQEKVTMMKKFC 370
DB 332 FNNHCHPISQCAFNGIFLPPQDGFAGPSAFYFVNMKFLNLTSEK--VSQEKVTMMKKFC 391
QY 371 AQPWEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIFIKIQSGDAGW 430
DB 392 SKSWEETKTSYPSVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIFIKIQSGDAGW 450
QY 431 TLGYMLNLTNMPAEQPLSTPLSHST 456
DB 451 TLGYMLNLTNMPAEQPLSTPLSHST 476

RESULT 5
Q86VW3 PRELIMINARY; PRT; 372 AA.
ID Q86VW3
AC Q86VW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356EE3 CRC64;

Query Match 74.5%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.6e-133;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 MESEELADRLVDVVERSLSNYPDFQGARIIITQBEAGYGVITINLLGKFSQKTRWFSI 178
DB 1 MESEELADRLVDVVERSLSNYPDFQGARIIITQBEAGYGVITINLLGKFSQKTRWFSI 60
QY 179 VPYETNNQETFGALDLGGASTQVTPVQNTTIESPDNALQFLYKGVNVTYTHSLCYGK 238
DB 61 VPYETNNQETFGALDLGGASTQVTPVQNTTIESPDNALQFLYKGVNVTYTHSLCYGK 120
QY 239 DOALWOKLAKIOVASNEILRDPCHFGYKGVNVTYTHSLCYGK 298
DB 121 DOALWOKLAKIOVASNEILRDPCHFGYKGVNVTYTHSLCYGK 180
QY 299 IGNYQQCHQSILELNTSYCPYSCAFNGIFLPPQDGFAGPSAFYFVNMKFLNLTSEKVS 358
DB 181 IGNYQQCHQSILELNTSYCPYSCAFNGIFLPPQDGFAGPSAFYFVNMKFLNLTSEKVS 240
QY 359 QEKVTMMKKFCQAPWEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIF 418
DB 241 QEKVTMMKKFCQAPWEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIF 300
QY 419 FIGIKQSDAGTGLGYMLNLTNMPAEQPLSTPLSHST 456
DB 301 FIGIKQSDAGTGLGYMLNLTNMPAEQPLSTPLSHST 338

RESULT 6
ENPI_RAT STANDARD; PRT; 511 AA.
ID ENPI_RAT
AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=92121928;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
apyrase (CD39) gene.",
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Cochlea; DOI=10.1016/S0169-328X(99)00244-2;
 RX MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
 RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 termination of purinergic transmission.";
 RL Brain Res. Mol. Brain Res. 73:85-92(1999).
 RN [3]
 RP SEQUENCE OF 432-511 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=96031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
 RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 rat brain.";
 RL Neuropharmacology 36:1189-1200(1997).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
 kidney, liver, muscle, thymus, lung and spleen.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U81295; AAC53195.1; -;
 DR EMBL; Y15685; CAA75730.1; -;
 DR RGD; 69265; Rntpd1.
 DR InterPro: IP000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 FT DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 511 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 332 332 F -> L (in Ref. 2).
 SQ SEQUENCE 511 AA; 57408 MW; 4CC123D3B64C193 CRC64;
 Query Match 73.6%; Score 1795.5; DB 1; Length 511;
 Best Local Similarity 73.8%; Pred. No. 3.9e-131;
 Matches 329; Conservative 52; Mismatches 62; Indels 3; Gaps 3;
 QY 13 IFLSTONKALPENVKYGLVDAGSSHTSLVIYKWPAREKNDGTGVHVEBCRVKGGPIS 72
 DB 33 IAVGLTHNKLPEPNVKYGLVDAGSSHTSLVIYKWPAREKNDGTGVHVEBCRVKGGPIS 92
 QY 73 KFOVKNEIGYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELDADRLVDV 132
 DB 93 KYAOKTDEIAAYLAECMKMSTERIPASKOHTPPVYLGATAGMRLLRMESEKQSADEVLA 152
 QY 133 ERSLSNPPDFQGARIIITQEGAYGWTINYLKGSOKTRWSPVPEYNNQETGAL 192
 DB 153 SRSLSKSPYDFQGARIIITQEGAYGWTINYLKGRFTQEOSWLNLFIS-DSQKQATFGAL 211

QY 193 DLGCASTQVTFVPQNOTIETSDNALQFRLYGKDYNYVTHSFLCYGKDALWQKLAKDIQV 252
 DB 212 DLGSGSTQVTFVPLNQLTLEAPETSLQFRLYGTDYTVVTHSFLCYGKDALWQKLAKDIQV 271
 QY 253 ASNEILRDCPFHFGYKKNVNSDLYKTPCTKRPMETLPTQOFPIQIGNYQOCHOSILEL 312
 DB 272 SSGGILKDCPFYKKNVNSDLYKTPCTKRPEKLFPNQFQVQGTGDEYEQCHOSILKF 331
 QY 313 FNTSYCPYSOCAENGIFLPLQDGFAPSAFYVMKFL-NLTSEKV-SQSKVTMMKKPC 370
 DB 332 FNNSHCPYSOCAENGIFLPLQDGFAPSAFYVMDFFKWANDSVSSQERMEITIKNFC 391
 QY 371 AQPWEIKTYSAGYKELSEYCFSGTYILSLQLQGYHFTADSWEHIFTKIGKQSGDAGW 430
 DB 392 SKPWEVKASYPTVKEKYLSEYCFSGTYILSLQLQGYHFTADSWDQHFHFKIKDSNAGW 451
 QY 431 TLGYMLNLTMNIPAEQPLSTPLSHST 456
 DB 452 TLGYMLNLTMNIPAEQPLSTPLPHST 477
 RESULT 7
 ENPI_PIG ID ENPI_PIG STANDARD; PRT; 510 AA.
 AC QSMYU4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 03-JUL-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPase) (Ecto-ATP diphosphohydrolase) (ATPDase) (lymphoid cell
 DE activation antigen) (Ecto-apyrase) (CD39 antigen).
 GN Name=ENTPD1; Synonyms=CD39;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic endothelium;
 RX MEDLINE=20325090; PubMed=10866813;
 RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O.,
 RA Savigny J.;
 RT "Distribution, cloning, and characterization of porcine nucleoside
 RT triphosphate diphosphohydrolase-1.";
 RL Eur. J. Biochem. 267:4106-4114(2000).
 RN [2]
 RP SEQUENCE OF 202-220.
 RC TISSUE=Pancreas;
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Koziak K., Savigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach P.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Highest expression found in vascular
 endothelium, smooth muscle, spleen and lung.
 CC -1- PTM: Cleaved into two polypeptides that seem to stay together by
 noncovalent interactions.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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ENBL; AJ133746; CAB95871.1; -,		Ectonucleoside triphosphate
InterPro; IPR000407; GDAI_CD39_NTPase.		diphosphohydrolase 1.
Pfam; PF011150; GDAI_CD39; 1.		Ectonucleoside triphosphate
PROSITE; PS01238; GDAI_CD39_NTPASE; 1.		diphosphohydrolase 1 27 kDa subunit.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;		Ectonucleoside triphosphate
Magnesium; Transmembrane.		diphosphohydrolase 1 54 kDa subunit.
CHAIN 1 510		Cytoplasmic (Potential).
FT FT		Potential.
FT CHAIN 1 201		Extracellular (Potential).
FT FT		Potential.
FT CHAIN 202 510		Potential.
FT FT		Cytoplasmic (Potential).
FT DOMAIN 1 16		N-linked GlcNAc. .) (Potential).
FT TRANSMEM 17 37		N-linked GlcNAc. .) (Potential).
FT DOMAIN 38 477		N-linked GlcNAc. .) (Potential).
FT TRANSMEM 478 498		N-linked GlcNAc. .) (Potential).
FT DOMAIN 499 510		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 73 73		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 245 245		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 274 274		N-linked GlcNAc. .) (Potential).
FT CARBOHYD :291 291		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 333 333		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 370 370		N-linked GlcNAc. .) (Potential).
FT CARBOHYD 457 457		N-linked GlcNAc. .) (Potential).
FT CONFLICT 203 203		G > S (in Ref. 2).
SQ SEQUENCE 510 AA; 57757 MW; 82F8689040D7735 CRC64;		

Query Match	70.4%;	Score 1717;	DB 1;	Length 510;
Best Local Similarity	70.4%;	Pred. No. 5e-125;		
Matches 312; Conservative	63;	Mismatches 66;	Indels 2;	Gaps 2;

15	QY	LSSTQNKALPENVKYGIIVLDAGSSHTSLYYTKWPAEKENDTGVVHQVEBCRVKPGISKF	74
35	DB	LGHTQNKPLPENVKFGLVLDAGSSHTSLYYTKWPAEKENDTGVVSVQVEECKLXPGISEF	94
75	QY	VQKVNEIGIYLTDCMERAREVIPSROHOETPVYLGATAGMRLLRMESEELADRVLDVVER	134
95	DB	AKLGEIDIYLEACMERARIVVPKSHAETPVYLGATAGMRLLRKMNENLASKILSTVAE	154
135	QY	SLSNYPDFDQAGARIITGOEBGAYGWITINYLKCKFSQKTRFWISVPYETNNQETFGALD	194
155	DB	SITRYPDFDQAGARIITGOEBGAYGWITINYLKDKFIQKSGWNLKPKRGDTQETYGALD	214
195	QY	GGASTQTVFPVONQTTESPDNALQFRLYGKDVNVYTHSFICYGKQALMOKLAKDIOVAS	254
215	DB	GGASTQITVPFVONQVLESSENTLHFRLYGKNYSVYTHSFICYGKQDQALLQKLRKDLK-NT	273
255	QY	NEILRDPCHFGYKVVNVSDLYKTPCTKGFEMTLPQOQFEIOIGINYQOCHOSIILEFN	314
274	DB	NGTHBPCFHSYGQRRNVNLSHYEAPCTRREFTLSLPEPELIEIOGTGDFQKQCSIRPLFN	333
315	QY	TSYCPYSQCAPNGIFLPPLOGDGCASAFYFVWKFLNLTSEKVS-QBKVTEMMKKFCAQP	373
334	DB	TSYCPYSRCSFDGFLPLPQGDFAAFSAFYVNGFLNLTSEGSFOSKVTSTLEAFCSRP	393
374	QY	WEBIKTSYAGVKEKYLSEYCSFTYIILSLLLQGVHFTADSWEHIHFIGIKQSDAGWTLG	433
394	DB	WAELOMYFGDVKEKYLSEYCSFTYIILTLLLSGVHFTAEWTKNIHFMKVQSTSVGMTLG	453
434	QY	YMLNLNTMIPAEQPLSTPSHST	456
454	DB	YMLNLNTMIPSEFPSSSTRISHST	476

RESULT 8		
ENP1_BOVIN		
ID	ENP1_BOVIN	STANDARD;
AC	O18956;	PRT; 513 AA.
	DT 16-OCT-2001	(Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (CD39 antigen) (Ecto-apyrase).
Name=ENTPD1; Synonyms=CD39;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Aortic endothelium;
Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
TISSUE=Aorta;
MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
Kaczmarek E., Kozlak K., Seivigny J., Siegel J.B., Anrather J.,
Beaudoin A.R., Bach F.H., Robson S.C.;
Identification and characterization of CD39/vascular ATP
diphosphohydrolase.;
J. Biol. Chem. 271:33116-33122(1996).
-1- FUNCTION: In the nervous system, could hydrolyze ATP and other
nucleotides to regulate purinergic neurotransmission. Could also
be implicated in the prevention of platelet aggregation.
Hydrolyzes ATP and ADP equally well.
-1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
-1- COFACTOR: Requires calcium and magnesium.
-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.

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or send an email to license@isb-sib.ch).

EMBL; AF005940; AB62382.1; -	DR
InterPro; IPR000407; GDAL_CD39_NTPase.	DR
Pfam; PF01150; GDAL_CD39; 1.	DR
PROSITE; PS01238; GDAL_CD39_NTPASE; 1.	DR
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;	KW
Magnesium; Transmembrane.	KW
DOMAIN 1 16	FT
TRANSMEM 17 37	FT
DOMAIN 38 481	FT
TRANSMEM 482 502	FT
DOMAIN 503 513	FT
CARBOHYD 73 73	FT
CARBOHYD 227 227	FT
CARBOHYD 245 245	FT
CARBOHYD 307 307	FT
CARBOHYD 336 336	FT
CARBOHYD 373 373	FT
CARBOHYD 460 460	FT
CONFLICT 97 97	FT
CONFLICT 101 103	FT
CONFLICT 464 464	FT
SEQUENCE 513 AA; 58113 MW; 20FE98F2786D2F96 CRC64;	SQ

Query Match 69.4%; Score 1692.5; DB 1; Length 513;
Best Local Similarity 69.5%; Pred. No. 4.1e-123;
Matches 310; Conservative 64; Mismatches 67; Indels 5; Gaps 3;

QY 15 LSTQNKALPENVKYGIVLDAAGSHSTSLIIYKWPAAEKENDTGVHVQVECRVKGPGISKF 74
35 LGHTONKALPENVKFGIVLDAAGSHSTSLIIYKWPAAEKENDTGVVTOIEBNNKVGPGISGF 94
Db


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QY 75 VQKNEIGYLTDCMERAREVIPSQHOETPVYIGATAGMRLRMESEELADRVLDVVER 134
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 95 AKVNEINVLTACWERAQKVPISIQHMETPVYLGATAGMRLRMENKQWADKILAAVAS 154
QY 135 SLSNYPDFOGARIITGOEBGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFGALDL 194
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 155 SISEYPPDFOGARIISGOEBGAYGWTINVLGKFTOKLSWENLKPSKODTQETYGALDL 214
QY 195 GGASTQVTFVFPQNTIESPDNALQFRLYGKDYNNVTHSFLCYGKQDQALWOKLAKDIQVAS 254
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 215 GGASTQITVFPQNETTSPNNLYFRLYGKNYSVYTHSFLCYGKQDQALLGLGLQ-GT 273
QY 255 NEILRDCFPHPGYKVVNVDLYTKPTKPEMT---LPQCFEIQIGNYQOCHQSILE 311
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 274 NGIITHEPCFHSYMRKIMVNLBNFGCTKRLHNSFSFYPLVDIIRGAGNFORCQSIQ 333
QY 312 LFNTSYCPYSCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEK-VSQEKTVMEMMKFC 370
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 334 LFNTSYCPYSCSFGVFLPLHCGQGAFAFYVMKFLNLTSESVSVQLEKLEFC 393
QY 371 AQPWEETKTSYAGVEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHTKIQSGDAGW 430
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 394 AQRWEEVQKNGEVEKYLSEYCFSGTYIIVLLVINGVHFTAESWKNIFHFNKVRSTDVGW 453
QY 431 TLGYMLNLTNMPAEQPLSTPLSHST 456
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 454 TLGYMLNLTNKPABEPMSPPLPHST 479

RESULT 9
Q8CEB1 PRELIMINARY; PRT; 420 AA.
ID Q8CEB1
AC Q8CEB1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732419M6 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence. (fragment).
GN MusMusculi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Hashiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1;
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; P:ATP catabolism; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
Query Match 64.5%; Score 1574; DB 2; Length 420;
Best Local Similarity 74.5%; Pred. No. 5.3e-114;
Matches 289; Conservative 42; Mismatches 53; Indels 4; Gaps 3;
QY 71 ISKPVQKNEIGYLTDCMERAREVIPSQHOETPVYIGATAGMRLRMESEELADRVLD 130
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 ISKYAQKTDEIGAYLAECMELTELPTSKHHQTPVYLGATAGMRLRMESEGADEVLA 60
QY 131 VVERSLSNYPDFOGARIITGOEBGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFG 190
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 61 AVSTLSKSYFDFQGAIIITGOEBGAYGWTINVLGKFTQEQSWLSLIS-DSQKQSTFG 119
QY 191 ALDLGGASTQVTFVFPQNTIESPDNALQFRLYGKDYNNVTHSFLCYGKQDQALWOKLAKDI 250
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 120 ALDLGGASTQITVFPQNETTSPNNLYFRLYGKNYSVYTHSFLCYGKQDQALLGLGLQ 179
QY 251 QVASNETLRDPCFHPGYKVVNVDLYTKPTKPEMTLPQCFEIQIGNYQOCHQSIL 310
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 180 QVSSGGVLKDCPCFNPGYKVVNVDLYTKPTKPEMTLPQCFEIQIGNYQOCHQSIL 239
QY 311 ELFNNTSYCPYSCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEK--VSQEKVTMMKK 368
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 240 ELFNNTSYCPYSCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEK--VSQEKVTMMKK 299
QY 369 FCAQFWEEIKTSYAGVEKYLSEYCFSGTYIISLLQGYHFTADSWEHIFHTKIQSGDA 428
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Db 300 FCSKSWETKTSYPSVKKYLSEYCFSGAYILS-LLQYNTFGSSWEQIHFHWGKIKDSNA 358
Qy 429 GWTGLYMLNLTNMPAEQPLSTPLSHST 456
Db 359 GWTGLYMLNLTNMPAEQPLSTPLSHST 386

RESULT 10
Q6DFS1
ID Q6DFS1 PRELIMINARY; PRT; 508 AA.
AC Q6DFS1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Enpdl-prov prov.
GN Name=entpdl-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076662; AAH76662.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39 Nipase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39 NTPASE; 1.
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 59.6%; Score 1455; DB 2; Length 508;
Best Local Similarity 57.3%; Pred. No. 1.2e-104;
Matches 268; Conservative 80; Mismatches 102; Indels 18; Gaps 4;

Qy 4 RNOQTWPEG--IFLSS-----TONKALPENVKYGLVDAGSSHTSLYIKW 47
Db 8 KQKTHKKVIFLGFALFVLGVSILVAIVQNKPLPKNIKIGVLDAGSSHTSVIYEW 67
Qy 48 PAEKENDTGVVHVEEKRKVGSKFQVKVNEIGYILTDCEWREAREVIPSQHQETPVY 107
Db 68 PAEKENDTGVVQIQNECKVEGNGISSYGHPEPKAGLSLQKCNKARQVPEKQRETPVY 127
Qy 108 LGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITQEGEGAWITINLLG 167
Db 128 LGATAGMRLRLTNATMAEEVLSSVENTLRSFPDFQGARITQEGEGAWITINLLG 187
```

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Qy 168 KFSQKTRWFSTIVPVETNNQETFGALDGGASTQVTFVQNOTIESPDNALQRLYKGDYN 227
Db 188 NFIQDSQGWFKYIP-NFKPTETSGALDGGASTQITFESKRE-IESQENSLHFLYKGSYD 245
Qy 228 VYTHSFCLYCKDQALWQKLAKDIQVASNEILRDCFHCPGKVKVNVSDLYKTPCTKREM 287
Db 246 IYTHSFCLYCKDQALRIQIANSIHKDATSIDLLDFCNFGRNASTNDLSSPCISKURI 305
Qy 288 TLPFQPEIQIGNYQQCHOSILELFTNTSYCPYSQCAFNGIFLPLQGDGFAFAFYFVM 347
Db 306 PTAPSTLDIRGTGNYQJCKRNQVAFNRTHCTYSHCSFNGVFPQSLDGTGFAFSAYFVM 365
Qy 348 KFLNLTSEKVSQEKVTEMKKFCAQPWEIEKTSYAGVKEKYLSEYCFSGTYLSLLQGY 407
Db 366 NFLNLTNEQMSLDKVKETVERHCSRPWDEVKDPKIKEKYLSEYCFSGTYLSLLQGY 425
Qy 408 HPTADSWEHITHFICKIQSGDAGWTGLGYMLNLTNMPAEQPLSTPLSHS 455
Db 426 GFSSENWDIRFLGKIKDSAGWTGLGYMLNLTNMPAEQPLSTPLSHA 473

RESULT 11
Q6GP74
ID Q6GP74 PRELIMINARY; PRT; 508 AA.
AC Q6GP74;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MGC80631 protein.
GN Name=MGC80631;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
```


RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6; TISSUE=Liver;
RA Bignonnesse F., Levesque S.A., Kukulski F., Lecka J., Robson S.C.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY364442; AA04519.1; -
DR GO: GO:0004050; F:aprase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase.
SQ SEQUENCE 497 AA; 5450 MW; 00DE822BEEB1BDF CRC64;

Query Match 43.0%; Score 1048; DB 2; Length 497;
Best Local Similarity 45.7%; Pred. No. 5.7e-73;
Matches 213; Conservative 79; Mismatches 136; Indels 40; Gaps 11;

Qy 8 TWFGIGFLS-----STQKALPENVKYGIIVLDAGSSHTSLIYKQPA 49
Db 4 SWKRVFMALLGVAAASGLTWLVLILVKAINVLLPADTKFGIVDFDAGSSHTSLFYQWPA 63

Qy 50 EKENDTGVHVECRVKPGISKFVQKVEIGIYLTDCMERAREVIPSQHOETPVVLG 109
Db 64 NKEDTGVSWQALTCQIEGPGISSTSDPTQAGESLKSCLSEALALPQAOHPETPTFLG 123

Qy 110 ATAGMRLIRMESEELADRLVDVRSLSNYPDFQAGRIITGOBEGAYGWTITNYLLG-- 167
Db 124 STAGMRLLSQNSOARDILAAVQSLSKSPVDFWAGKILAGQDEAGFGWITINVLGML 183

Qy 168 -KFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTIESPDNALQFLYKDY 226
Db 184 LKYS-SGQW--ILPEE---GMLVAGALDGGASTQISFVPPQNPILDQ-STQVTFRLYGANY 236

Qy 227 NVYTHSLFYCKDQALQKLAQ-----DIOVASNEILRDCFHPGKVVVNSDLYKTP 280
Db 237 SVYTHSLFYCKDQALQKLAQ-----VRHPCYHSYGQAILPLSLSDSP 293

Qy 281 CTRAFEMTLPQFOEIQIGNYOCHOSILELFTSYCP-YSQAFNGIFLPPILQGDGFA 339
Db 294 CIHTTDSLNTQNLTVETGDPGNCVVALSLFNFSSCKGKDCAFNGIYPPVHGQFYA 353

Qy 340 PSAYFYVKKFLNLTSEKVSQEKVEMKKFCAQWEEIKTSYAGVKYLSYCFSGTYI 399
Db 354 FSNFYTFHFLNLTSRQ-SLNTVNDTVKFCQKPKLVEVSPG-QERWLRDYCASGLYI 411

Qy 400 LSLLLQGVHFTADSEHIFHTGKLGSDAGWTGLGYMLNLTNMIAPAEQ 447
Db 412 LVLLLEGYKFSSETWPNFQFOKQAGDITDGTGLGMLNLTGMIAPAEAP 459

RESULT 14
ENPI_CHICK
ID_ENPI_CHICK ; STANDARD; PRT; 493 AA.
AC O93295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE activation antigen (Ecto-ATP diphosphohydrolase) (Arpase) (Lymphoid cell
GN Name=ENTPD1; Synonyms=CD39;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE=Oviduct;
RX MEDLINE=98298108; PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RT "Molecular cloning of the chicken oviduct ecto-ATP-

diphosphohydrolase."; J. Biol. Chem. 273:16043-16049(1998).
[2]
SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RX MEDLINE=97442428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
RA Lewis-Carl S., Kirley T.L.;
RT "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-apyrase."; J. Biol. Chem. 272:23645-23652(1997).
CC -I- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -I- COFACTOR: Requires calcium and magnesium (By similarity).
CC -I- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL: AF041355; AAC26491.1; -
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPase; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 7 Cytoplasmic (Potential).
FT TRANSMEM 8 283 Potential.
FT DOMAIN 29 463 Extracellular (Potential).
FT TRANSMEM 464 486 Potential.
FT DOMAIN 487 493 Cytoplasmic (Potential).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
FT CONFLICT 16 16 C -> W (in Ref. 2).
FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
SQ SEQUENCE 493 AA; 54034 MW; F14FP4C3AA2F3603 CRC64;

Query Match 41.1%; Score 1004; DB 1; Length 493;
Best Local Similarity 45.7%; Pred. No. 1.5e-69;
Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

Qy 23 LPENVKYGIVLDAGSSHTSLIYKVPKAEKNDTGTVHQBECRVKPGISGKVKQVNEIG 82
Db 35 LPPTKTKGLVDFDAGSTHTALYVYQWPKADKGTGVSVQSVCTVNGSGISSYADDPAG 94

Qy 83 IYLTDCMERAREVIPSQHOETPVYLGATGMRLIRMESEELADRLVDVRSLSNYPFD 142
Db 95 ASLKPCLDKAMAVIPVEQQWQPTPYLGATGMRLIRMESEELADRLVDVRSLSNYPFD 154

Qy 143 FQAGRIITGOBEGAYGWTITNYLLG---KFSQKTRWFSIVPYETNNQETFGALDGGAST 199
Db 155 FRGAQILTGNEBGSFGWITVNYLLETLIKFSFAGKW-----EHPQNTFVGLDGGAST 209

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Qy 200 QVTFVQNQTIESPDNALQRLYKDYNNVYTHSFLCYGKQQA---LWQKLAKDIOVASNE 256
Db 210 QITFQP-GVTIEDKNTSVLRLYGTNSLYTHSVLCYGOIQASKRLMAALHQDGSYQN- 267
Qy 257 ILRDPCHPGYKVVNSDLYKTPCTKRFEWTLPPQOFEIQGIGNYOOCHQSILELFNPS 316
Db 268 -ISHPCYPKGYRRIITIAEIVDSPVTPSMLSPAQILTVTGTGNPAACPTAILKLFNLT 326
Qy 317 YCPYSQCAFNGIFLPLQGDGAFSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 376
Db 327 CGANRTCGFDGVYQPPVRGGOFFAFAGFYTFSPFLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
Qy 377 IKTSYAGVKKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIKGIQSDAGWTLGYML 436
Db 386 LVETFPQNK-E-HLHTYCVVGLYILTLVLDGKYPDEHTWSNIHFSQKAGNADIGWTLGFML 444
Qy 437 NLTNMIPAE 445
Db 445 NLTNMIPT 453

RESULT 15
Q90X66 PRELIMINARY; PRT; 493 AA.
AC Q90X66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21982040; PubMed=11985621;
RA Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
RT "Purification, characterization, cloning, and expression of the
RL chicken liver ecto-ATP-diphosphohydrolase."
DR Eur. J. Biochem. 269:2373-2382 (2002).
DR EMBL; AF426405; AAL25086.1; -
DR GO; GO:0004050; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;
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Query Match 40.9%; Score 997; DB 2; Length 493;
Best Local Similarity 45.7%; Pred. No. 5.3e-69;
Matches 196; Conservative 72; Mismatches 145; Indels 16; Gaps 7;

Qy 23 LPENVKYGIVLDAGSSHTSLIYKYPAAEKNDTGWHVQVBEKRVKPGISKVQKNEIG 82
Db 35 LPPGKTKGLVFDAGSTHALYVQWPAKNGTGIQVQVESCCTVNGSGISSYADDPAG 94
Qy 83 IYLTDCMERAREVIPSQHQETPYVLGATAGMRLLRMESEBELADRLVDVVERSLSNYPFD 142
Db 95 ASLKPCLDKAMAVIPVEQWQTPYVLGATAGMRLLRQNSTKAEQVFAEYSKAIRPEPVD 154
Qy 143 FQGARITGQEGAYGNTINYLIG---KFSQKTRWFSIVPYETNNQETFGALDGGAST 199
Db 155 FRGAQILTNGEGSGFMITVNYLLETLIKFSAGKW-----EHPQNTFVLGALDGGAST 209
Qy 200 QVTFVQNQTIESPDNALQRLYKDYNNVYTHSFLCYGKQQA---LWQKLAKDIOVASNE 256
Db 210 QITFQP-GVTIEDKNTSVLRLYGTNSLYTHSVLCYGOIQASKRLMAALHQDGSYQN- 267
Qy 257 ILRDPCHPGYKVVNSDLYKTPCTKRFEWTLPPQOFEIQGIGNYOOCHQSILELFNPS 316
Db 268 -ISHPCYPKGYQENITIAEIVDSPVTPSMLSPAQILTVTGTGNPAACRTAILKLFNFT 326
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Qy 317 YCPYSQCAFNGIFLPLQGDGAFSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 376
Db 327 CGANRTCGFDGVYQPPVRGGOFFAFAGFYTFSPFLNLTGQQ-SLSHVNATVWDFCNKNWSE 385
Qy 377 IKTSYAGVKKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIKGIQSDAGWTLGYML 436
Db 386 LVETFPQNK-E-HLHTYCVVGLYILTLVLDGKYPDEHTWSNIHFSQKAGNADIGWTLGFML 444
Qy 437 NLTNMIPAE 445
Db 445 NLTNMIPT 453
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Search completed: March 7, 2005, 13:22:44
Job time : 64.8824 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 74.4923 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147a-3_COPY_21_476
Perfect score: 2440
Sequence: 1 VSHRNQQTWEGIFLSSTQN.....NLTNMIPAEQPLSLSHST 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04.*
- 1: Geneseqpl1980s.*
 - 2: Geneseqpl1990s.*
 - 3: Geneseqpl2000s.*
 - 4: Geneseqpl2001s.*
 - 5: Geneseqpl2002s.*
 - 6: Geneseqpl2003as.*
 - 7: Geneseqpl2003bs.*
 - 8: Geneseqpl2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2440	100.0	476	3 AAY70911	Aay70911 Human CD3
2	2440	100.0	476	3 AAY70888	Aay70888 Protein e
3	2373	97.3	476	3 AAY70912	Aay70912 Human CD3
4	2373	97.3	476	3 AAY70889	Aay70889 Protein e
5	2356	96.6	454	3 AAY70913	Aay70913 Human sol
6	2356	96.6	454	3 AAY70890	Aay70890 Protein e
7	2356	96.6	473	3 AAY70924	Aay70924 Human sol
8	2356	96.6	473	3 AAY70901	Aay70901 Protein e
9	2356	96.6	474	3 AAY70923	Aay70923 Human sol
10	2356	96.6	474	3 AAY70900	Aay70900 Protein e
11	2356	96.6	478	3 AAY70914	Aay70914 Human sol
12	2356	96.6	478	3 AAY70891	Aay70891 Protein e
13	2353	96.4	463	3 AAY70925	Aay70925 Human sol
14	2353	96.4	463	3 AAY70902	Aay70902 Protein e
15	2353	96.4	464	3 AAY70922	Aay70922 Human sol
16	2353	96.4	464	3 AAY70899	Aay70899 Protein e
17	2348	96.2	439	4 AAB71918	Aab71918 Soluble h
18	2348	96.2	487	3 AAY70921	Aay70921 Human sol
19	2348	96.2	487	3 AAY70898	Aay70898 Protein e
20	2348	96.2	510	2 AA04334	AA04334 Human lym
21	2348	96.2	510	2 AA04264	AA04264 Human CD3
22	2348	96.2	510	3 AAY70910	Aay70910 Human sol
23	2348	96.2	510	3 AAY70887	Aay70887 Human sol
24	2348	96.2	510	4 AAB71917	Aab71917 Human CD3
25	2348	96.2	510	7 ADJ57262	Adj57262 Human CD3

26	2348	96.2	510	8 ADL24295	Adl24295 Human CD3
27	2348	96.2	510	8 ADQ99453	Adq99453 Human CD3
28	2348	96.2	510	8 ADR69210	Adr69210 Human CD3
29	2348	96.2	510	8 ADR69042	Adr69042 Human CD3
30	2348	96.2	510	8 ADS17924	Ads17924 Human CD3
31	2348	96.2	510	8 ABO84674	Ab084674 Human can
32	2348	96.2	510	8 ADR87821	Adr87821 Human CD3
33	2348	96.2	511	8 ADK60421	Adk60421 Angiogene
34	2348	96.2	511	8 ADK60722	Adk60722 Angiogene
35	2348	96.2	511	8 ADP73345	Adp73345 CD39 1ymp
36	2348	96.2	517	7 ADN95839	Adn95839 Human BEC
37	2348	96.2	517	8 ADK60221	Adk60221 Angiogene
38	2348	96.2	517	8 ADK60522	Adk60522 Angiogene
39	2348	96.2	517	8 ADP73145	Adp73145 Angiogene
40	2348	96.2	522	8 ABO84672	Ab084672 Human can
41	2294	94.0	529	8 ABM83376	Abm83376 Human dia
42	2136	87.5	503	8 ABM83377	Abm83377 Human dia
43	1969	80.7	402	8 ABO84671	Ab084671 Human can
44	1841	75.5	377	7 ADI62735	Adi62735 Human apo
45	1118	45.8	311	8 ABO84673	Ab084673 Human can

ALIGNMENTS

RESULT 1

AAY70911
ID AAY70911 standard; protein; 476 AA.

XX AC AAY70911;

XX DT 17-AUG-2000 (first entry)

XX DE Human CD39-L4-1 protein construct.

XX KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
unstable angina; myocardial infarction; stroke; coronary artery disease;
atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
antiaanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
cardiant; vasotropic; thrombolytic.

OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Region 1..37

XX FT Cleavage-site /note= "Human CD39-L4 protein N-terminal end"

XX FT /note= "Cleavage site of leader sequence"

XX FT Region 38..476

XX FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US022955.

XX PR 16-OCT-1998; 98US-0104585P.

XX PR 06-NOV-1998; 98US-0107466P.

XX PR 13-AUG-1999; 99US-0149010P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

XX PT New soluble CD39 polypeptides having apyrase activity, useful for
inhibiting angiogenesis and treating unstable angina, myocardial

XX DT 17-AUG-2000 (first entry)
XX XX Protein encoded by CD39-L4 construct.
XX XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW coronary ischaemia; cerebral ischaemia; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW thrombotic disorder; vascular occlusion.
XX XX Homo sapiens.
OS Synthetic.
XX XX
XX XX
XX XX Location/Qualifiers
XX XX Region 1..48
XX XX /note= "Derived from CD39-L4"
XX XX Cleavage-site 20..21
XX XX Misc-difference 39
XX XX /note= "Any amino acid preferably Cys or Ser"
XX XX 49..476
XX XX /note= "Soluble portion of CD39"
XX XX
XX XX WO200023094-A2.
XX XX
XX XX 27-APR-2000.
XX XX
XX XX 13-OCT-1999; 99WO-US023641.
XX XX
XX XX 16-OCT-1998; 98US-0104585P.
XX XX 06-NOV-1998; 98US-0107466P.
XX XX 13-AUG-1999; 99US-0149010P.
XX XX
XX XX (IMNV) IMMUNEX CORP.
XX XX (CORR) CORNELL RES FOUND INC.
XX XX
XX XX Maliszewski CR, Gayle RB, Marcus AJ;
XX XX WPI; 2000-339518/29.
XX XX
XX XX Inhibiting platelet activation and recruitment, useful for treating a
XX XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX XX coronary artery disease or injury, comprises administering soluble CD39
XX XX polypeptides.
XX XX
XX XX Claim 6; Page 91-93; 118pp; English.
XX XX
XX XX The present sequence is a fusion construct of human soluble CD39 encoded
XX XX by CD39-L4-2 and CD39-L4-3 constructs. CD39-L4 is a secreted apyrase
XX XX belonging to the CD39 family. The fusion construct is used for the
XX XX expression and activity of soluble CD39 in CHO (Chinese hamster ovary)
XX XX cells. Soluble CD39 retains the capacity of wildtype CD39 to metabolise
XX XX ATP and ADP at physiologically relevant concentrations as well as the
XX XX ability to block and reverse ADP-induced platelet activation and
XX XX recruitment including platelet aggregation. This is used in the treatment
XX XX of unstable angina, myocardial infarction, stroke, coronary artery
XX XX disease or injury, atherosclerosis, peripheral vascular occlusion,
XX XX preclampsia, embolism, platelet-associated ischaemic disorder including
XX XX lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic
XX XX disorder including coronary artery thrombosis, cerebral artery
XX XX thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
XX XX thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
XX XX pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
XX XX useful for preventing thrombus formation or reformation, occlusion,
XX XX reocclusion, stenosis or restenosis of blood vessels or stroke
XX XX
XX XX Sequence 476 AA;
XX XX

Query Match 97.3%; Score 2373; DB 3; Length 476;
Best Local Similarity 97.6%; Pred. No. 1.3e-234;
Matches 445; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 1 VSHRNQQTWTEGIFLSSSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQ 60
DB 21 VSHRNQQTWTEGIFLSSSMKPINVSASTLYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQ 80
QY 61 VEECRVKGPGISGVQKVNIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRME 120
DB 81 VEECRVKGPGISGVQKVNIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRME 140
QY 121 SEELADRLVDVRSLSNYPDPQGARITITQEGAGVMTINVLGLKFSQKTRWFSIVP 180
DB 141 SEELADRLVDVRSLSNYPDPQGARITITQEGAGVMTINVLGLKFSQKTRWFSIVP 200
QY 181 YETNNQETFGALDGGASTQVTFVPPQNQTIESPDNALQFRLYKDVNVYTHSFLCYGKDQ 240
DB 201 YETNNQETFGALDGGASTQVTFVPPQNQTIESPDNALQFRLYKDVNVYTHSFLCYGKDQ 260
QY 241 ALWQKLAQIOVASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLFPQOFEIOGIG 300
DB 261 ALWQKLAQIOVASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLFPQOFEIOGIG 320
QY 301 NYOQCHOSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFVVMKFLNLTSEKVSQE 360
DB 321 NYOQCHOSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFVVMKFLNLTSEKVSQE 380
QY 361 KVTEMMKKFCAQPWEIEIKTSYAGVKSEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFI 420
DB 381 KVTEMMKKFCAQPWEIEIKTSYAGVKSEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFI 440
QY 421 GKIQGS DAGWTGLGYMLNLTNMI PAEQPLSTPLSHST 456
DB 441 GKIQGS DAGWTGLGYMLNLTNMI PAEQPLSTPLSHST 476
RESULT 5
AAAY70913
ID AAAY70913 standard; protein; 454 AA.
XX AC AAAY70913;
XX AC
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.
XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX OS Homo sapiens.
OS Synthetic.
XX XX
XX XX Location/Qualifiers
XX XX Key 1..15
XX XX Protein /label= Mature human interleukin_2
XX XX /note= "N-terminal region"
XX XX Protein 16..454
XX XX /note= "Human soluble CD39 protein"
XX XX WO200023459-A1.
XX XX
XX XX 27-APR-2000.
XX XX
XX XX 13-OCT-1999; 99WO-US022955.
XX XX


```
CC restenosis of blood vessels or stroke
XX
SQ Sequence 454 AA;

Query Match          96.6%; Score 2356; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 6.9e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGVVHQVEECRVKGGISKVF 75
DB 14 SSTQNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGVVHQVEECRVKGGISKVF 73

QY 76 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERS 135
DB 74 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERS 133

QY 136 LSNYPDFQGARITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 195
DB 134 LSNYPDFQGARITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 193

QY 196 GASTQVTFVFNQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKDQALWQKLAKDIOVASN 255
DB 194 GASTQVTFVFNQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKDQALWQKLAKDIOVASN 253

QY 256 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILELFPNT 315
DB 254 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILELFPNT 313

QY 316 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVFMKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
DB 314 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVFMKFLNLTSEKVSQEKVTMMKKFCAQPWE 373

QY 376 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 435
DB 374 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 433

QY 436 LNLNMPAEQPLSTPLSHST 456
DB 434 LNLNMPAEQPLSTPLSHST 454

RESULT 7
AAAY70924
ID AAAY70924 standard; protein; 473 AA.
XX
AC AAAY70924;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, pIL2LTrim4.
XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiatic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX
OS Homo sapiens.
OS Synthetic.
XX
PH Key
FT Peptide
FT 1..24 Location/Qualifiers
FT /label= Leader peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT Cleavage-site 26..27
FT /note= "Cleavage site of leader sequence"
FT Protein 35..473
FT /note= "Human soluble CD39 protein"
XX
FN WO200023459-A1.
```

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XX 27-APR-2000.
XX
PF 13-OCT-1999; 99WO-US022955.
XX
PR 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
FA (IMMV ) IMMUNEX CORP.
XX
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX
XX WPI; 2000-339644/29.
XX
FT New soluble CD39 polypeptides having apyrase activity, useful for
FT inhibiting angiogenesis and treating unstable angina, myocardial
FT infarction, stroke, coronary artery disease or injury.
XX
PS Claim 6; Page 114-116; 122pp; English.
XX
CC The present sequence is the fusion protein construct, pIL2LTrim4. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity.
CC Soluble CD39 is constructed by removing the N- and C-terminal
CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
CC at relevant concentrations and the ability to block and reverse ADP-
CC induced platelet activation and recruitment, including platelet
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
CC myocardial infarction, coronary artery disease or injury, embolism,
CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
CC associated ischaemic disorders including lung, coronary and cerebral
CC ischaemia, thrombotic disorders including coronary, peripheral and
CC cerebral artery thrombosis, intracardiac and venous thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
SQ Sequence 473 AA;

Query Match          96.6%; Score 2356; DB 3; Length 473;
Best Local Similarity 100.0%; Pred. No. 7.4e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGVVHQVEECRVKGGISKVF 75
DB 33 SSTQNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGVVHQVEECRVKGGISKVF 92

QY 76 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERS 135
DB 93 QKNEIGIYITDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERS 152

QY 136 LSNYPDFQGARITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 195
DB 153 LSNYPDFQGARITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 212

QY 196 GASTQVTFVFNQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKDQALWQKLAKDIOVASN 255
DB 213 GASTQVTFVFNQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKDQALWQKLAKDIOVASN 272

QY 256 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILELFPNT 315
DB 273 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILELFPNT 332

QY 316 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVFMKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
DB 333 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVFMKFLNLTSEKVSQEKVTMMKKFCAQPWE 392

QY 376 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 435
DB 393 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 452
```

QY 436 LNLTMIPAEQPLSTPLSHST 456
 XX ||||||||||||||||||
 Db 453 LNLTMIPAEQPLSTPLSHST 473

RESULT 8

AAV70901
 ID AAV70901 standard; protein; 473 AA.

XX AC AAV70901;

DT 17-AUG-2000 (first entry)

XX DE Protein encoded by Trim 4 construct.

XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion; pIL2Trim4 variant.

XX OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers
 FH Cleavage-site 26..27
 FT Protein 35..473

FT /note= "Soluble portion of CD39"

XX WO200023094-A2.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US023641.

XX PR 16-OCT-1998; 98US-0104585P.

XX PR 06-NOV-1998; 98US-0107466P.

XX PR 13-AUG-1999; 99US-0149010P.

XX PA (IMMV) IMMUNEX CORP.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Maliszewski CR, Gayle RB, Marcus AJ;

XX WIPI; 2000-339518/29.

XX PT Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.

XX PS Example 11; Page 114-116; 118pp; English.

XX CC The present sequence is the protein encoded by Trim4 construct. pIL2Trim4
 CC variant was constructed by removing the human IL2 residues from solCD39
 CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
 CC human IL2 to the solCD39 coding region results in high levels of both
 CC expression and activity in the supernatants of transfected cells. SolCD39
 CC is used in the treatment of unstable angina, myocardial infarction,
 CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
 CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
 CC disorder including lung ischaemia, coronary ischaemia and cerebral
 CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
 CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.

CC Soluble CD39 is also useful for preventing thrombus formation or
 CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
 CC vessels or stroke

XX SQ Sequence 473 AA;

Query Match 96.6%; Score 2356; DB 3; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.4e-233;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISKPV 75
 Db ||||||||||||||||||

QY 33 SSTQNKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISKPV 92
 Db ||||||||||||||||||

QY 76 QKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 135
 Db ||||||||||||||||||

QY 93 QKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 152
 Db ||||||||||||||||||

QY 136 LSNYPFDFQAGRIITGQEGAYGWTITNYLIGKFSQKTRWFSIVPYETNNQETFGALDLG 195
 Db ||||||||||||||||||

QY 153 LSNYPFDFQAGRIITGQEGAYGWTITNYLIGKFSQKTRWFSIVPYETNNQETFGALDLG 212
 Db ||||||||||||||||||

QY 196 GASTQVTFVPPONQIESPDNALQRLYKGVNVYTHSFLCYGKQDALWQKLAKDIQVASN 255
 Db ||||||||||||||||||

QY 213 GASTQVTFVPPONQIESPDNALQRLYKGVNVYTHSFLCYGKQDALWQKLAKDIQVASN 272
 Db ||||||||||||||||||

QY 256 EILRDPFCFHPGCKKVVNVSDLYKTPCTKRFEMTLPFQOFBIQIGIGNYQQCHQSILELFT 315
 Db ||||||||||||||||||

QY 273 EILRDPFCFHPGCKKVVNVSDLYKTPCTKRFEMTLPFQOFBIQIGIGNYQQCHQSILELFT 332
 Db ||||||||||||||||||

QY 316 SYCPYSQCAPNGIFLPLQGDGAFSAFYPMVKFLNTLTSKVSQEKVTEMKKFCAQPWE 375
 Db ||||||||||||||||||

QY 333 SYCPYSQCAPNGIFLPLQGDGAFSAFYPMVKFLNTLTSKVSQEKVTEMKKFCAQPWE 392
 Db ||||||||||||||||||

QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIKIGKQSDAGWTIGYM 435
 Db ||||||||||||||||||

QY 393 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIFIKIGKQSDAGWTIGYM 452
 Db ||||||||||||||||||

QY 436 LNLTMIPAEQPLSTPLSHST 456

QY 453 LNLTMIPAEQPLSTPLSHST 473

RESULT 9

AAV70923

ID AAV70923 standard; protein; 474 AA.

XX AC AAV70923;

XX DT 17-AUG-2000 (first entry)

XX DE Human soluble CD39 fusion protein construct, pIL2LTrim3.

XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers
 XX Peptide 1..24
 FT /label= Leader peptide

FT /note= "Derived from human interleukin 2 (hIL2)"

FT Cleavage-site 24..25

FT /note= "Cleavage site of leader sequence"

FT Protein 36..474

FT /note= "Human soluble CD39 protein"

XX PN WO200023459-A1.
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US022955.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX DR WPI; 2000-339644/29.
XX PT New soluble CD39 polypeptides having apyrase activity, useful for
XX PT inhibiting angiogenesis and treating unstable angina, myocardial
XX PT infarction, stroke, coronary artery disease or injury.
XX PS Claim 6; Page 113-114; 122pp; English.
XX CC The present sequence is the fusion protein construct, pIL2Ltrm3. This
XX CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
XX CC and soluble CD39 (solCD39) protein region, having apyrase activity.
XX CC Soluble CD39 is constructed by removing the N- and C-terminal ATP and ADP
XX CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
XX CC at relevant concentrations and the ability to block and reverse ADP-
XX CC induced platelet activation and recruitment, including platelet
XX CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
XX CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
XX CC myocardial infarction, coronary artery disease or injury, embolism,
XX CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
XX CC associated ischaemic disorders including lung, coronary and cerebral
XX CC ischaemia, thrombotic disorders including coronary, peripheral and
XX CC cerebral artery thrombosis, intracardiac and venous thrombosis,
XX CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
XX CC transient ischaemic attack. Soluble CD39 is also useful for preventing
XX CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
XX CC restenosis of blood vessels or stroke
XX SQ Sequence 474 AA;
Query Match 96.6%; Score 2356; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 7.4e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16 SSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVF 75
34 SSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVF 93
76 QKVNEIGYLTDCMERAREVTPRSQHTPVYLGATAGMRLRLRMESEBELADRVLDVVERS 135
94 QKVNEIGYLTDCMERAREVTPRSQHTPVYLGATAGMRLRLRMESEBELADRVLDVVERS 153
136 LSNYPDFQGARITGQEGAYGMITINVLGKFSQKTRWFSIVPYETNNQETFGALDLG 195
154 LSNYPDFQGARITGQEGAYGMITINVLGKFSQKTRWFSIVPYETNNQETFGALDLG 213
196 GASTQVTFVPPNQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKDQALWQKLAKDIQVASN 255
214 GASTQVTFVPPNQNTIESPDNALQFLRYGKDYNNVTHSFLCYGKDQALWQKLAKDIQVASN 273
256 BILRDPCHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFIEQIGNYQOCHQSILELFPNT 315
274 BILRDPCHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFIEQIGNYQOCHQSILELFPNT 333
316 SYCPSQCAQNGIFLPPQGFAPSAFYVVKMFLNLTSEKVSQEKVTMMKKFCAQDWE 375
334 SYCPSQCAQNGIFLPPQGFAPSAFYVVKMFLNLTSEKVSQEKVTMMKKFCAQDWE 393
376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 435

Db 394 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 453
Qy 436 LNLTNMIPAEQPLSTPLSHST 456
Db 454 LNLTNMIPAEQPLSTPLSHST 474
RESULT 10
AAAY70900
ID AAY70900 standard; protein; 474 AA.
XX AC AAY70900;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by Trim 3 construct.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antiaxial; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pIL2Ltrm3 variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Cleavage-site 24..25
FT Protein 36..474
FT /note="Soluble portion of CD39"
XX PN WO200023094-A2.
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US023641.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMMV) IMMUNEX CORP.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX DR WPI; 2000-339518/29.
XX PT Inhibiting platelet activation and recruitment, useful for treating a
XX PT mammal suffering from unstable angina, myocardial infarction, stroke,
XX PT coronary artery disease or injury, comprises administering soluble CD39
XX PT polypeptides.
XX PS Example 11; Page 113-114; 118pp; English.
XX CC The present sequence is the protein encoded by Trm3 construct. pIL2Ltrm3
XX CC variant was constructed by removing the human IL2 residues from solCD39
XX CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
XX CC human IL2 to the solCD39 coding region results in high levels of both
XX CC expression and activity in the supernatants of transfected cells. SolCD39
XX CC is used in the treatment of unstable angina, myocardial infarction,
XX CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
XX CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
XX CC disorder including lung ischaemia, coronary ischaemia and cerebral
XX CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
XX CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery

CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
CC Soluble CD39 is also useful for preventing thrombus formation or
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke
XX
SQ Sequence 474 AA;

Query Match 96.6%; Score 2356; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 7.4e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 SSTQKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 75
Db 34 SSTQKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 93

Qy 76 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 135
Db 94 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 153

Qy 136 LSNYPDFQGARIIITQGEAGYMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 195
Db 154 LSNYPDFQGARIIITQGEAGYMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 213

Qy 196 GASTQVTFVQNTIESPDNALQFRLYKGDVNYTHSFLCYGKDOALWQKLAKDIQVASN 255
Db 214 GASTQVTFVQNTIESPDNALQFRLYKGDVNYTHSFLCYGKDOALWQKLAKDIQVASN 273

Qy 256 EILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEGIGNYOQCHOSILELNT 315
Db 274 EILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEGIGNYOQCHOSILELNT 333

Qy 316 SYCPSQCAFNGIFLPPLOQDGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQDWE 375
Db 334 SYCPSQCAFNGIFLPPLOQDGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQDWE 393

Qy 376 EIKTSYAGVKYKLYSEYCFSGTYILSLLLQYHFTADSWEHIFTKIQGSDAGWTLYM 435
Db 394 EIKTSYAGVKYKLYSEYCFSGTYILSLLLQYHFTADSWEHIFTKIQGSDAGWTLYM 453

Qy 436 LNLNTPAEQPLSLSHST 456
Db 454 LNLNTPAEQPLSLSHST 474

RESULT 11
ID AAY70914 standard; protein; 478 AA.
XX
AC AAY70914;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, pIL2solCD39.
XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FH 1. .24
FT /label= Leader_peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT 25. .36
FT /label= Mature_human_interleukin_2

FT Region /note= "Derived from N-terminal end of human IL2"
FT 37. .39
FT /note= "Linker"
FT Protein 40. .478
FT /note= "Human soluble CD39 protein"
XX
FN WO200023459-A1.
XX
PD 27-APR-2000.
XX
PF 13-OCT-1999; 99WO-US022955.
XX
PR 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
DR N-PSDB; AAD00207.
XX
PT New soluble CD39 polypeptides having apyrase activity, useful for
FT inhibiting angiogenesis and treating unstable angina, myocardial
FT infarction, stroke, coronary artery disease or injury.
XX
PS Disclosure; Page 99-101; 122pp; English.
XX
CC The present sequence is a fusion construct pIL2solCD39, comprising the
CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,
CC having apyrase activity. This produces high levels of solCD39 expression
CC and activity in the transfected cells. Soluble CD39 is constructed by
CC removing the N- and C-terminal transmembrane domains. It retains the
CC capacity to metabolise ATP and ADP at relevant concentrations and the
CC ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
CC embolism, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX
SQ Sequence 478 AA;

Query Match 96.6%; Score 2356; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 7.5e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 SSTQKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 75
Db 38 SSTQKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVECRVKGPGISKFV 97

Qy 76 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 135
Db 98 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 157

Qy 136 LSNYPDFQGARIIITQGEAGYMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 195
Db 158 LSNYPDFQGARIIITQGEAGYMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLG 217

Qy 196 GASTQVTFVQNTIESPDNALQFRLYKGDVNYTHSFLCYGKDOALWQKLAKDIQVASN 255
Db 218 GASTQVTFVQNTIESPDNALQFRLYKGDVNYTHSFLCYGKDOALWQKLAKDIQVASN 277

Qy 256 EILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEGIGNYOQCHOSILELNT 315
XX
XX

Db 278 EILRDCPCFHGKYKVVNSDLYKTPCTKRFEMLTPFQCFEIQGIGNYQQCHQSILELFPNT 337
 QY 316 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
 Db 338 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
 QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 435
 Db 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 457
 QY 436 LNLTNMIPAEQPLSTPLSHST 456
 Db 458 LNLTNMIPAEQPLSTPLSHST 478

RESULT 12

AAV70891
 ID AAV70891 standard; protein; 478 AA.

AC AAV70891;

XX 17-AUG-2000 (first entry)

DE Protein encoded by pIL2Lsol CD39.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /note= "huIL2 leader sequence"
 FT Protein 25..36
 FT /note= "Mature human IL2"
 FT Region 37..39
 FT /note= "Linker"
 FT Protein 40..478
 FT /note= "SolCD39 protein"

WO200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

PA (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

DR N-PSDB; AAD00202.

XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.

PS Disclosure; Page 99-101; 118pp; English.

XX The present sequence is protein encoded by the coding region of
 CC pIL2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase
 CC activity. Fusion of 12 amino acids from the N-terminus of mature human
 CC IL2 to the solCD39 coding region results in high levels of both
 CC expression and activity in the supernatants of transfected cells. This is
 CC used in the treatment of unstable angina, myocardial infarction, stroke,
 CC coronary artery disease or injury, atherosclerosis, peripheral vascular
 CC occlusion, preclampsia, embolism, platelet-associated ischaemic disorder
 CC including lung ischaemia, coronary ischaemia and cerebral ischaemia, a
 CC thrombotic disorder including coronary artery thrombosis, cerebral artery
 CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
 CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
 CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
 CC useful for preventing thrombus formation or reformation, occlusion,
 CC reocclusion, stenosis or restenosis of blood vessels or stroke

SQ Sequence 478 AA;

Query Match 96.6%; Score 2356; DB 3; Length 478;
 Best Local Similarity 100.0%; Pred. No. 7.5e-233;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGGISKFV 75
 Db 38 SSTQNKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGGISKFV 97
 QY 76 QKVEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS 135
 Db 98 QKVEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS 157
 QY 136 LSNYPDFQCARITGQEGAYCMTITNYLLGKFSQKTRWFSIVPYTNQETFGALDLG 195
 Db 158 LSNYPDFQCARITGQEGAYCMTITNYLLGKFSQKTRWFSIVPYTNQETFGALDLG 217
 QY 196 GASTQVTFVFNQNTIESPDNALQFRLYKDYNYVTHSFLCYGKQDALWQKLADIQVSN 255
 Db 218 GASTQVTFVFNQNTIESPDNALQFRLYKDYNYVTHSFLCYGKQDALWQKLADIQVSN 277
 QY 256 EILRDCPCFHGKYKVVNSDLYKTPCTKRFEMLTPFQCFEIQGIGNYQQCHQSILELFPNT 315
 Db 278 EILRDCPCFHGKYKVVNSDLYKTPCTKRFEMLTPFQCFEIQGIGNYQQCHQSILELFPNT 337
 QY 316 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
 Db 338 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
 QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 435
 Db 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 457
 QY 436 LNLTNMIPAEQPLSTPLSHST 456
 Db 458 LNLTNMIPAEQPLSTPLSHST 478

RESULT 13

AAV70925
 ID AAV70925 standard; protein; 463 AA.

XX AAV70925;

XX 17-AUG-2000 (first entry)

XX Human soluble CD39 fusion protein construct, IgkappaLsolCD39.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;

antiangular, cerebroprotective; antiarteriosclerotic; anticoagulant;
cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig;
immunoglobulin kappa.

OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FH Peptide 1..20
FT /label= Leader peptide
FT /note= "Derived from human immunoglobulin Ig kappa"
FT
FT Cleavage-site 20..21
FT /note= "Cleavage site of leader sequence"
FT Region 21..24
FT /note= "Residues derived from human interleukin 2 (IL2)"
FT Protein 25..463
FT /note= "Human soluble CD39 protein"
XX WO200023459-A1.
XX
XX 27-APR-2000;
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 116-118; 122pp; English.
XX
XX The present sequence is the fusion protein construct, IgkappaSolCD39.
XX This construct comprises of the leader peptide from human immunoglobulin
XX Ig kappa, linked to the soluble CD39 (solCD39) protein region by few
XX residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase
XX activity and is constructed by removing the N- and C-terminal
XX transmembrane domains. It retains the capacity to metabolise ATP and ADP
XX at relevant concentrations and the ability to block and reverse ADP-
XX induced platelet activation and recruitment, including platelet
XX aggregation. Soluble CD39 polypeptides are useful for inhibiting
XX angiogenesis. It is useful for the treatment of unstable angina, stroke,
XX myocardial infarction, coronary artery disease or injury, embolism,
XX atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
XX associated ischaemic disorders including lung, coronary and cerebral
XX ischaemia, thrombotic disorders including coronary, peripheral and
XX cerebral artery thrombosis, intracardiac and venous thrombosis,
XX coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
XX transient ischaemic attack. Soluble CD39 is also useful for preventing
XX thrombus formation or reformation, occlusion, reocclusion, stenosis or
XX restenosis of blood vessels or stroke
XX
XX Sequence 463 AA;

Query Match 96.4%; Score 2353; DB 3; Length 463;
Best Local Similarity 99.8%; Pred. No. 1.5e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGGISKFV 75
Db :
23 TSTQNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKGGISKFV 82
QY 76 QKVEIGIYLTDCMERAREVTPRSQHTPVYLGATAGMRLLRMESEELADRVLDVVERS 135
Db 83 QKVEIGIYLTDCMERAREVTPRSQHTPVYLGATAGMRLLRMESEELADRVLDVVERS 142

QY 136 LSNYPFDQGARIIITQEGEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDIG 195
Db :
143 LSNYPFDQGARIIITQEGEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDIG 202
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Db :
203 GASTQVTFVPPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKDQALWQKLAKDIOVASN 262
QY 256 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEWTLPPFQOFBEIQGIGNYQQCHQSIILELFT 315
Db :
263 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEWTLPPFQOFBEIQGIGNYQQCHQSIILELFT 322
QY 316 SYCPYSQCAFNGIIFLPLQGDGFAGSAFYFMKFLNLTSEKVSQKVTMMKKFCAQPMW 375
Db :
323 SYCPYSQCAFNGIIFLPLQGDGFAGSAFYFMKFLNLTSEKVSQKVTMMKKFCAQPMW 382
QY 376 EIKTSYAGVKKYLSEYCFSGTYILSLLLQYHFTADSWEHIFHFGIKIQGSDAGWTGLYM 435
Db :
383 EIKTSYAGVKKYLSEYCFSGTYILSLLLQYHFTADSWEHIFHFGIKIQGSDAGWTGLYM 442
QY 436 LNLNMIAPAEQPLSTPLSHST 456
Db :
443 LNLNMIAPAEQPLSTPLSHST 463

RESULT 14
AAY70902
ID AAY70902 standard; protein; 463 AA.
XX
XX AC AAY70902;
XX
XX DT 17-AUG-2000 (first entry)
XX
XX DE Protein encoded by IgkappaSolCD39 construct.
XX
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antiangular; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion; IgkappaSolCD39 construct.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Igkappa leader sequence"
FT Cleavage-site 20..21
FT Region 21..24
FT /note= "Derived from IL-2"
FT Region 25..463
FT /note= "Soluble portion of CD39"
FT Region 25..32
FT /note= "Derived from solCD39"
XX
XX WO200023094-A2.
XX
XX PD 27-APR-2000.
XX
XX PF 13-OCT-1999; 99WO-US023641.
XX
XX PR 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX PA (IMMV) IMMUNEX CORP.

(CORR) CORNELL RES FOUND INC.

PA XX PI Maliszewski CR, Gayle RB, Marcus AJ;

XX XX WPI; 2000-339518/29.

DR XX Inhibiting platelet activation and recruitment, useful for treating a

PT PT mammal suffering from unstable angina, myocardial infarction, stroke,

PT PT coronary artery disease or injury, comprises administering soluble CD39

PT PT polypeptides.

XX XX Claim 6; Page 116-118; 118pp; English.

PS XX The present sequence is the protein encoded by IgpapelsolCD39 construct.

XX CC This is used for transient expression of soluble(sol)CD39 in recombinant

CC CC cells for determining enzymatic activity and platelet inhibitory activity

CC CC for each protein product. SolCD39 is used in the treatment of unstable

CC CC angina, myocardial infarction, stroke, coronary artery disease or injury,

CC CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,

CC CC platelet-associated ischaemic disorder including lung ischaemia, coronary

CC CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary

CC CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,

CC CC peripheral artery thrombosis, venous thrombosis, thrombosis,

CC CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),

CC CC transient ischaemic attack. Soluble CD39 is also useful for preventing

CC CC thrombus formation or reformation, occlusion, reocclusion, stenosis or

CC CC restenosis of blood vessels or stroke

XX XX Sequence 463 AA;

QY Query Match 96.4%; Score 2353; DB 3; Length 463;

Db Best Local Similarity 99.8%; Pred. No. 1.5e-232;

XX Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGTVHVECRVKGFGISKVF 75

Db :|||||

QY 76 QKVNIEGILYTDCHMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 135

Db |||||||

QY 83 QKVNIEGILYTDCHMERAREVIPSQHOETPVYLGATAGMRLRMESELADRVLDVVERS 142

Db |||||||

QY 136 LSNYPDFQGARIIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 195

Db |||||||

QY 143 LSNYPDFQGARIIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 202

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QY 196 GASTQVTFVQNTQIESPDNALQRLYCKQVNVYTHSFLCYGKQDQALWOKLADIQVAN 255

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QY 256 EILRDPCHFPGYKXVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQOCHOSILELFTNT 315

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QY 263 EILRDPCHFPGYKXVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQOCHOSILELFTNT 322

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QY 316 SYCYSQCAFNGIFLPLQGFQAFSAFYFWKFLNLTSEKVSQEKVTMMKKFCAQFWE 375

Db |||||||

QY 323 SYCYSQCAFNGIFLPLQGFQAFSAFYFWKFLNLTSEKVSQEKVTMMKKFCAQFWE 382

Db |||||||

QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQYHFTADSWHEIHFGIKQSDAGWTILGYM 435

Db |||||||

QY 383 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQYHFTADSWHEIHFGIKQSDAGWTILGYM 442

Db |||||||

QY 436 LNLNMPAPAEQPLSTPLSHST 456

Db |||||||

QY 443 LNLNMPAPAEQPLSTPLSHST 463

Db |||||||

RESULT 15

AA70922

ID AA70922 standard; protein; 464 AA.

XX XX AA70922;

AC XX

XX XX

DT 17-AUG-2000 (first entry)

XX Human soluble CD39 fusion protein construct, pIL2LTrim1.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;

KW unstable angina; myocardial infarction; stroke; coronary artery disease;

KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;

KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;

KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;

KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;

KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX Homo sapiens.

OS Synthetic.

OS

XX Key Location/Qualifiers

FT Peptide 1..24

FT /label= "Leader peptide

FT /note= "Derived from human interleukin 2 (hIL2)"

FT Cleavage-site 24..25

FT /note= "Cleavage site of leader sequence"

FT Protein 26..464

FT /note= "Human soluble CD39 protein"

FT WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107456P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

XX New soluble CD39 polypeptides having apyrase activity, useful for

PT inhibiting angiogenesis and treating unstable angina, myocardial

PT infarction, stroke, coronary artery disease or injury.

XX Claim 6; Page 111-112; 122pp; English.

XX The present sequence is the fusion protein construct, pIL2LTrim1. This

CC construct comprises of the leader peptide from human interleukin 2 (hIL2)

CC and soluble CD39 (solCD39) protein region, having apyrase activity. The

CC two regions are joined by an intervening Ala residue. Soluble CD39 is

CC constructed by removing the N- and C-terminal transmembrane domains. It

CC retains the capacity to metabolise ATP and ADP at relevant concentrations

CC and the ability to block and reverse ADP-induced platelet activation and

CC recruitment, including platelet aggregation. Soluble CD39 polypeptides

CC are useful for inhibiting angiogenesis. It is useful for the treatment of

CC unstable angina, stroke, myocardial infarction, coronary artery disease

CC or injury, embolism, atherosclerosis, peripheral vascular occlusion,

CC pre-eclampsia, platelet-associated ischaemic disorders including lung,

CC coronary and cerebral ischaemia, thrombotic disorders including coronary,

CC peripheral and cerebral artery thrombosis, intracardiac and venous

CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary

CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful

CC for preventing thrombus formation or reformation, occlusion, reocclusion,

CC stenosis or restenosis of blood vessels or stroke

XX XX Sequence 464 AA;

QY Query Match 96.4%; Score 2353; DB 3; Length 464;

Best Local Similarity 99.8%; Pred. No. 1.5e-232;

Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGTVHVECRVKGFGISKVF 75

Db	24	SATONKALPENVKYGI	VLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPGISKEV	83
Qy	76	QKWEIGIYLTDCMERAREV	IPRSOHOBTVPYLGCATAGMELLRWSEELADRVLDVVERS	135
Db	84	QKWEIGIYLTDCMERAREV	IPRSOHOBTVPYLGCATAGMELLRWSEELADRVLDVVERS	143
Qy	136	LSNYPDPFGQARIIT	QOBEGAYGMITNYLLGKFSQKTRWFSIVPVETNNQETFGALD	195
Db	144	LSNYPDPFGQARIIT	QOBEGAYGMITNYLLGKFSQKTRWFSIVPVETNNQETFGALD	203
Qy	196	GASTQVTFVPQONTIES	PDNALQFRLYKQYNNVTHSFLCYGKDQALWOKLANDIQVASN	255
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Qy	316	SYCPYSQACAFNGIF	LPLPQDGFAGSAFYFWKFLNLTSEKVSOEKVEMMKFCAQPWE	375
Db	324	SYCPYSQACAFNGIF	LPLPQDGFAGSAFYFWKFLNLTSEKVSOEKVEMMKFCAQPWE	383
Qy	376	EIKTSYAGYKELYSEY	CFSGTYIISLLQGYHFTADSWEHIFIGIKIQSGDAGWTGLGYM	435
Db	384	EIKTSYAGYKELYSEY	CFSGTYIISLLQGYHFTADSWEHIFIGIKIQSGDAGWTGLGYM	443
Qy	436	LNLTNNIPAEQPLST	PLSHST 456	
Db	444	LNLTNNIPAEQPLST	PLSHST 464	

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Job time : 75.6034 secs.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 53.496 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147a-3_COPY_21_476
Perfect score: 2440
Sequence: 1 VSHRQQTWFEGIFLSSTON.....NLTNIPAEQPLSLSHST 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	2373	97.3	476	9	US-09-835-147-4
3	2356	96.6	454	9	US-09-835-147-6
4	2356	96.6	473	9	US-09-835-147-29
5	2356	96.6	474	9	US-09-835-147-28
6	2356	96.6	478	9	US-09-835-147-8
7	2353	96.4	463	9	US-09-835-147-30
8	2353	96.4	464	9	US-09-835-147-27
9	2348	96.2	439	9	US-09-374-586-2
10	2348	96.2	487	9	US-09-835-147-26
11	2348	96.2	502	13	US-10-092-063-38
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13	2348	96.2	510	9	US-09-374-586-1

14	2348	96.2	510	10	US-09-781-796B-1	Sequence 1, Appli
15	2348	96.2	510	16	US-10-646-308-30	Sequence 30, Appli
16	1010	41.4	495	9	US-09-823-356-4	Sequence 4, Appli
17	910.5	37.3	529	9	US-09-923-304-4	Sequence 4, Appli
18	907.5	37.2	458	13	US-10-052-586-496	Sequence 496, App
19	907.5	37.2	458	14	US-10-174-590-496	Sequence 496, App
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ALIGNMENTS

RESULT 1

US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-3

Query Match 100.0%; Score 2440; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.7e-209;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VSHRNOQTWFE	GIFLSS	TQNKALP	ENVKYGI	VL	DAGSS	HTSLY	YIKWPA	EKENDTGV	WHQ	60														
Db	21	VSHRNOQTWFE	GIFLSS	TQNKALP	ENVKYGI	VL	DAGSS	HTSLY	YIKWPA	EKENDTGV	WHQ	80														
Qy	61	VEECRVK	GGIGIS	KFKVQ	NEIGI	YL	TDCMER	AREVI	PR	SQHOET	PVVLG	ATACMRLLRWE	120													
Db	81	VEECRVK	GGIGIS	KFKVQ	NEIGI	YL	TDCMER	AREVI	PR	SQHOET	PVVLG	ATACMRLLRWE	140													
Qy	121	SEELADRV	LDDV	VERSLN	YP	DFQ	GARI	ITQ	CEB	GAYC	WITIN	YLLG	KFSQKTRWFSI	180												
Db	141	SEELADRV	LDDV	VERSLN	YP	DFQ	GARI	ITQ	CEB	GAYC	WITIN	YLLG	KFSQKTRWFSI	200												
Qy	181	YETNNOET	FGALD	LGAS	TQVTF	PQ	NOTI	ESP	ONAL	Q	FLRY	KDYN	VYTHSL	CLCYGKQD	240											
Db	201	YETNNOET	FGALD	LGAS	TQVTF	PQ	NOTI	ESP	ONAL	Q	FLRY	KDYN	VYTHSL	CLCYGKQD	260											
Qy	241	ALWQKL	KADI	QIVAS	NEIL	RDC	PC	FH	GGYK	VVNV	SDLY	KT	PC	T	KRFEM	TLFP	QOFEI	QGIG	300							
Db	261	ALWQKL	KADI	QIVAS	NEIL	RDC	PC	FH	GGYK	VVNV	SDLY	KT	PC	T	KRFEM	TLFP	QOFEI	QGIG	320							
Qy	301	NYOQCH	QSIL	EL	FN	TSY	CPY	SOC	AFNG	I	FL	PL	QD	FG	AFSA	FV	V	MK	FN	LNTL	TS	SEKVSQ	360			
Db	321	NYOQCH	QSIL	EL	FN	TSY	CPY	SOC	AFNG	I	FL	PL	QD	FG	AFSA	FV	V	MK	FN	LNTL	TS	SEKVSQ	380			
Qy	361	KVTEM	MK	CAQ	PWE	IE	KT	S	VAG	VEK	YLS	YC	FS	GYI	LS	LL	Q	GH	V	HT	F	ADS	WEI	HI	420	
Db	381	KVTEM	MK	CAQ	PWE	IE	KT	S	VAG	VEK	YLS	YC	FS	GYI	LS	LL	Q	GH	V	HT	F	ADS	WEI	HI	440	
Qy	421	GKI	QGS	DAG	WT	L	GY	M	L	N	T	N	M	I	P	A	B	O	P	L	S	T	S	H	S	456
Db	441	GKI	QGS	DAG	WT	L	GY	M	L	N	T	N	M	I	P	A	B	O	P	L	S	T	S	H	S	476

```

RESULT 2
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

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Db	21	VSHRNQOTWFGIIFLSSMKXPINVASSTLYGLVDAGSSHTSLYIYKPAEKENDTGVVHQ	80
Qy	61	VEECRVKPGGISKFKVOKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME	120
Db	81	VEECRVKPGGISKFKVOKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME	140
Qy	121	SEELADRVLDVVERSLSNYPDFQOGARIITGOEGAGWIITNYLLGKFSQKTRWFSIVP	180
Db	141	SEELADRVLDVVERSLSNYPDFQOGARIITGOEGAGWIITNYLLGKFSQKTRWFSIVP	200
Qy	181	YETNNQETFGALDLGGASTQVTFVPQNGTIESPDNALQFRLYGKDNVYVTHSFLCYGKQD	240
Db	201	YETNNQETFGALDLGGASTQVTFVPQNGTIESPDNALQFRLYGKDNVYVTHSFLCYGKQD	260
Qy	241	ALWOKLAKDIQVASNEILRDCPFHPGYKKVNVNSDLYKTPCTKREMTLPFOQPIQIGIG	300
Db	261	ALWOKLAKDIQVASNEILRDCPFHPGYKKVNVNSDLYKTPCTKREMTLPFOQPIQIGIG	320
Qy	301	NYQCHOSIILELNTSYCPYSCQAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQGE	360
Db	321	NYQCHOSIILELNTSYCPYSCQAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQGE	380
Qy	361	KVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCSFGTYILSLLQGYHFTADSWEHIFPI	420
Db	381	KVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCSFGTYILSLLQGYHFTADSWEHIFPI	440
Qy	421	GKIOGSAGWTLYGYMLNTJNMIPAEQPLSTPLSHST	456
Db	441	GKIOGSAGWTLYGYMLNTJNMIPAEQPLSTPLSHST	476

RESULT 3
 US-09-835-147-6
 ; Sequence 6, Application US/09835147
 ; Patent No. US2002002277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliszewski, Charles R.
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Gimpel, Steven D.
 ; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 ; FILE REFERENCE: 2879-US
 ; CURRENT APPLICATION NUMBER: US/09/835,147
 ; CURRENT FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: US 60/104,585
 ; PRIOR FILING DATE: 1998-10-16
 ; PRIOR APPLICATION NUMBER: US 60/107,466
 ; PRIOR FILING DATE: 1998-11-06
 ; PRIOR APPLICATION NUMBER: US 60/149,010
 ; PRIOR FILING DATE: 1999-08-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/22955
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion
 ; OTHER INFORMATION: construct of human CD39
 US-09-835-147-6

Query Match 97.3%; Score 2373; DB 9; Length 476;
Best Local Similarity 97.6%; Pred. No. 2.6e-203;
Matches 445; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
Qy 1 VSHRNOQTWEGIFLSTONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDGVVH 60

Db 74 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMFLRLMESEELADRLVDVVERS 133
QY 136 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 195
Db 134 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 193
QY 196 GASTQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN 255
Db 194 GASTQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN 253
QY 256 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHOSILELNT 315
Db 254 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHOSILELNT 313
QY 316 SYCPYSCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWE 375
Db 314 SYCPYSCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWE 373
QY 376 EIKTSVAGVKEKYLSEYCFSGTVILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 435
Db 374 EIKTSVAGVKEKYLSEYCFSGTVILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 433
QY 436 LNLTNMIPAEQPLSTPLSHST 456
Db 434 LNLTNMIPAEQPLSTPLSHST 454

RESULT 4

US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 96.6%; Score 2356; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 8.6e-202;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 SSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 75
Db 33 SSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 92
QY 76 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMFLRLMESEELADRLVDVVERS 135
Db 93 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMFLRLMESEELADRLVDVVERS 152
QY 136 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 195

Db 153 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 212
QY 196 GASTQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN 255
Db 213 GASTQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN 272
QY 256 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHOSILELNT 315
Db 273 EILRDPCEPHGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHOSILELNT 332
QY 316 SYCPYSCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWE 375
Db 333 SYCPYSCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWE 392
QY 376 EIKTSVAGVKEKYLSEYCFSGTVILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 435
Db 393 EIKTSVAGVKEKYLSEYCFSGTVILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 452
QY 436 LNLTNMIPAEQPLSTPLSHST 456
Db 453 LNLTNMIPAEQPLSTPLSHST 473

RESULT 5

US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 96.6%; Score 2356; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 8.6e-202;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 SSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 75
Db 34 SSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 93
QY 76 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMFLRLMESEELADRLVDVVERS 135
Db 94 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMFLRLMESEELADRLVDVVERS 153
QY 136 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 195
Db 154 LSNYPDFOGARIITGOEGAYGWIITNYLLGKFSQKTRWFSIVPVETNNQETFGALDGLG 213
QY 196 GASTQVTFVPOQTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIOVASN 255

Db 214 GASTQVTFVFPQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIOVASN 273
QY 256 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 315
Db 274 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 333
QY 316 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
Db 334 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 393
QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 435
Db 394 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 453
QY 436 LNLTMNIPAEQPLSTPLSHST 456
Db 454 LNLTMNIPAEQPLSTPLSHST 474

RESULT 6

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 478
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match 96.8%; Score 2356; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 8.7e-202;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 SSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVF 75
Db 38 SSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVF 97
QY 76 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVRS 135
Db 98 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVRS 157
QY 136 LSNYPDFQAGARIITQEGEGAYGWITINVLKFSQKTRWFSIVPYETNNQETFGALDGL 195
Db 158 LSNYPDFQAGARIITQEGEGAYGWITINVLKFSQKTRWFSIVPYETNNQETFGALDGL 217
QY 196 GASTQVTFVFPQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIOVASN 255
Db 218 GASTQVTFVFPQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIOVASN 277
QY 256 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 315

Db 278 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 337
QY 316 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 375
Db 338 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
QY 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 435
Db 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLGYM 457
QY 436 LNLTMNIPAEQPLSTPLSHST 456
Db 458 LNLTMNIPAEQPLSTPLSHST 478
RESULT 7
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 96.4%; Score 2353; DB 9; Length 463;
Best Local Similarity 99.8%; Pred. No. 1.5e-201;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 16 SSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVF 75
Db 23 TSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPGISKVF 82
QY 76 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVRS 135
Db 83 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVRS 142
QY 136 LSNYPDFQAGARIITQEGEGAYGWITINVLKFSQKTRWFSIVPYETNNQETFGALDGL 195
Db 143 LSNYPDFQAGARIITQEGEGAYGWITINVLKFSQKTRWFSIVPYETNNQETFGALDGL 202
QY 196 GASTQVTFVFPQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIOVASN 255
Db 203 GASTQVTFVFPQNTIESPDNALQFLYKDYNNVYTHSFLCYGKQALWQKLAKDIOVASN 262
QY 256 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 315
Db 263 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELFT 322
QY 316 SYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 375

Db 323 SYCPYOCAPNGIFLPPLQDGFAGFAFYVWKFNLTSKVSQEKVTEMMKKFCAQPWE 382
QY 376 EIKTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 435
Db 383 EIKTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 442
QY 436 LNTNMIPAEQPLSTPLSHST 456
Db 443 LNTNMIPAEQPLSTPLSHST 463

RESULT 8
US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-27

Query Match 96.4%; Score 2353; DB 9; Length 464;
Best Local Similarity 99.8%; Pred. No. 1-5e-201;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 SSTONKALPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGTVVHQVEECRVKGPISKFV 75
Db 24 SATONKALPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGTVVHQVEECRVKGPISKFV 83

QY 76 OKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 135
Db 84 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 143

QY 136 LSNYPDFQAGARIITGOEAGYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 195
Db 144 LSNYPDFQAGARIITGOEAGYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 203

QY 196 GASTQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASN 255
Db 204 GASTQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASN 263

QY 256 EILRDCPFHPCYKVVNVSPLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 315
Db 264 EILRDCPFHPCYKVVNVSPLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 323

QY 316 SYCPYOCAPNGIFLPPLQDGFAGFAFYVWKFNLTSKVSQEKVTEMMKKFCAQPWE 375
Db 324 SYCPYOCAPNGIFLPPLQDGFAGFAFYVWKFNLTSKVSQEKVTEMMKKFCAQPWE 383

QY 376 EIKTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 435

Db 384 EIKTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYM 443
QY 436 LNTNMIPAEQPLSTPLSHST 456
Db 444 LNTNMIPAEQPLSTPLSHST 464

RESULT 9
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 96.2%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 4e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TQNKALPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGTVVHQVEECRVKGPISKFVQK 77
Db 1 TQNKALPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGTVVHQVEECRVKGPISKFVQK 60

QY 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 137
Db 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 120

QY 138 NYPPDFQAGARIITGOEAGYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 197
Db 121 NYPPDFQAGARIITGOEAGYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 180

QY 198 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 257
Db 181 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASNEI 240

QY 258 LRDPCHFPGYKVVNVSPLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 317
Db 241 LRDPCHFPGYKVVNVSPLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 300

QY 318 CPYSOCAPNGIFLPPLQDGFAGFAFYVWKFNLTSKVSQEKVTEMMKKFCAQPWE 377
Db 301 CPYSOCAPNGIFLPPLQDGFAGFAFYVWKFNLTSKVSQEKVTEMMKKFCAQPWE 360

QY 378 KTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 437
Db 361 KTSVAGVKEKYLSEYCSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 420

QY 438 LNTNMIPAEQPLSTPLSHST 456
Db 421 LNTNMIPAEQPLSTPLSHST 439

RESULT 10
US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.

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; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-26

Query Match          96.2%; Score 2348; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.6e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TONKALPENVKYGVILVDAGSSHTSLIYKPAEKENDTGVVHVQVEECRVKGGISKFVQK 77
DB 49 TONKALPENVKYGVILVDAGSSHTSLIYKPAEKENDTGVVHVQVEECRVKGGISKFVQK 108
QY 78 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 137
DB 109 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 168
QY 138 NYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 197
DB 169 NYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 228
QY 198 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 257
DB 229 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 288
QY 258 LRDPCHFPGYKVVVNSDLYKTPCTKRFEMLTPFQOFEIQGIGNYQOCHQSILELFTSY 317
DB 289 LRDPCHFPGYKVVVNSDLYKTPCTKRFEMLTPFQOFEIQGIGNYQOCHQSILELFTSY 348
QY 318 CPYSQCAFNGIFLPLQGDGFAFSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 377
DB 349 CPYSQCAFNGIFLPLQGDGFAFSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 408
QY 378 KTSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLGYMLN 437
DB 409 KTSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLGYMLN 468
QY 438 LTNMIPAEQPLSTPLSHST 456
DB 469 LTNMIPAEQPLSTPLSHST 487

RESULT 11
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
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; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-10-092-063-38

Query Match          96.2%; Score 2348; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.8e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TONKALPENVKYGVILVDAGSSHTSLIYKPAEKENDTGVVHVQVEECRVKGGISKFVQK 77
DB 38 TONKALPENVKYGVILVDAGSSHTSLIYKPAEKENDTGVVHVQVEECRVKGGISKFVQK 97
QY 78 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 137
DB 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
QY 138 NYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 197
DB 158 NYPDFQGARITGQEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
QY 198 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 257
DB 218 STQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 277
QY 258 LRDPCHFPGYKVVVNSDLYKTPCTKRFEMLTPFQOFEIQGIGNYQOCHQSILELFTSY 317
DB 278 LRDPCHFPGYKVVVNSDLYKTPCTKRFEMLTPFQOFEIQGIGNYQOCHQSILELFTSY 337
QY 318 CPYSQCAFNGIFLPLQGDGFAFSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 377
DB 338 CPYSQCAFNGIFLPLQGDGFAFSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 397
QY 378 KTSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLGYMLN 437
DB 398 KTSYAGVKERYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQSDAGWTGLGYMLN 457
QY 438 LTNMIPAEQPLSTPLSHST 456
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 12
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
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; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match          96.2%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.9e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 77
DB 38 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 97
QY 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 137
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 138 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 197
DB 158 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 217
QY 198 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 257
DB 218 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 277
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DB 278 LRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFNSTY 337
QY 318 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 377
DB 338 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 397
QY 378 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 437
DB 398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 438 LTNMIPAEQPLSTPLSHST 456
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 14
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match          96.2%; Score 2348; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.9e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 77
DB 38 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 97
QY 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 137
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 138 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 197
DB 158 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 217
QY 198 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 257
DB 218 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 277
QY 258 LRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFNSTY 317
DB 278 LRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFNSTY 337
QY 318 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 377
DB 338 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 397
QY 378 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 437
DB 398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 438 LTNMIPAEQPLSTPLSHST 456
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 13
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match          96.2%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.9e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 77
DB 38 TONKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQAECRKGISKFVOK 97
QY 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 137
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 138 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 197
DB 158 NYPDFQGARIIITGOEGAGYMITINYLKGFSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 217
QY 198 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 257
DB 218 STQVTFVQONQTIESPNDALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIOVASNEI 277
QY 258 LRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFNSTY 317
DB 278 LRDPCHFPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQCHQSILELFNSTY 337
QY 318 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 377
DB 338 CPYSCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQFWBEI 397
QY 378 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 437
DB 398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 438 LTNMIPAEQPLSTPLSHST 456
DB 458 LTNMIPAEQPLSTPLSHST 476
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QY 138 NYPFDQAGARIITGQEGAYGWITINVLKGFQKTRWFSIVPYETNNQETFGALDLGA 197
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Db 158 NYPFDQAGARIITGQEGAYGWITINVLKGFQKTRWFSIVPYETNNQETFGALDLGA 217
|||
QY 198 STQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEI 257
|||
Db 218 STQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEI 277
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QY 258 LRDPCEPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFETQIGNYQOCHQSILELNTSY 317
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Db 278 LRDPCEPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFETQIGNYQOCHQSILELNTSY 337
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QY 318 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPWBEI 377
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Db 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPWBEI 397
|||
QY 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYMLN 437
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Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYMLN 457
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QY 438 LTNMIPAEQPLSTPLSHST 456
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Db 458 LTNMIPAEQPLSTPLSHST 476
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RESULT 15

US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 96.2%; Score 2348; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.9e-201;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 TQNKALPENVKYGVILDAGSSHTSLYIKWPAEKENDTGWHQVVECRVKGPGISKPVOK 77
|||
Db 38 TQNKALPENVKYGVILDAGSSHTSLYIKWPAEKENDTGWHQVVECRVKGPGISKPVOK 97
|||
QY 78 VNEIGLYLDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLS 137
|||
Db 98 VNEIGLYLDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLS 157
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QY 138 NYPFDQAGARIITGQEGAYGWITINVLKGFQKTRWFSIVPYETNNQETFGALDLGA 197
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Db 158 NYPFDQAGARIITGQEGAYGWITINVLKGFQKTRWFSIVPYETNNQETFGALDLGA 217
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QY 198 STQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEI 257
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Db 218 STQVTFVPOQNTIESPDNALQFRLYKDYNNVYTHSFLCYGKQALWQKLAKDIQVASNEI 277
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QY 258 LRDPCEPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFETQIGNYQOCHQSILELNTSY 317
|||
Db 278 LRDPCEPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFETQIGNYQOCHQSILELNTSY 337
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QY 318 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPWBEI 377
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Db 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPWBEI 397
|||
QY 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYMLN 437
|||
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYMLN 457
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QY 438 LTNMIPAEQPLSTPLSHST 456
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Db 458 LTNMIPAEQPLSTPLSHST 476
|||

Search completed: March 7, 2005, 14:12:37
Job time : 54.496 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 19.4328 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-3_COPY_21_476

Perfect score: 2440
Sequence: 1 VSHRNQQTWFEIGFLSTQN.....NLTNIPABQLSTPLSHST 456

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	96.2	502	4	US-09-557-800C-55
2	2348	96.2	502	4	US-09-370-625A-38
3	2348	96.2	510	3	US-08-930-921-1
4	2348	96.2	510	4	US-09-781-796C-1
5	910.5	37.3	529	3	US-09-240-639-4
6	910.5	37.3	529	4	US-09-908-510A-4
7	910.5	37.3	529	4	US-09-905-744B-4
8	910.5	37.3	529	4	US-10-107-660-4
9	910.5	37.3	529	4	US-10-107-576-4
10	910.5	37.3	529	4	US-09-905-732B-4
11	910.5	37.3	529	4	US-09-923-304-4
12	910.5	37.3	529	4	US-09-949-016-6049
13	910.5	37.3	529	4	US-09-905-743B-4
14	910.5	37.3	556	4	US-09-949-016-11328
15	865	35.5	479	4	US-09-949-016-11559
16	847.5	34.7	282	4	US-09-949-016-7977
17	803	32.9	153	3	US-09-240-639-13
18	803	32.9	153	4	US-09-908-510A-13
19	803	32.9	153	4	US-09-905-744B-13
20	803	32.9	153	4	US-10-107-660-13
21	803	32.9	153	4	US-10-107-576-13
22	803	32.9	153	4	US-09-905-732B-13
23	803	32.9	153	4	US-09-905-743B-13
24	604	24.8	154	3	US-09-240-639-14
25	604	24.8	154	4	US-09-908-510A-14
26	604	24.8	154	4	US-09-905-744B-14
27	604	24.8	154	4	US-10-107-660-14

28	604	24.8	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	24.8	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	24.8	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	18.1	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	18.1	153	4	US-09-908-510A-15	Sequence 15, Appl
33	442.5	18.1	153	4	US-09-905-744B-15	Sequence 15, Appl
34	442.5	18.1	153	4	US-10-107-660-15	Sequence 15, Appl
35	442.5	18.1	153	4	US-10-107-576-15	Sequence 15, Appl
36	442.5	18.1	153	4	US-09-905-732B-15	Sequence 15, Appl
37	442.5	18.1	153	4	US-09-905-743B-15	Sequence 15, Appl
38	441	18.1	428	3	US-09-608-285A-7	Sequence 7, Appl
39	441	18.1	428	3	US-09-350-836B-7	Sequence 7, Appl
40	441	18.1	428	4	US-03-370-265-7	Sequence 7, Appl
41	441	18.1	428	4	US-09-557-800C-7	Sequence 7, Appl
42	441	18.1	428	4	US-09-370-625A-7	Sequence 7, Appl
43	426	17.5	428	3	US-09-608-285A-3	Sequence 3, Appl
44	426	17.5	428	3	US-09-608-285A-5	Sequence 5, Appl
45	426	17.5	428	3	US-09-240-639-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 96.2%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	18	TQNKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKPGISKFYOK	77
Db	38	TQNKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKPGISKFYOK	97
Qy	78	VNEIGVILTCMCERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL	137
Db	98	VNEIGVILTCMCERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL	157
Qy	138	NYPDFQAGRIITQEEGAYGWTINYLKGFOSKTRWFSIVPYETNNQETFGALDLGGA	197

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Db 158 NYPDFQAGRIITGOEAGAGWITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
Qy 198 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 257
Db 218 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 277
Qy 258 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 317
Db 278 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 337
Qy 318 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 377
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Qy 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 437
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 457
Qy 438 LTNMIPAEQPLSTPLSHST 456
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 2
US-09-370-625A-38
; Sequence 38, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-38

Query Match 96.2%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVQK 77
Db 38 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVQK 97
Qy 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSL 137
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSL 157
Qy 138 NYPDFQAGRIITGOEAGAGWITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 197
Db 158 NYPDFQAGRIITGOEAGAGWITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
Qy 198 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 257
Db 218 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 277
Qy 258 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 317
Db 278 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 337
Qy 318 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 377
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Qy 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 437
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 457
Qy 438 LTNMIPAEQPLSTPLSHST 456
Db 458 LTNMIPAEQPLSTPLSHST 476
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Qy 318 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 377
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Qy 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 437
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 457
Qy 438 LTNMIPAEQPLSTPLSHST 456
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 3
US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1

Query Match 96.2%; Score 2348; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.4e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVQK 77
Db 38 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVQK 97
Qy 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSL 137
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSL 157
Qy 138 NYPDFQAGRIITGOEAGAGWITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 197
Db 158 NYPDFQAGRIITGOEAGAGWITINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
Qy 198 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 257
Db 218 STQTVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDAQALWOKLAKDIQVASNEI 277
Qy 258 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 317
Db 278 LRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOEIQQIGNYQOCHOSILELFNTSY 337
Qy 318 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 377
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Qy 378 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 437
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQGSDAGWTLGYMLN 457
Qy 438 LTNMIPAEQPLSTPLSHST 456
Db 458 LTNMIPAEQPLSTPLSHST 476
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RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 96.2%; Score 2348; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.4e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 TONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGTVHQBECRVKPGISKVFQK 77
Db 38 TONKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGTVHQBECRVKPGISKVFQK 97
Qy 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLESEELADRLVDVVERSL 137
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLESEELADRLVDVVERSL 157
Qy 138 NYPDFQGARITIGQEEGAYGWIITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA 197
Db 158 NYPDFQGARITIGQEEGAYGWIITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA 217
Qy 198 STQVTFPQNOTIESPDNALQFRLYGKDYNYVTHSFQKTRWFSIVPYETNNQETFGALDLGGA 257
Db 218 STQVTFPQNOTIESPDNALQFRLYGKDYNYVTHSFQKTRWFSIVPYETNNQETFGALDLGGA 277
Qy 258 LRDPCEHPGKVKVNVSDLYKTPCTKPEMTLPFOQFEIQQGNYQOCHQSILELNTSY 317
Db 278 LRDPCEHPGKVKVNVSDLYKTPCTKPEMTLPFOQFEIQQGNYQOCHQSILELNTSY 337
Qy 318 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 377
Db 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
Qy 378 KTSVAGVKYKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTGLYMLN 437
Db 398 KTSVAGVKYKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTGLYMLN 457
Qy 438 LTNMIPAEQPLSTPLSHST 456
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 37.3%; Score 910.5; DB 3; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;
Qy 19 QNKALPENVKYIGVLDAGSSHTSLIYKPAEKENDTGTVHQBECRVKPGISKVFQKV 78
Db 47 KOEVLPPGLKXIGVLDAGSSRTTVVYQWPAEKENNTGVVSQTFKCSVKSGSISSYGNP 106
Qy 79 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLESEELADRLVDVVERSLN 138
Db 107 QDVPRAFEECMQKVKGVQVPSHLHGSTPIHLGATAGMRLLESEELADRLVDVVERSLN 166
Qy 139 YPFDQGARITIGQEEGAYGWIITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA 198
Db 167 QPFDQGARITIGQEEGAYGWIITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA 224
Qy 199 TQVTFPQNOTIESPDNALQFRLYGKDYNYVTHSFQKTRWFSIVPYETNNQETFGALDLGGA 257
Db 225 TQISFVAGERMDLNTSDIMQVSLYGVVYLYTHSFQKTRWFSIVPYETNNQETFGALDLGGA 284
Qy 258 LRDPCEHPGKVKVNVSDLYKTPCT--KRFEMTLPPFOQFEIQQGNYQOCHQSILELNT 315
Db 285 LTNPCYPRDYSISPTMGHVFDSLCTVDPQRPESYNPNVDITPFGTGPDLCKEKVASI 344
Qy 316 SYC--PYSCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPW 374
Db 345 KACHDQCTCSFDGVIQKIPGFVAFAGFYTAGALNL--SGSFSLDTFNSSTWNPFCQNW 403
Qy 375 EEIKTSYAGVKYKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTGLY 434
Db 404 SOLPELLPKPDEVYARSYCFSSANYIYHLFYNGYKFTETETWPIHFEKEVGNSSIAWS 463
Qy 435 MLNLTNMPAEQPL 448
Db 464 MSLTNQIPAESPL 477

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

Query Match		37.3%;	Score 910.5;	DB 4;	Length 529;	
Best Local Similarity		41.5%;	Pred. No. 1.3e-88;			
Matches		180;	Conservative	79;	Mismatches 168;	Indels 7; Gaps 5;
Qy	19	QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGPISKFQKV	78			
Db	47	KQEVLPGLKYGIVLDAGSSRTTYYVYQWPAEKENNTGVVQTFKCVKSGSGISSYGNP	106			
Qy	79	NEIGIYLTDCMERAREVIPSQHOETPVYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	138			
Db	107	QDVPRAFEECMQKVGQVPSHLHGSTIHLGATAGMELLRLQNETAANEVLESIQSYFKS	166			
Qy	139	YPPDFQAGRIITGOEGAGYGMITINYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	198			
Db	167	QPFDFRGAQIISGQEGYGMITINYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	224			
Qy	199	TQVTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAKDIOVA-SNEI	257			
Db	225	TQISFVAGERKMDLNTSDIMQVSLYGYVYVYQWPAEKENNTGVVQTFKCVKSGSGISSYGNP	284			
Qy	258	LRDPCFHPGKVKVNVSDLYKTPCT--KRFEMTLFQOFEIQGIGNYQOCHQSILELFT	315			
Db	285	LTNFCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGDPSLCKEKVASIFDF	344			
Qy	316	SYC-PYSQCAFNGIFLPLQDGFAGFAPYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW	374			
Db	345	KACHDQETCSFDGVYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403			
Qy	375	BEIKTSYAGVKEKYLSEYCFSGSTYLSLLQGYHFTADSWEHIFIGIKQSGDAGWTLY	434			
Db	404	SQPLPALLPKFDEVYARSYCFSANIYHLLFVNGYKFTETWPIHFKEKEVGNSSIAWSLGY	463			
Qy	435	MLNLTNMPAEQPL 448				
Db	464	MLSLTNQIPAESPL 477				
RESULT 8						
US-10-107-660-4						
; Sequence 4, Application US/10107660						
; Patent No. 6780977						
; GENERAL INFORMATION:						
; APPLICANT: Chadwick, Brian Paul						
; APPLICANT: Frischauf, Anna-Maria						
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE						
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS						
; FILE REFERENCE: 9598-066						
; CURRENT APPLICATION NUMBER: US/10/107,660						
; CURRENT FILING DATE: 2002-03-27						
; PRIOR APPLICATION NUMBER: US/09/240,639						
; PRIOR FILING DATE: 1998-01-29						
; NUMBER OF SEQ ID NOS: 29						
; SOFTWARE: Patent in Ver. 2.0						
; SEQ ID NO 4						
; LENGTH: 529						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-107-660-4						
Query Match						
Best Local Similarity						
Matches						
Qy	19	QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGPISKFQKV	78			
Db	47	KQEVLPGLKYGIVLDAGSSRTTYYVYQWPAEKENNTGVVQTFKCVKSGSGISSYGNP	106			
Qy	79	NEIGIYLTDCMERAREVIPSQHOETPVYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	138			
Db	107	QDVPRAFEECMQKVGQVPSHLHGSTIHLGATAGMELLRLQNETAANEVLESIQSYFKS	166			
Qy	139	YPPDFQAGRIITGOEGAGYGMITINYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	198			
Db	167	QPFDFRGAQIISGQEGYGMITINYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	224			
Qy	199	TQVTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAKDIOVA-SNEI	257			
Db	225	TQISFVAGERKMDLNTSDIMQVSLYGYVYVYQWPAEKENNTGVVQTFKCVKSGSGISSYGNP	284			
Qy	258	LRDPCFHPGKVKVNVSDLYKTPCT--KRFEMTLFQOFEIQGIGNYQOCHQSILELFT	315			
Db	285	LTNFCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGDPSLCKEKVASIFDF	344			
Qy	316	SYC-PYSQCAFNGIFLPLQDGFAGFAPYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW	374			
Db	345	KACHDQETCSFDGVYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403			
US-09-905-744B-4						
; Sequence 4, Application US/09905744B						
; Patent No. 6780410						
; GENERAL INFORMATION:						
; APPLICANT: Chadwick, Brian Paul						
; APPLICANT: Frischauf, Anna Maria						
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND						
; TITLE OF INVENTION: ACIDS						
; FILE REFERENCE: 28110/36120A						
; CURRENT APPLICATION NUMBER: US/09/905,744B						
; CURRENT FILING DATE: 2001-07-13						
; PRIOR APPLICATION NUMBER: 09/240,639						
; PRIOR FILING DATE: 1999-01-29						
; NUMBER OF SEQ ID NOS: 32						
; SOFTWARE: Patent in version 3.1						
; SEQ ID NO 4						
; LENGTH: 529						
; TYPE: PRT						
; ORGANISM: Homo Sapiens						
US-09-905-744B-4						
Query Match						
Best Local Similarity						
Matches						
Qy	19	QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGPISKFQKV	78			
Db	47	KQEVLPGLKYGIVLDAGSSRTTYYVYQWPAEKENNTGVVQTFKCVKSGSGISSYGNP	106			
Qy	79	NEIGIYLTDCMERAREVIPSQHOETPVYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	138			
Db	107	QDVPRAFEECMQKVGQVPSHLHGSTIHLGATAGMELLRLQNETAANEVLESIQSYFKS	166			
Qy	139	YPPDFQAGRIITGOEGAGYGMITINYLKGFQKTRWFSIVPVETNNQETFGALDVGAS	198			

Qy	375	EETKTSYAGVKEKYLSVCFCSTYILSLLLGQYHFTADSWEHIIHFIOKIIGSDAGWTGLG	434
	:	:::::	:
Db	404	SQPLLLPKDFDVSARYSCFSANYIYHLFVNQYKFTBETWFIHQFEKVGNSSIAWSLG	463
Qy	435	MLNLTNMIPAEQL	448
	:		:
Db	464	MLSLTNQIPAESPL	477

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RESULT 9
US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4

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Query Match	37.3%;	Score 910.5;	DB 4;	Length 529;
Best Local Similarity	41.5%;	Pred. No. 1.3e-88;		
Matches 180;	Conservative 79;	Mismatches 168;	Indels 7;	Gaps 5

RESULT 10
US-09-905-732B-4
; Sequence 4, Application US/09905732B
; Patent No. 6787328

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RESULT 11
US-09-923-304--4
; Sequence 4, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UTSC:65RUS
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

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Db 345 KACHDQETCSFDGVYQPKIRGFFVAPAGFYTASALNL-SGSFSLDTFNSSTWFCQNW 403
Qy 375 BEIKTSVAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHIFIGIKIQSDAGWTIGY 434
Db 404 SOLPLLPKFDVVARSYCFSANIYIHLFVNGYKFTETWQIHFKEVGNSSIAWSLGY 463
Qy 435 MLNLTNMPARQPL 448
Db 464 MSLTNTQIPAESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 37.3%; Score 910.5; DB 4; Length 556;
Best Local Similarity 41.5%; Pred. No. 1.4e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 19 ONKALPENVKYGIIVLDAGSSHTSLYIKVPAEKENDTGVVHVQVECRVKGIGSKFQKV 78
Db 74 KQELPPLKLYGIIVLDAGSSRTYVYVQWPAEKENDTGVVQVTKCSYKSGISSYGNP 133
Qy 79 NEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLRMESBELADRLVDVVERSLN 138
Db 134 QDVPRATEECMKVKGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS 193
Qy 139 YPPDFQGARITGOEGAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 198
Db 194 QPPDFRGAQIISGOEGYGVWITANYLMGNFLEKNLWHMWV--HPHGVETTGALDLGAS 251
Qy 199 TQVTFVQNTIESPDNALQRLYKGYVYTHSFCLCYGKQDALWQKLAKDIQVA-SNEI 257
Db 252 TQISFVAGEKMDLNTSDIMQVSLYGYVYVTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 311
Qy 258 LRDPCEFHPGYKKVNVSDLYKTPCT--KRPEMTLPFQGFBEIQGIGNYQOCHQSILEFNT 315
Db 312 LTNECYPRDYSISTMGHVFDSLCTVQRPESYNPNVDITEGSDPSLCKEKVASIPDF 371
Qy 316 SYC-PYSQCAFNGIFLPPLOQDFGAFYFVMKFLNLTSEKVSQEKVTENMMKFKCAQPW 374
Db 372 KACHDQETCSFDGVYQPKIRGFFVAPAGFYTASALNL-SGSFSLDTFNSSTWFCQNW 430
Qy 375 BEIKTSVAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHIFIGIKIQSDAGWTIGY 434
Db 431 SOLPLLPKFDVVARSYCFSANIYIHLFVNGYKFTETWQIHFKEVGNSSIAWSLGY 490
Qy 435 MLNLTNMPARQPL 448
Db 491 MSLTNTQIPAESPL 504
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RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 35.5%; Score 865; DB 4; Length 479;
Best Local Similarity 41.3%; Pred. No. 8.5e-84;
Matches 183; Conservative 69; Mismatches 137; Indels 54; Gaps 9;

Qy 18 TONKALPENVKYGIIVLDAGSSHTSLYIKVPAEKENDTGVVHVQVECRVKGIGSKFQKV 77
Db 36 TRDVREPPALKYGIIVLDAGSSHTSMFYIKWPAKENDTGVVQHSKCDVPGGIGSSYADN 95
Qy 78 VNEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLRMESBELADRLVDVVERSLN 137
Db 96 PSGASQSLVGLCEALQDVPKRHAGTPLYLGATAGMRLNLTNPEASTSVLMAVTHTLT 155
Qy 138 NYPPDFQGARITGOEGAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDL 194
Db 156 QYPPDFRGAQLISQOEGYGVWITANYLLENFIKYGVGRWF-----RPRKGTILGMDL 209
Qy 195 GGASTQVTFVQNTIESPDNA--LQPRLYKGYVYTHSFCLCYGKQDALWQKLAKDIQV 252
Db 210 GGASTQITF--ETTSPEADRASEVQLHLYGQHYRVYTHSFCLCYGRDQVLRLLASALQT 266
Qy 253 ASNEILLRDPCEFHPGYKKVNVSDLYKTPCTKRPENTLPFQOF-----EIQGIGNYQOCH 306
Db 267 HGFH----PCWPRGFSTQVLLGDVYQSPT----MAQRPNQFNSSARVSLSGSDPHLCR 318
Qy 307 QSILELENTSYCYPSQCAFNGIFLPPLOQDFGAFYFVMKFL--NLTSEKVSQEKVTE 364
Db 319 DLVSGLESFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCFSCF 378
Qy 365 MMKKFKCAQPBEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHIFIGIKI 424
Db 379 AAVNVCNQTAQ-----QLLSRGYGFDERAPGCVIFQKCAA 414
Qy 425 GSDAGWTILGMLNLTNMPARQPL 447
Db 415 DTAVGWALGYMLNLTNLPADPP 437

Search completed: March 7, 2005, 13:27:55
Job time : 21.4328 secs
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Result No.	Score		Query		Length	DB	ID	Description
	Score	Match	Match	%				
1	2297	94.4	510	2	I56242	lymphoid cell acti		
2	502	20.6	483	2	D86276	hypothetical prote		
3	469.5	19.3	405	2	E86276	hypothetical prote		
4	448	18.4	630	2	S50463	hypothetical prote		
5	411	16.9	572	2	T40856	probable nucleotid		
6	409.5	16.8	516	2	G84442	probable nucleosid		
7	395.5	16.3	508	2	C86276	7A19.33 protein -		
8	388.5	16.0	485	2	T34147	hypothetical prote		
9	383.5	15.8	557	2	T16696	hypothetical prote		
10	380.5	15.6	556	2	T39109	probable guanosine		
11	374	15.4	455	2	S48859	nucleoside triphos		
12	336.5	13.8	454	2	JC4616	aprase (EC 3.6.1.		
13	332	13.7	1052	2	T04439	hypothetical prote		
14	329.5	13.5	479	2	T23508	hypothetical prote		
15	313.5	12.9	518	2	A40732	guanosine-diphosph		
16	167	6.9	628	2	A55421	nucleoside-triphos		
17	104.5	4.3	3848	2	T17414	TiPc protein - ali		
18	103.5	4.3	404	2	T21251	hypothetical prote		
19	101.5	4.2	716	2	T21516	hypothetical prote		
20	100	4.1	307	2	T27332	hypothetical prote		
21	99	4.1	1951	2	B43963	RNA viral polymera		
22	98.5	4.1	590	2	AB1411	autolysin, N-acety		
23	98.5	4.1	797	2	D86247	hypothetical prote		
24	98.5	4.1	1509	2	B89985	hypothetical prote		
25	98	4.0	288	1	B48583	spore germination		
26	98	4.0	665	2	T18979	hypothetical prote		
27	97.5	4.0	392	2	A96738	hypothetical prote		
28	97	4.0	494	2	T03774	probable histidine		
29	97	4.0	4436	2	E71086	hypothetical prote		

RESULT 7

C86276
7A19.33 protein - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86276
R/TheoClogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: C86276
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-508 <STO>
A/Cross-references: UNIPROT:Q9XI63; GB:AR005172; NID:95080800; PIDN:AAD39310.1; GSPDB:GN
C/Genetics:
A/Map position: 1
C/Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.3%; Score 395.5; DB 2; Length 508;
Best Local Similarity 28.4%; Pred. No. 6.5e-24;
Matches 125; Conservative 69; Mismatches 175; Indels 71; Gaps 20;
QY 22 NVSASTLGVLDAGSHTSLYIKWPAEKENDTGVVHVVECRVK-GPGISKFEVQVNE 80
DB 59 NRRVLSHYIIDDGSSGTRVHVGYRIEYSGKPVDFGEENYASLKLSPGLSAYADNPEG 118
QY 81 IGIYLTDCMERARVIPSQHOETPVVLGATAGNRLRLMESEELADRLVDVVERSLSNYP 140
DB 119 VSEVTELVFAKRVHVKGLKSDIRLMATAGNRLLELPQE---QILDVTRVLSSG 175
QY 141 FDFQAGRIITQGEAGYGVITINYLKGFQKTRWFSIVPYETNN-QETFGALDLG--- 195
DB 176 FDF-----RDWASVIGILENFQDLMKVYMLGLLI 207
QY 196 --GASTOVTFVFNQTTIESPDNALQFLRYGK-DYNVYTHSFLCYGKQDALWQKLADI-Q 251
DB 208 MRSVRLEVTYF---STELVPSEFSTRLAYGNVSNLYSHSFLDFGQD-AAQEKLSLYN 263
QY 252 VASNE---ILRDPCHFGYKVVNV-SDLYKTPCTK-RPEMTLPFOQFEIQGIGNYQOC 305
DB 264 SAANSTEGIVDPDIPKGYILETNLQDLPGFLADKGTATL-----QAAGNPEEC 316
QY 306 HQSILELF--NTSYCPYSQCAFNGIFLPLQDGFAGSFYFVNMFLNLTSEKVSQKVT 363
DB 317 RSAAFAMQBEKCKTKYKCSIGSIFTPNLQGSPLATENFHTSKPGL-GEK---EWLS 372
QY 364 EMM---KKFCAQPEEIKTSVAGKVKLYSEYCSGYILSLLOGHYHTADSWEHIFI 420
DB 373 EMILAGKRCFGEESKLVKYPTKDNELLYRCFSSAYIISMLHDSLGVALDD-ERIKYA 431
QY 421 GKIQGSD--AGWTLG-YMLN 437
DB 432 SKAGEEDIPLDWALGAFILN 451

RESULT 8

T34147
hypothetical protein C33H5.14 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34147
R/Bradshaw, H.; Stelliyes, L.
submitted to the EMBL Data Library, November 1995

A/Description: The sequence of C. elegans cosmid C33H5.

A/Reference number: Z21482
A/Accession: T34147
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-485 <BRA>
A/Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:C33H5.14
A/Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C/Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.0%; Score 388.5; DB 2; Length 485;
Best Local Similarity 26.4%; Pred. No. 2.2e-23;
Matches 114; Conservative 68; Mismatches 187; Indels 63; Gaps 15;
QY 29 YGIVLDAGSHTSLYIKWPAEKENDTGV---VHVVECRVK-GPGISKFEVQVNEIGIY 84
DB 25 YGVICDAGSSGTRFLVYTLKPLSGGLTNDLHSESEPVVKVTPGLSSFGDKPEQVVEY 84
QY 85 LTDCMERARVIPSQHOETPVVLGATAGNRLRLMESEELADRLVDVVERSLSNYPDFQ 144
DB 85 LTPLRFABEHIPEQLGETDLLIFATAGNRLLEPAQKDAIINKLQNLKSVTALRVSDS 144
QY 145 GARIITQGEAGYGVITINYLKGFQKTRWFSIVPYETNNQETFGALDLGCGASTOVTFV 204
DB 145 NRIIDGAWEGYVIAVNVILGRFKE-----NDSKVMIDMGGSVQIAFE 192
QY 205 PQNTTIESPD--NALQFLRYGKD-----YNVYTHSFLCYGKQDALWQKLADIQVASNE 256
DB 193 IANEK-ESYNGNVYENLGSITNEDYKYIYSTTFLGYGANEGL-KKYENSLVKSGNS 250
QY 257 ILRDPCHFGYKVVNVSDLYKTPCTKREMTLPFOQFEIQGIGNYQOCHQSILELPTS 316
DB 251 --NDCSPRGLENLIG-----EFTVNGTGEWDVCLAQVSSLLIGDK 288
QY 317 ---YCPYSQCAFNGIFLPLQ---GDFGAFSAFYFVNMFLNLTSEKVSQKVTMMKKFC 370
DB 289 AQSCSNPTCFRLNVIAPSNLSTVQLYGFSEYWTTSNFGSGE-YHYQKFTDEVKRYC 347
QY 371 AQPWEI-----KTSYAGVKBYKLYSEYCSGYILSLLOGHYHTADSWEHI-HFIQIKI 424
DB 348 QKDNDIQDGFKEKNEFPNADIERLGTNCPKAAVWTVSLHDG--FNVDKTKHLFQSVLKIA 405
QY 425 GSDAGTGLYML 436
DB 406 GEEMQWALGAML 417

RESULT 9

T16696
hypothetical protein R07E4.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: T16696
R/Miller, N.
submitted to the EMBL Data Library, October 1995
A/Description: The sequence of C. elegans cosmid R07E4.
A/Reference number: Z18561
A/Accession: T16696
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-557 <MIL>
A/Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:R07E4.4
A/Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match 15.8%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 6.9e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;

RESULT 11

S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: *Pisum sativum* (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S65147; S48859
R:Haieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated,
A:Reference number: S65141; MUID:96197404; PMID:8616230
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <RSD>
A:Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:G563611; PIDN:CAA83655.1;
C:Superfamily: nucleoside triphosphatase chromatin-associated.
C:Keywords: nucleus

Query Match

QY	29	YGIVLDAGSHTSLYIYKQPAEKENDTVVH-----QVEECRVKGGPGSKFQVKVNEIGIYL	85
Db	44	YAVVFDAGTSGSRHHYHF-----NQNLDDLHIGKGYEYTNKIITPGLSSVANNPEQAAKSL	99
QY	86	TDCEAREAREVIPSQHQETPVVLGATAGMRLLMSEELADRVLDVVERSLN-YPPDFQ	144
Db	100	IPLEQAEADVDPDLQPKTPVRLGATAGRLRLNGDASE---KILQSVRDMLSNRSTFNQ	156

Db
100 IP LLEQAE DV PDD LQ P K T P V R L G A T A G L R L L N G D A S E - - - K I L Q S V R D M L S N R S T F N V Q 156

Qy	145	--GARIITQBEGAYGWITINYLLKPSQKTRWFSVPYETNNQETFGALDLGGASQTVT	202
		: : :	
Db	157	PDAVSIIDGTQBSYLWVTNYVALGNLKK-----YTKTGVLDIGGGSVOMA	204
		: : :	

OV 203 EVPONOTIESPDNAL-----OFRLYGKDVNVYTHSEFLCYGKDOALWOKLAKDIOVAS 254

[illegible]

DB	205	YAVSRKATKAPKAVDGDPPYIKKKVWLKGIPIYDLVYVHSYLVHFR-----EASR	252
QY	255	NEILR-----DPCFHPGYKKVNVNSDLYKTPCTKGFEMTLPPQPEIQIGICNYQQCHQS	308

DB	QY	309	ILELFNTSY-CPYSQCAFNGFLPPIQGDGFG	---	AFSAFYFVMKFLNLTSEK---	356
		253	AEILKLTTPRSPNCLLAGFNGLIYTSG---	---	EEFKAT---	AYTSGANFNCKNT 299

DB	300	IRKALKLNPCYPQNTCTFGW- - - - - NGGGNGQKRLFASSFFLYLPEDTGMVDASTPNF	355
QY	357	-VSQEKVTEMMKKFCQAPWBIKTSYAGVKEKYLSEY -CPSGTIYLSLLQGYHFTADSW	414

Db	356	ILRPVDIETKAKEACALNFEDAKSTYFPLDKKNVASVVCMDLIYQYVLLVDG--FGLDPL	413
Qy	415	EHIFHGKIQGSD---AGWTLYGYMLNTNNIP	443

Db 414 QKITSKEIEYQDAIVEAAWPLGNAVEAISALP 446

JC4616

aprase (EC 3.6.1.5) precursor - potato
N;Alternate names: adenylylphosphatase; ATP-diphosphohydrolase
C;Species: Solanum tuberosum (potato)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4616; PC4147
R;Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A;Reference number: JC4616; MUID:96158985; PMID:8579614
A;Accession: JC4616
A;Molecule type: mRNA
A;Residues: 1-454 <HAN>
A;Cross-references: UNIPROT:P80595; GB:U58597; PID:G1381632; PIDN:AAB02720.1; PID:G1381632
A;Accession: PC4147
A;Molecule type: protein
A;Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. It is involved in starch synthesis.
C;Genetics:
A;Gene: ctop1
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TM>
F;31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F;44-65/Region: actin-head shock protein 70-hexokinase beta-phosphate binding
F;44-65/Region: nucleotide binding #status predicted
F;192-212/Region: actin-head shock protein 70-hexokinase gamma-phosphate binding
F;192-212/Region: nucleotide binding #status predicted
F;390-410, 427-446/Region: hydrophobic carboxyl end
F;151-262/Binding site: carboxylate (Asn) #status predicted

Query Match	13.8%;	Score	336.5;	DB.2;	Length	454;			
Best Local Similarity	24.8%;	Pred. No.	3.2e-19;						
Matches	121;	Conservative	83;	Mismatches	193;	Indels	91;	Gaps	19;
<hr/>									
Qy	5	NQQTWFGEFGLS	-----SMKPINVSA-----	STLXGIVLDGSSHTSYIY	45				
Db	3	NQNSHFIIILAI	FLVPLSLSSKNVNAQIPLRRHLLSHSEHYAVIFDAGSTGSRHV	62					
Qy	46	KWPAEKENDTV	GVHQVECRVKGPKSKFVQKVNEIGIYITDCMERAREVITPRSQHOETP	105					
Db	63	RFD-EKLGLLPI	GNINIEFYMATPEPLGSLSYAEDPKAAANSLPEPLDGAEGVVPQLOSETP	121					
Qy	106	VYLGATAGMLLR	MESEELADRLDVVE--RSLSNVPFDFQGAARIITQOEGAYGMITI	162					
Db	122	LELGATAGLRML	KGDA--AEKIQAVNLVKNQSTTHSKDKQWTTILDGTQEGSYMAAI	178					
Qy	163	NYLLCKFSQKTR	WFPSIVPYETNNQETFFCALDGGASTQVTFVPQN-QTIESPDN	215					
Db	179	NYLLGNLCK	-----DYKSTTATIDLGGSVQMAVAISNEQFAKAPQNEDEGEPY	226					
Qy	216	ALQFRLYKQD	VNVYTHSFLCYGKQOALMOKIAKIQIVASNEILRDPCHPHGPKKVVNSD	275					
Db	227	VQKHLMSKO	NLYVHYSYLYNQ-LAGRAEIFKASRNESNCALEGC--DGYYSYGGVD-	282					
Qy	276	LYKTPCTKRF	WTLPPFOQFIEQIGNYQOCHOSILELFN-PSYCPYSOCANFGLPLPLQ	334					
Db	283	-YKVKAPKKG	-----SSWKKCRRLTHALKNAKCNIECTNGW----	323					
Qy	335	GDFG	-----AFSAFYFMKFLNLTSEKVSQE-----KVTEMKKFCAQPMIEKTSYA	382					
Db	324	GGGDGQKNI	HASSFFYDIGAQGVIVDTKFPSALAKPIQYLNAAKAVACQTNVADIKSIFP	383					
Qy	383	GVKEKYLEY	CFSGTYIISLLLOGHYFTADSWEHYHFIKTKQSD----AGTWLGYMLNL	438					
Db	384	KTQDRNI	PYLCMDLIYEYTLVDG--FGLNPHKEITVTHDVOYKNYLVGAAPWLGCAIDL	441					
Qy	439	---TNMI	442						

A; Introns: 36/3; 83/3; 189/1; 300/2; 412/3

A; Introns: 36/3; 83/3; 189/1; 300/2; 412/3
C; Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	13.5%	Score 329.5;	DB 2;	Length 479;
Best Local Similarity	26.8%;	Pred. No. 1.3e-18;		
Matches 122;	Conservative 71;	Mismatches 197;	Indels 65;	Gaps 19;

Qy	22 NVSASTLYGIVLDAGSHSTSLIYKW---PAEKENDTGUVHQVEE---CRVKPGGISKPV 75
Db	36 NQHTRCFVTVIDDAGSGTGRLLHYKFTHDPATASH--GMPPKYKEIKFQEVK-PGLSSFA 92

QY		76	QKVNEIGIYLTCMERAREVIPSQHSTPVYLGATAGMRLLRMESELADRVLDVVERS	135	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
	:	:	:	:	
Dδ		93	KSPSAAADSLEPLLORARKEVHFEMFWEKPTITLKATAGRL---	PGMADDILSVSR	149

Qy	136	LSNYPP--DFQCA-RIITGOEGAYGWITINYLKG-PSQKTRWFSIVPYETNNQETGCA	191
Db	150	IFNSGGFAAFPDADVNMVPGSDGVYFWFTNLILLETFTDE-----PTVGHKKPAARHVSAA	205

Qy 192 LDLGASTQVTFVPQNTIESP-----DNALQFRLYKGDYNNVYTHSFCLYCGKDQALWQ--K 245

Db 206 FDLGGSTGLTYWPNNAVAFESHVGYRDIPE--EGHTRIVTFSEFENGLIARPTNTIO 263

Oy	246	LAKDIOQVASEILRDP	CFHPGKYKVVNSDL	KTPCTKRFEMLPFOQ	EIQIGNYOQC	305
Dh	264	LETNDRETESTUOL	ITSCWDEGVC-----	TEFVALKVNNINGCC	CHCCHCC	319

Qy 306 HQSILELFNTSYCPYSQCAFNGIFLPIQLQGDFGAFSPYFVMKFLNL-----TSEKVSQ 359
:
:
:
Dh 311 VGTTKNEVESST-----MKLPRTKGS-DVIVTSYFENPDAI NSGIWVGNECCATPY 269
:
:
:

Qy 360 BKVTMMKKFCAQPWEBIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHF 419

361 POPKFAAFINPBBEVTLLDGC-----CHUMPGQI STTYIVYLLPBYVCF EDNOKYV 412

QY 420 IGKIQGSDAGWTLGYMLNTNIP-AEQPLSTPLS 453
|||:|:
414 AKYIKYEVHSCGCGIATATLHPCFQTCATVTL 448

RESULT 15

guanosine-diphosphatase (EC 3.6.1.42) - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein YEL042w
C/Species: *Saccharomyces cerevisiae*.

C/Accession: A40732; B40732; S30837; S50502
R/Abelion, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschbe
J. Cell Biol. 122, 307-323, 1993

A;Reference number: A40732; PMID:93308137; PMID:8391537
A;Accession: A40732
A;Molecule type: DNA

A;Cross-references: UNIPROT:P32621; EMBL:L19560; NID:G349392; PIDN:AAA34656.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIIP:134711).
A;Accession: B40732

A; Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>
R; Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.;
submitted to the EMBL Data Library, February 1993.

A;Accession number: J30612
A;Accession: S30837
A;Molecule type: DNA
A;Residues: 1-518 <MUL>

R; Dietrich, F.S.
A:Description: The sequence of S. cerevisiae cosmid
8198. 8334. and 9871
Accession-Numbers: GS0108179; EMBL:D106830; NID:G003625; FIDN:AAB55000.1; FID:5

A;reference number: S504391
A;Accession: S50502
A;Molecule type: DNA
A;Residues: 1-518 <DIE>

A;Cross-references: EMBL:U18779; NID:g603625;
C;Genetics:
A;Gene: SGD:GDA1
A;Cross-references: SGD:S0000768; MIPS:YEL042w
A;Map position: 5L

C;Function: hydrolase
A;Description: nucleoside triphosphatase chromatin-associated
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F;10-24/Domain: transmembrane #status predicted <TMM>
F;41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	12.3%	Score 313.5	DB 2	Length 518
Best Local Similarity	26.6%	Pred. No. 2.8e-17		
Matches 119: Conservative	70	Mismatches 186	Indels 73	Gaps 20

Qy	29	YGVLDAGSSHTSLYTYKWPAAEKENDTGVVHQVEECRVKPGISKVFQKVNEIGI--VLT	86
Dh	93	YVIMIDAGSGTSRVVHYTKFQDVCTSPPTLI--DEKFMLEPGLSSP--DTDSVGAANSID	147

87 DCMERAREVIPSQHQTVPVLGATAGMRL--RMESEELADVLDDVVSRLSNYPF---D 142
::: : :::: : :::: : :::: : :::
149 DIVLVAVNVITKACCTGVIVVTTCILPLICQAAVKYII SVAEPIIK- DYDEIPEP 204

QY 143 FQARITTQEGAGVWITINLLGKFSQKTRWFSIVPYETNNQE--TFGALDLGGASTQ 200

QY	201	VTFVPO	--NOTIESPDNALQFR	LYKGDYNYVTHSFLCYG	-----KDQALWOKLAKDI	250
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QY 251 QVASNE-----ILRDPCHFPGYKKVVNSDLYKTPCTKRFENTLPQOPEIQIG-----N 301

QY 302 YQQCHQSILELEN-TSYCPYQCAFNGLFLPEL-----QGDFGAFSAFYVMKFLNITS 354

QY 355 EKVSQEKVTENMKKFC--AQWEEIKTSYAGVKEKYLSE--YCFSGTYILSLILQGYHFT 410

Qy 411 ADSWEIHFIQKIQSDAGWTLGYMLNL 438

Search completed: March 7, 2005, 13:24:57

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 63.8824 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-4_COPY_21_476

Perfect score: 2432

Sequence: 1 VSHRNQQTWPEGIFLSSMKP.....NLTNMPABQPLSTPLSHST 456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2297	94.4	510	1	ENP1_HUMAN	P49961 homo sapien
2	1818	74.8	372	2	Q86VV3	Q86VV3 homo sapien
3	1788	73.5	510	1	ENP1_MOUSE	P55772 mus musculu
4	1788	73.5	539	2	Q8CDV7	Q8CDV7 mus musculu
5	1783	73.3	510	2	Q92106	Q92106 mus musculu
6	1751.5	72.0	511	1	ENP1_RAT	P97687 rattus norv
7	1668	68.6	510	1	ENP1_PIG	Q9MYU4 sus scrofa
8	1639.5	67.4	513	1	ENP1_BOVIN	O18956 bos taurus
9	1574	64.7	420	2	Q8CEB1	Q8CEB1 mus musculu
10	1416	58.2	508	2	Q6DFR1	Q6DFR1 xenopus tro
11	1379	56.7	508	2	Q6GP74	Q6GP74 xenopus lae
12	1280.5	52.7	492	2	Q8DC46	Q8DC46 brachydanio
13	1040	42.8	497	2	Q6UQ22	Q6UQ22 mus musculu
14	992	40.8	493	1	ENP1_CHICK	Q93295 gallus gall
15	985	40.5	493	2	Q90X66	Q90X66 gallus gall
16	973.5	40.0	454	2	Q6ZM69	Q6ZM69 brachydanio
17	961	39.5	455	2	Q7T014	Q7T014 brachydanio
18	956.5	39.3	495	1	ENP2_RAT	Q35795 rattus norv
19	949.5	39.0	495	1	ENP2_MOUSE	O55026 mus musculu
20	949.5	39.0	495	2	Q921R1	Q921R1 mus musculu
21	942	38.7	494	1	ENP2_CHICK	P79784 gallus gall
22	940	38.7	502	2	Q66L64	Q66L64 brachydanio
23	931	38.3	500	2	Q6NV19	Q6NV19 xenopus tro
24	922	37.9	526	2	Q6GN44	Q6GN44 xenopus lae
25	906.5	37.3	529	2	Q80Z26	Q80Z26 rattus norv
26	896.5	36.9	495	1	ENP2_HUMAN	Q9Y513 homo sapien
27	892.5	36.7	529	1	ENP3_HUMAN	O75355 homo sapien
28	891.5	36.7	458	2	Q6UVZ0	Q6UVZ0 homo sapien
29	885.5	36.4	529	2	Q8BFW6	Q8BFW6 m mus muscu
30	856.5	35.2	453	2	Q6ZM68	Q6ZM68 brachydanio
31	807.5	33.2	452	2	Q8N6K2	Q8N6K2 homo sapien

32 661 27.2 544 2 Q7YTA4 schistosoma
33 620.5 25.5 300 2 Q8KOL2 mus musculu
34 596.5 24.5 209 2 Q8UVX9 torpedo mar
35 512 21.1 488 2 Q6NQA8 arabidopsis
36 502 20.6 483 2 Q9X162 arabidopsis
37 492 20.2 503 2 Q94AP8 arabidopsis
38 492 20.2 503 2 Q8HID8 arabidopsis
39 487 20.0 634 2 Q6FRC2 arabidopsis
40 484 19.9 537 2 Q6Z543 oryza sativ
41 483 19.9 428 1 ENP5_HUMAN
42 483 19.9 428 2 Q96RX0 homo sapien
43 482.5 19.8 336 2 Q8CCV2 homo sapien
44 474.5 19.5 555 2 Q94E22 mus musculu
45 469.5 19.3 405 2 Q9M9T7 arabidopsis

ALIGNMENTS

RESULT 1
ENP1_HUMAN STANDARD; PRT; 510 AA.
AC P49961; Q9UQO9; Q9Y3Q9;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) [ecto-ATP diphosphohydrolase] (ATPDase) (lymphoid cell activation antigen) (ecto-apyrase) (CD39 antigen).
GN Name=ENTPD1; Synonyms=CD39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J., Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;
RA "The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization.";
RT J. Immunol. 153:3574-3583(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RX TISSUE=Umbilical vein;
RC MEDLINE=97149443; PubMed=8996251;
RA Robson S.C., Kaczmarek E., Siegel J.B., Cardinas D., Kozlak K., Millan M., Hancock W.W., Bach F.H.;
RA "Loss of ATP diphosphohydrolase activity with endothelial cell activation.";
RT J. Exp. Med. 185:153-163(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).
RX TISSUE=Placenta;
RC MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;
RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T., Titani K., Fujimura Y., Narita N.;
RA "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II.";
RT FEBS Lett. 453:335-340(1999).
RN [4]
RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
RX TISSUE=Placenta;
RC MEDLINE=96096723; PubMed=8529670;
RA Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;
RA "Purification and properties of human placental ATP diphosphohydrolase.";
RT Eur. J. Biochem. 234:66-74(1995).
RN [5]
RP SEQUENCE OF 1-30; 49-85; 94-97; 88-93; 193-223; 245-265; 382-385 AND 399-405 (ISOFORM PLACENTAL I).
RX TISSUE=Placenta;


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Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356EE3 CRC64;

Query Match 74.8%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.2e-132;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 MESELDADRVLDVVERSLNSNYPFQGGARIITGOEGAYGMITNYLLGKFSQKTRWFSI 178
Db 1 MESELDADRVLDVVERSLNSNYPFQGGARIITGOEGAYGMITNYLLGKFSQKTRWFSI 60

Qy 179 VPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQRLYKGVNVTYHFLCYGK 238
Db 61 VPYETNNQETFGALDLGGASTQVTFVPOQNTIESPDNALQRLYKGVNVTYHFLCYGK 120

Qy 239 DOALWQKLAKDIQVANSNIELDPCHFGYKVVNVSDLYKTPCTKRPFTLPPQPFQIQ 298
Db 121 DOALWQKLAKDIQVANSNIELDPCHFGYKVVNVSDLYKTPCTKRPFTLPPQPFQIQ 180

Qy 299 IGNTYQOCHQSTLELFTNTSCYPSYSCAFNGIFLPLQDGFAGFSFYFVWKFNLITSEKVS 358
Db 181 IGNTYQOCHQSTLELFTNTSCYPSYSCAFNGIFLPLQDGFAGFSFYFVWKFNLITSEKVS 240

Qy 359 QEKVTMMKXCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHII 418
Db 241 QEKVTMMKXCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHII 300

Qy 419 FIGIKQSDAGWTGLGYMLNLTNMPAEQPLSTPLSHST 456
Db 301 FIGIKQSDAGWTGLGYMLNLTNMPAEQPLSTPLSHST 338
```

```
RESULT 3
ENP1_MOUSE
ID ENP1_MOUSE STANDARD; PRT; 510 AA.
AC P55772;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J.,
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
RA "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization.";
RL J. Immunol. 153:3574-3583(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RA MEDLINE=98399871; PubMed=9730622;
RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
RA Gayle R.B. III, Maliszewski C.R.;
RT "Gene structure and chromosome location of mouse Cd39 coding for an
RT ecto-apyrase.";
RL Cytogenet. Cell Genet. 81:287-289(1998).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H2O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
EMBL; AF037366; AA922259.1; -
DR EMBL; AF041818; AAC83203.1; -
DR EMBL; AF041812; AAC83203.1; JOINED.
DR EMBL; AF041813; AAC83203.1; JOINED.
DR EMBL; AF041814; AAC83203.1; JOINED.
DR EMBL; AF041815; AAC83203.1; JOINED.
DR EMBL; AF041816; AAC83203.1; JOINED.
DR EMBL; AF041817; AAC83203.1; JOINED.
DR MGI; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0004050; P:apyrase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
FT DOMAIN 1 16 Cytoplasmic (Potential).
```



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QY 72 SKFQKVNIEIGIYLDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
D 121 SKYAKTDEIGAYLAECMELSTELIPTSKHQTPVYLGATAGMRLLRMESEESQSADEVLA 180
QY 132 VERSLSNYPPOFQAGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 191
D 181 VSTSLKGPYDFQAKIITGOEGAYGWTITNYLLGRTQSQWLSLIS-DSQKQETFGA 239
QY 192 LDLGASQTQVTFVQNOTIESPDNALQFRLYKGDYNNVTHSFCLYCGKQDQALWQKLADIQ 251
D 240 LDLGASQTQVTFVQNSTIESPNSLQRLYGEDYTVVTHSFCLYCGKQDQALWQKLADIQ 299
QY 252 VASNEILRDPCHFPGYKKNVNSDLYKTPCTKRFEMTLPPQFETQIGNTQQCHQSILE 311
D 300 VSSGVLKDPFCNFGYKKNVNSDLYKTPCTKRFEMTLPPQFETQIGNTQQCHQSILE 359
QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSFYFVMKFLNLTSEK--VSQKVTMMKKF 369
D 360 LFNNSHCPYSQCAFNGIFLPLHSGFAGSFYFVMDFKKVAKNSVISQKMTETIKNF 419
QY 370 CAQWEEIKTSYAGVKEKYLSEYCFSGTYILSLQGHVHTADSWEHHTFGIKQGSAG 429
D 420 CSKSWEETKTSYPSVKEKYLSEYCFSGTYILSLQGHVHTADSWEHHTFGIKQGSAG 478
QY 430 WTLGYMLNLTNNMIPAEQPLSPPLSHST 456
D 479 WTLGYMLNLTNNMIPAEQPLSPPLSHST 505

RESULT 5
Q921Q6 PRELIMINARY; PRT; 510 AA.
ID AC Q921Q6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Entpdl protein.
GN Name=Entpdl;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
STRAIN=C2Ech II; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

SEQUENCE FROM N.A.
STRAIN=C2Ech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011278; AAH11278.1;

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DR MGD; MGI:102805; Entpdl.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:aprase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDAI CD39; 1.
DR PROSITE; PS01238; GDAI CD39 NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77B644AE1413A0 CRC64;

Query Match 73.3%; Score 1783; DB 2; Length 510;
Best Local Similarity 73.8%; Pred. No. 9.1e-130;
Matches 330; Conservative 47; Mismatches 62; Indels 8; Gaps 4;

QY 12 GIFLSSKXPNVNSASTLYGIVLDGSSHTSIYIKVPAEKENDTGVVQVQLEECQVKGP 71
D 36 GLTONKPLPENVK----YGVLDGSSHTNIYIKVPAEKENDTGVVQVQLEECQVKGP 91
QY 72 SKFQKVNIEIGIYLDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
D 92 SKYAKTDEIGAYLAECMELSTELIPTSKHQTPVYLGATAGMRLLRMESEESQSADEVLA 151
QY 132 VERSLSNYPPOFQAGARIITGOEGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 191
D 152 VSTSLKGPYDFQAKIITGOEGAYGWTITNYLLGRTQSQWLSLIS-DSQKQETFGA 210
QY 192 LDLGASQTQVTFVQNOTIESPDNALQFRLYKGDYNNVTHSFCLYCGKQDQALWQKLADIQ 251
D 211 LDLGASQTQVTFVQNSTIESPNSLQRLYGEDYTVVTHSFCLYCGKQDQALWQKLADIQ 270
QY 252 VASNEILRDPCHFPGYKKNVNSDLYKTPCTKRFEMTLPPQFETQIGNTQQCHQSILE 311
D 271 VSSGVLKDPFCNFGYKKNVNSDLYKTPCTKRFEMTLPPQFETQIGNTQQCHQSILE 330
QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSFYFVMKFLNLTSEK--VSQKVTMMKKF 369
D 331 LFNNSHCPYSQCAFNGIFLPLHSGFAGSFYFVMDFKKVAKNSVISQKMTETIKNF 390
QY 370 CAQWEEIKTSYAGVKEKYLSEYCFSGTYILSLQGHVHTADSWEHHTFGIKQGSAG 429
D 391 CSKSWEETKTSYPSVKEKYLSEYCFSGTYILSLQGHVHTADSWEHHTFGIKQGSAG 449
QY 430 WTLGYMLNLTNNMIPAEQPLSPPLSHST 456
D 450 WTLGYMLNLTNNMIPAEQPLSPPLSHST 476

RESULT 6
ENP1 RAT STANDARD; PRT; 511 AA.
ID AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-aprase) (CD39 antigen).
GN Name=Entpdl; Synonyms=CD39;
OS Rattus norvegicus [Rat].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

SEQUENCE FROM N.A.; AND CHARACTERIZATION.
STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=9221928;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-aprase: evidence for only one ecto-
aprase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302 (1997).
RN [2]

```

RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Cochlea;
RX MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
RT "Evidence for alternative splicing of ecto-ATPase associated with
RL termination of purinergic transmission";
RN Brain Res. Mol. Brain Res. 73:85-92(1999).
RP SEQUENCE OF 432-511 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
RL rat brain";
RN Neuropharmacology 36:1189-1200(1997).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
CC kidney, liver, muscle, thymus, lung and spleen.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U81295; AAC53195.1; -;
CC EMBL; Y15685; CAA75730.1; -;
CC RGD; 69265; Entpdl.
CC InterPro; IPR000407; GDA1_CD39_NTPase.
CC Pfam; PF01150; GDA1_CD39; 1.
CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
FT DOMAIN 1 16 Cytoplasmic (Potential).
FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 478 Extracellular (Potential).
FT TRANSMEM 479 499 Potential.
FT DOMAIN 500 511 Cytoplasmic (Potential).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
FT CONFLICT 332 332 F -> L (in Ref. 2).
SQ SEQUENCE 511 AA; 57408 MW; 4CC12D3B644C193 CRC64;

Query Match 72.0%; Score 1751.5; DB 1; Length 511;
Best Local Similarity 72.3%; Pred. No. 2.5e-127;
Matches 323; Conservative 53; Mismatches 64; Indels 7; Gaps 4;

QY 12 GFLSMKPNVNSASTLYGVLIDAGSSHTSLVIYKPAEKENDTGVHVQVECRVKGPGI 71
DB 36 GLTHNKPENVK-----YGVLDAGSSHTSLVIYKPAEKENDTGVVQLLECCVKGPGI 91
QY 72 SKFVQKVNIGIYLTDCMERAREVPSRQHPVTYVLGATAGWRLLRMESEELADRVLDV 131
DB 92 SKVAQKTDIAAYLAECMKMSTERIPASKQHQTPTVLGATAGWRLLRMESKQSADEVLA 151
QY 132 VRSLSNYPDFQAGRIITQEGAGWTITNYLLGKFSQKTRFWSIVPYETNNQETGA 191
DB 152 VRSLSKSPDFQAGRIITQEGAGWTITNYLLGKFSQKTRFWSIVPYETNNQETGA 210

QY 192 LDLGASTQVTFVPPONOTIESPDNALQRLYKGDYVNVYTHSFLCYGKQDALWQKLADIQ 251
DB 211 LDLGSSSTQVTFVPPUNQLEAPETSLQRLYGTDTVTYTHSFLCYGKQDALWQKLADIQ 270
QY 252 VASNEILRDPCHPGYKVVNVVDLYKTPCTKRFEMTLPPQOFEGTGNVQCHQSILE 311
DB 271 VSSGILKDCPCFYPGYKVVNVVDLYKTPCTKRFEMTLPPQOFEGTGNVQCHQSILK 330
QY 312 LFNYSYCPYSQAFNGIFLPPLOQDFGAFSAFYFWKFL-NLTSEKV-SOEKVTEMKKF 369
DB 331 FFNNSHCPYSQAFNGFVLPPLQSGFGAFSAFYFYVMDFFKMWANDSVSSQEKMTITKNF 390
QY 370 CAQWEEIKTSYAGVKEKYSYCFSGTVILSLLOQYHFTADSWEHILHFIKIQSGDAG 429
DB 391 CSKPEEVEKASVPTVKELYSYCFSGTVILSLLOQYHFTADSWEHILHFIKIQSGDAG 450
QY 430 WTLGYMLNLTNMIPAEQPLSTPLSHST 456
DB 451 WTLGYMLNLTNMIPAEQPLSTPLSHST 477

RESULT 7
ENPI_PIG STANDARD; PRT; 510 AA.
ID ENPI_PIG
AC QSMYTA;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=ENTPDL; Synonyms=CD39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ortic endothelium;
RX MEDLINE=20325090; PubMed=10866813;
RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O.,
RA Sevigny J.;
RT "Distribution, cloning, and characterization of porcine nucleoside
RT triphosphate diphosphohydrolase-1";
RL Eur. J. Biochem. 267:4106-4114(2000).
RN [2]
RP SEQUENCE OF 202-220.
RC TISSUE=Pancreas;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Highest expression found in vascular
CC endothelium, smooth muscle, spleen and lung.
CC -!- PTM: Cleaved into two polypeptides that seem to stay together by
CC noncovalent interactions
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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DR EMBL; AJ133746; CAB95871.1; --
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT CHAIN 1 510
FT   Ectonucleoside triphosphate
FT   diphosphohydrolase 1.
FT CHAIN 1 201
FT   Ectonucleoside triphosphate
FT   diphosphohydrolase 1 27 kDa subunit.
FT CHAIN 202 510
FT   Ectonucleoside triphosphate
FT   diphosphohydrolase 1 54 kDa subunit.
FT FT
FT DOMAIN 1 16
FT   Cytoplasmic (Potential).
FT TRANSMEM 17 37
FT   Potential.
FT DOMAIN 38 477
FT   Extracellular (Potential).
FT TRANSMEM 478 498
FT   Potential.
FT DOMAIN 499 510
FT   Cytoplasmic (Potential).
FT FT CARBOHYD 73 73
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 245 245
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 274 274
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 291 291
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 333 333
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 370 370
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 457 457
FT   N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 203 203
FT   G -> S (in Ref. 2).
FT SEQUENCE 510 AA; 57757 MW; 82f86869040d7735 CRC64;
Query Match 68.6%; Score 1668; DB 1; Length 510;
Best Local Similarity 68.4%; Pred. No. 7.6e-121;
Matches 305; Conservative 65; Mismatches 70; Indels 6; Gaps 3;
Qy 12 GIFLSSMKPINVASSTLYGVLDAGSSHTSLIYIKVPAEKENDTGTVVHVQVECRVKGP 71
Db 36 GLTONKALPENVK----FGIVLDAGSSHTSLIYIKVPAEKENDTGTVVHVQVECRVKGP 91
Qy 72 SKPVQKNEIGYLTDCWERAEVPRSOHETPVYLGATAGMELLRMESEELADRVLDV 131
Db 92 SEPANKLGEIDYLEACMERARTVVPKSOHAETPVYLGATAGMELLRMKENLASKILST 151
Qy 132 VERLSNYPDFQAGRIITGEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VASGITRYPDFQAGRIITGEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
Qy 192 LDLGASTQVTFVQNTQIESPDNALQFRLYKGDYVYTHSFLCYGKDQALWQKLAKDIQ 251
Db 212 LDLGASTQITFVQNTQIESPDNALQFRLYKGDYVYTHSFLCYGKDQALWQKLAKDIQ 271
Qy 252 VASNEILRDCPHGPKYKVVNVNLDYKTPCTKREMTLPFOFIQIGNVYQOCHOSTLE 311
Db 272 -NTNGTITHEPCFSGYQRRMNVNLDYKTPCTKREMTLPFOFIQIGNVYQOCHOSTLE 330
Qy 312 LFNISYCPYSOCAFNGFLPLPQDGFQAFSAFYFMKFLNLTSEKVS-QEKVTMMKKFC 370
Db 331 LFNISYCPYSRCSFDGVFLPLPQDGFQAFSAFYFMKFLNLTSEKVSQSVTLEAFC 390
Qy 371 AQPHEEIKTSVAGVEKYLSCYSGVYVLSLLQGVHFTADSWEHIFIKIGSGDAGW 430
Db 391 SRPAELQWYFGDVKELSCYSGVYVLSLLQGVHFTADSWEHIFIKIGSGDAGW 450
Qy 431 TLGVMLNLTNMPAEQSLTSLSHST 456
Db 451 TLGVMLNLTNMPAEQSLTSLSHST 476
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RESULT 8
ENPI_BOVIN
ID_ENPI_BOVIN STANDARD; PRT; 513 AA.
AC O18956;
DT 16-Oct-2001 (Rel. 40, Created)

```
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPDI; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Aortic endothelium;
RC Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RP TISSUE=Aorta;
RC MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Seviigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase."
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
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EMBL; AF005940; AAB62382.1; --
InterPro; IPR000407; GDAI_CD39_NTPase.
Pfam; PF01150; GDAI_CD39; 1.
PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 16
FT   Cytoplasmic (Potential).
FT TRANSMEM 17 37
FT   Potential.
FT DOMAIN 38 481
FT   Extracellular (Potential).
FT TRANSMEM 482 502
FT   Potential.
FT DOMAIN 503 513
FT   Cytoplasmic (Potential).
FT FT CARBOHYD 73 73
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 227 227
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 245 245
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 307 307
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 336 336
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 373 373
FT   N-linked (GlcNAc. . .) (Potential).
FT FT CARBOHYD 460 460
FT   N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 97 97
FT   K -> N (in Ref. 2).
FT CONFLICT 101 103
FT   INV -> CGF (in Ref. 2).
FT CONFLICT 464 464
FT   K -> V (in Ref. 2).
FT SEQUENCE 513 AA; 58113 MW; 20F98F27B6D2F96 CRC64;
Query Match 67.4%; Score 1639.5; DB 1; Length 513;
Best Local Similarity 67.3%; Pred. No. 1.2e-118;
Matches 302; Conservative 66; Mismatches 72; Indels 9; Gaps 4;
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Qy 12 GIFLSSMKPINVASSTLYGVLDAGSSHTSLIYIKVPAEKENDTGTVVHVQVECRVKGP 71
Db 36 GLTONKALPENVK----FGIVLDAGSSHTSLIYIKVPAEKENDTGTVVHVQVECRVKGP 91

Qy	72	SKFVQVNEIGLYLTDQMERAREVTPRSHOETPVYLGATAGMRLRMESEELADRVLDV	131
Db	92	SGFAKVNENIVLITACMERAKQVIPSIOHNETPVYLGATAGMRLRMESEELADRVLDV	151
Qy	132	VERLSNYPDFQAGARIITGOBEGAYWITINYLKGFPSQKTRWFSIVPYETNQSTFGA	191
Db	152	VASSISEYFPDQAGARIISGQEEGAYGWTIVNYLLGKFTQKLSWFLNPKSKDDTQETGA	211
Qy	192	LDLGGASTQVTPVQNTQIESPDNALQRLYKDKYNYVTHSFCLYCGKQDQALWOKLAKDQ	251
Db	212	LDLGGASTQITVPQNETTESNNNLVFRLYGKNYSVYTHSFCLYCGKQDQALWOKLAKDQ	271
Qy	252	VASNETLRDPCFHPGKVVVNSDLYKTPCTKRPEMT--LPFOQFEIQIGIGNVQOCHQS	308
Db	272	-GTNGIITHPECFHRSYMRKIMSVLNEGFCYKRLHNSFPYPLVDIIRGAGNFQRCQS	330
Qy	309	ILELFNTSYCPYSCQAFNGIFLPPQLQDGFAGSAFYFVFMKFLNLTSEK-VSQEKVTEMMK	367
Db	331	IIQLFNTSYCPYSSCSFNGVFLPPLHGQGFAGSAFYVMBEFLNLTSESVSEQLTEKLE	390
Qy	368	KFCAQWBEIKTSYAGVKEKYLSEYCFSGVTILSLILQGYHFTADSWEHHTFKTGQSGD	427
Db	391	EFCARWEEVQKNFGEVKEKYLSEYCFSGVTILVLLNGYHFTAESWKNHFMNKVRSTD	450
Qy	428	AGWTLGYMLNLTNMPAEOPSLTPLSHST	456
Db	451	VGMTLGYMLNLTNMPAEOPSLTPLSHST	479
RESULT 9			
Q8CEB1	ID	Q8CEB1	PRELIMINARY; PRT; 420 AA.
AC	Q8CEB1	Q8CEB1	
DT	01-MAR-2003	{TREMBLrel. 23, Created}	
DT	01-MAR-2003	{TREMBLrel. 23, Last sequence update}	
DT	01-OCT-2003	{TREMBLrel. 25, Last annotation update}	
DE	Mus musculus, 10 days neonate skin cDNA, RIKEN full-length enriched		
DE	library, clone:4732419M16 product:ectonucleoside triphosphate		
DE	diphosphonhydrolase 1, full insert sequence. (Fragment).		
GN	Name=Entpdl;		
OS	Mus musculus; (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	[1]	SEQUENCE FROM N.A.	
RP	STRAIN=C57BL/6J; TISSUE=Skin;		
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RC	Carninci P., Hayashizaki Y.		
RA	"High-efficiency full-length cDNA cloning."		
RT	Meth. Enzymol. 303:19-44(1999).		
RP	[2]	SEQUENCE FROM N.A.	
RP	STRAIN=C57BL/6J; TISSUE=Skin;		
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RC	RIKEN FANTOM Consortium;		
RA	"Functional annotation of a full-length mouse cDNA collection."		
RT	Nature 409:685-690(2001).		
RP	[3]	SEQUENCE FROM N.A.	
RP	STRAIN=C57BL/6J; TISSUE=Skin;		
RC	The FANTOM Consortium.		
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;		
RA	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RT	Nature 420:563-573(2002).		
RP	[4]	SEQUENCE FROM N.A.	
RP	STRAIN=C57BL/6J; TISSUE=Skin;		
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RC	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,		
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.		

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Db 300 FCSKSWETKTSYPSVKEKYSEYCFSGAYILS-LLOGNYFTGSSWEQIHFMGKIKDSNA 358
Qy 429 GWTGLYMLNLTNMPAEQPLSTPLSHST 456
Db 359 GWTGLYMLNLTNMPAEQPLSTPLSHST 386

RESULT 10
Q6DPS1
ID Q6DPS1 PRELIMINARY; PRT; 508 AA.
AC Q6DPS1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Entpdl-prov protein.
GN Name=entpdl-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076662; AAH76662.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 58.2%; Score 1416; DB 2; Length 508;
Best Local Similarity 56.0%; Pred. No. 2.7e-101;
Matches 262; Conservative 82; Mismatches 106; Indels 18; Gaps 4;

Qy 4 RNOQTWPEG--IFLSSMKPINVSA-----STLYGIVLDAGSSHTSLYIKW 47
Db 8 KQKTHKKVIFLGFALFVLGIVSLVAIVQNPPLPKNIKIGIVLDAGSSHTSVIYEW 67
Qy 48 PAEKENDTVVHVECKRGKPGISKFKVQKNEIGIVLTDCEMAREVIPRSQHQETPVY 107
Db 68 PAEKENDTVVQIQNECKVEGNGISSYHGBELKAGLSLQKCMKARQVPEKQRETPVY 127
Qy 108 LGATAGHLLRMESSEELADRLVDVRSLSNYPDFQGARITQEGAGWIITNLLG 167
Db 128 LGATAGHLLRLTNATWABEVLSSVENTLRSFPDFQGARITQEGAGWIITNLLG 187
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Qy 168 KFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVFNQOTIBSPDNALQFRLYGKQYN 227
Db 188 NFIQDSQWFKYIP-NFKPTSTSGALDGGASTQITFESKRE-IESQENSLHFLRYGKSYD 245
Qy 228 VYTHSFLCYGKQDALWQKLAKIDQVANSNEILRDCFPHPGYKVVNVSDLYKTPCTKRFEM 287
Db 246 IYTHSFLCYGKQDALRLQIANIKDATSIDLDCFNSGYRNASTNDLYSSPCISKLR 305
Qy 288 TLPFQOFEIOGIGNVQOCHOSILEFNTSYCPYSQCAFNGIFLPLQGDGCAFSAFYFVM 347
Db 306 PTAPSTLDIRGTGNYQCKRNQVAFNRTHCTYSHCSFNGVQPSLQDGTGFAFYFVM 365
Qy 348 KFLNLTSEKVSQEKVEMMKFCAQPWEIEIKTSYAGVKEKYLSEYCFSGTYILSLLOQY 407
Db 366 NFLNLTNEQMSLDKVKETVERHCSRWDVCKDPKIKYKYLSEYCFSGTYILNLEGY 425
Qy 408 HPTADSEVHEHFIKIOGSDAGWTGLYMLNLTNMPAEQPLSTPLSHS 455
Db 426 GFSSSENWDIRFLGKIKDSAGWTGLYMLNLTNMPAEQPLSTPLSHA 473

RESULT 11
Q6GPF74
ID Q6GPF74 PRELIMINARY; PRT; 508 AA.
AC Q6GPF74;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC80631 protein.
GN Name=MGC80631;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341133; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
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RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC073267.1; -	
DR	GO; GO:0016787; F:hydrolase activity; IEA.	
DR	InterPro; IPR000407; GDAI_CD39_NTPase.	
DR	Pfam; PF01150; GDAI_CD39_1	
DR	KrZywnski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.;	
SQ	PROSITE; PS01238; GDAI_CD39_NTPASE; 1.	
	SEQUENCE 508 AA; 5049 MW; BD205818A06C523B CRC64;	
Query Match 56.7%; Score 1379; DB 2; Length 508;		
Best Local Similarity 56.1%; Pred. No. 2e-98;		
Matches 256; Conservative 74; Mismatches 110; Indels 16; Gaps 3;		
QY	15 LSSMKPINVA-----STLYGVLDSGSSHTSLYIKWPAEKENDTGVVHQ 60	
DB	21 LGALFPLGVIALVTIAVQNKPLPNKIKYGLVLDAGSSHTSVIYEPSEKENDTGVVQ 80	
QY	61 VEECRVKGPGISKVQKNEIGIYLTDCMERAREVIPSQHOETPVVYLGATAGMRLLRME 120	
DB	81 INDCRVEGNGLSSVGHPTKAGLSLQKMKARQVPEMQKETPVVYLGATAGMRLLRN 140	
QY	121 SEELADRVLDVVERSLNYPDFQARIITQEGEGAYGWTITNVLGKFSQKTRWFSIVP 180	
DB	141 NATMAEEVLSSVENMLRSFPDFQARIITQEGEGAYGWTITNVLGNFIQDSGWFKYMP 200	
QY	161 YETNNQETFGALDGGASTQVTFVPOQTIESPNALQFLRYGKDYNNYTHSFLCYGKQ 240	
DB	201 -NFKPTGSGALDGGASTQITFESKE-IESQNSLHFRUYGKSDYVYTHSFLCYGKQ 258	
QY	241 ALMOKLADIOVASNEILRDCFPHPGKVVNVSDLYKTPCTKRFEMTLFPQOFEIOGIG 300	
DB	259 ALRLQIANSVPTATDSILMDPCFNSGYRRNTSTSLYSSPCISNLRISTAPSLFDVKG 318	
QY	301 NYQOCHQSILELNTSYCPYSCAPNGIFLPLQDGCAPSAFYVMKFLNLTSEKVSQE 360	
DB	319 NYQLCKRNVAEITDTRCTYSHCSFNGIFQPLDGTGFAFSAYFVMDFLKTKGEISLD 378	
QY	361 KYTEMKMKFCQAPWEIEKTSYAGVKEKYLSEYCSFGTGYLILSLQGYHFTADSWEHIFI 420	
DB	379 KYKTEVERHCSFPWDEKKEPKKIEKYLSEYCSFGTGYLILSLQGYHFTADSWEHIFI 438	
QY	421 GKIQSDAGWTLYGMLNTNMIAPQPLSTPLSHST 456	
DB	439 GKIKSDAGWTLYGMLNTNMIAPSLPYSPPLSHAT 474	
RESULT 12		
Q6DC46	PRELIMINARY; PRT; 492 AA.	
ID	Q6DC46	
AC	Q6DC46;	
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Zgc:100819 protein.	
GN	Names=zgc:100819;	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRATN=Singapore local strain; TISSUE=Embryo;	
RC	PubMed=12477932; DOI=10.1073/pnas.242603899;	
RX	Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Tohyuki S., Carninci P., Prange C.,	
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywnski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRATN=Singapore local strain; TISSUE=Embryo;	
RC	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	
RL	Director MGC Project;	
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC078240; AAH78240.1; -	
DR	GO; GO:0016787; F:hydrolase activity; IEA.	
DR	InterPro; IPR000407; GDAI_CD39_NTPase.	
DR	Pfam; PF01150; GDAI_CD39_1	
DR	PROSITE; PS01238; GDAI_CD39_NTPASE; 1.	
SQ	SEQUENCE 492 AA; 55507 MW; B789AB6DFC6A032B CRC64;	
Query Match 52.7%; Score 1280.5; DB 2; Length 492;		
Best Local Similarity 54.8%; Pred. No. 8.5e-91;		
Matches 252; Conservative 66; Mismatches 105; Indels 37; Gaps 9;		
QY	13 IFLSMKPIN-----VSASTL-----YGIVLDAGSSHTSLYIKWPAEKENDTGVV 58	
DB	15 IFLMAVAVGIVMVSISVQHKPLPKQKYKYLVDAGSSHTSVIYKWPAAKENTGMV 74	
QY	59 HQVECRVKGPGISKVQKNEIGIYLTDCMERAREVIPSQHOETPVVYLGATAGMRLLR 118	
DB	75 QQHHTCNVKGKGTSSYFDPKPGAGASLECKMEKEKIPAHRSHTPVVYLGATAGMRLLR 134	
QY	119 MESEELADRVLDVVERSLNYPDFQARIITQEGEGAYGWTITNVLGKFSQKTRWFSI 178	
DB	135 MEDEMASEKILTSVAHSLKTYPFSGARILSGQEGAGWTITVNL-----SENLR- 186	
QY	179 VPYETNNQETFGALDGGASTQVTFVPOQTIESPNALQFLRYGKDYNNYTHSFLCYGK 238	
DB	187 -----KPAGTLGALDGGASTQITFVPQ-QIISSDINSIDFLRYGNDYHLYTHSFLCYGK 240	
QY	239 DQALMOKLADIOVASNE-----ILRDCPCHPGKVVNVSDLYKTPCTKRFEMTLFPQOF 294	
DB	241 DQALKLMAEKLRSTPDKTDAILLRDPCFHPGNTTKLTLESV-NTECMKFLKM--PKEQF 297	
QY	295 EIOGIGNYQOCHOSILELNTSYCPYSCAPNGIFLPLQDGCAPSAFYVMKFLNLT 354	
DB	298 SHVGLGNWSQCSIRKVENTSHCPYSGCSFNGVFPQTVGKFGAPSAFFVMDFLNLKN 357	
QY	355 EKVSQEKVTEMMKKFCAQPMWEIKTSYAGVKEKYLSEYCSFGTYILSLILQGYHFTADSW 414	
DB	358 D--SLDKTKQRLAMCYCSTPNQKIVQDHPKVKYKYLSEYCFSAFYIILTLLEHGYNFTSDNW 415	
QY	415 EHIHFTKIOGSDAGWTLYGMLNTNMIAPQPLSTPLSH 454	
DB	416 NDKIFKIKIGSDAGWTLYGMLNTNMIAPEDDPKPLMPH 455	
RESULT 13		
Q6UQ22	PRELIMINARY; PRT; 497 AA.	
ID	Q6UQ22	
AC	Q6UQ22;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Nucleoside triphosphate diphosphohydrolase-8 (EC 3.6.1.5).	
GN	Name=Entp8;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	


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Qy 204 VPQNTIESPDNALQFLRYGKDVNVTYTHSFLCYGKQQA---LWOKLAKDIQVASNEILRD 260
Db 214 QP-GVTIEDKNTSVLFRLYGNTSYLTHSYLCYQIQASKELMAALHQDGSYVQN--ISH 270
Qy 261 PCFHPGKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELENTSYCPY 320
Db 271 PCVPKGYRIITIAEIVDSCVPTPMSLPAQILTVTGTGNPAACPTAILKLFNLTCGAN 330
Qy 321 SOCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIITS 380
Db 331 RTCGFDGVYQPPVRGQFFAFAGFYITFSFLNLGTQQ--SLSHVNATVWDFCNKWSLVELT 389
Qy 381 YAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIKIGQSDAGWTLGYMLNLTN 440
Db 390 FPQNKKE-HLHTYCVVGLYILTLVLDGYKFDHTWSNIHFSQKAGNADIGWTLGFMLNLTN 448
Qy 441 MIPAE 445
Db 449 MIPT 453

RESULT 15
Q90X66 PRELIMINARY; PRT; 493 AA.
AC Q90X66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_taxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21982040; PubMed=11985621;
RA Knowles A.F., Nagy A.K., Strobil R.S., Wu-Weis M.;
RT "Purification, characterization, cloning, and expression of the
RL chicken liver ecto-ATP-diphosphohydrolase."
DR EMBL; AF426405; AAL25086.1;
DR GO; GO:0004050; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449B86167B70 CRC64;

Query Match 40.5%; Score 985; DB 2; Length 493;
Best Local Similarity 45.6%; Pred. No. 7.3e-68;
Matches 194; Conservative 72; Mismatches 143; Indels 16; Gaps 7;

Qy 27 TLYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGIGSKFVKVNEIGIYLT 86
Db 39 TKYGLVFDAGSTHALYVYQWPAKENGTVGSQVESCIVNGSGISSYVADDPAGAGSLX 98
Qy 87 DCMERAREVTPRSQOETPVYLGATAGMLRMESEELADRVLDVVERSLSNYPDFQGA 146
Db 99 PCLDKAMAVIPEVQWQWQTPYLGATAGMLRMESEELADRVLDVVERSLSNYPDFQGA 158
Qy 147 RIITGQEGAGVGTITINVLG--KFSQKTFWFSIVPVTNNQETFGALDGGASTQVTF 203
Db 159 QILTGNBEGSGWITVNYLLLETLTKFSPAGKW-----EHPQNTVEVLGALDGGASTQITF 213
Qy 204 VPQNTIESPDNALQFLRYGKDVNVTYTHSFLCYGKQQA---LWOKLAKDIQVASNEILRD 260
Db 214 QP-GVTIEDKNTSVLFRLYGNTSYLTHSYLCYQIQASKELMAALHQDGSYVQN--ISH 270
Qy 261 PCFHPGKVVNVDLYKTPCTKRFEMTLFPQOEIOGIGNYQOCHOSILELENTSYCPY 320
Db 271 PCVPKGYRIITIAEIVDSCVPTPMSLPAQILTVTGTGNPAACPTAILKLFNLTCGAN 330
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Qy 321 SOCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEIITS 380
Db 331 RTCGFDGVYQPPVRGQFFAFAGFYITFSFLNLGTQQ--SLSHVNATVWDFCNKWSLVELT 389
Qy 381 YAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIKIGQSDAGWTLGYMLNLTN 440
Db 390 FPQNKKE-HLHTYCVVGLYILTLVLDGYKFDHTWSNIHFSQKAGNADIGWTLGFMLNLTN 448
Qy 441 MIPAE 445
Db 449 MIPT 453
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Search completed: March 7, 2005, 13:22:45
Job time : 64.8824 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 74.4923 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147a-4_COPY_21_476
Perfect score: 2432
Sequence: 1 VSHRNQQTWFGIFLSNKP.....NLTNMPARQLPSTPLSHST 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Database		Description	
Result No.	Score	Match	Length	ID	DB	ID			
1	2430	99.9	476	3	AA70912	AA70912	Human CD3		
2	2430	99.9	476	3	AA70889	AA70889	Protein e		
3	2373	97.6	476	3	AA70911	AA70911	Human CD3		
4	2373	97.6	476	3	AA70888	AA70888	Protein e		
5	2297	94.4	510	2	AAW04334	AAW04334	Human lym		
6	2297	94.4	510	2	AAW04264	AAW04264	Human CD3		
7	2297	94.4	510	3	AA70910	AA70910	Human sol		
8	2297	94.4	510	3	AA70887	AA70887	Human CD3		
9	2297	94.4	510	4	AA70917	AA70917	Human CD3		
10	2297	94.4	510	7	ADJ57262	ADJ57262	Human CD3		
11	2297	94.4	510	8	ADL24295	ADL24295	Human CD3		
12	2297	94.4	510	8	ADQ99453	ADQ99453	Human CD3		
13	2297	94.4	510	8	ADR69210	ADR69210	Human CD3		
14	2297	94.4	510	8	ADR69042	ADR69042	Human CD3		
15	2297	94.4	510	8	ADS17924	ADS17924	Human can		
16	2297	94.4	510	8	ABO84674	ABO84674	Human can		
17	2297	94.4	510	8	ADR87821	ADR87821	Human CD3		
18	2297	94.4	511	8	ADK60421	ADK60421	Angiogene		
19	2297	94.4	511	8	ADK60722	ADK60722	Angiogene		
20	2297	94.4	511	8	ADP73345	ADP73345	CD39 lym		
21	2297	94.4	517	7	ADN95839	ADN95839	Human BEC		
22	2297	94.4	517	8	ADK60221	ADK60221	Angiogene		
23	2297	94.4	517	8	ADK60522	ADK60522	Angiogene		
24	2297	94.4	517	8	ADP73145	ADP73145	Angiogene		
25	2297	94.4	522	8	ABO84672	ABO84672	Human can		

ALIGNMENTS

RESULT 1

AA70912
ID AA70912 standard; protein; 476 AA.
XX AC AA70912;
XX DT 17-AUG-2000 (first entry)
XX DE Human CD39-L4-2/3 protein construct.
XX KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic.
XX OS Homo sapiens.
XX OS Synthetic.

Key	Location/Qualifiers
Region	1..48
Cleavage-site	/note= "Human CD39-L4 protein N-terminal end"
Misc-difference	39 /note= "Cleavage site of leader sequence"
Region	/label= Cys, Ser /note= "Xaa= Cys in CD39-L4-2 and Xaa=Ser in CD39-L4-3" 49..476 /note= "Human soluble CD39 protein"
Region	WO200023459-A1.
Region	27-APR-2000.
Region	13-OCT-1999; 99WO-US022955.
Region	16-OCT-1998; 98US-0104585P.
Region	06-NOV-1998; 98US-0107466P.
Region	13-AUG-1999; 99US-0149010P.
Region	(IMMV) IMMUNEX CORP.
Region	Maliszewski CR, Gayle RB, Price VL, Gimpel SD; WPI; 2000-339644/29.

QY 1 VSHRNOQTWTFEGIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIYKWPAAKENDTGVVHQ 60
Db 21 VSHRNOQTWTFEGIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIYKWPAAKENDTGVVHQ 80
QY 61 VEECRVKGPGISKVFQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME 120
Db 81 VEECRVKGPGISKVFQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME 140
QY 121 SEELADRLVDVVERSLNYPDFQGARITGOEGAYGWTITNYLLGKFSOKTRWFSIVP 180
Db 141 SEELADRLVDVVERSLNYPDFQGARITGOEGAYGWTITNYLLGKFSOKTRWFSIVP 200
QY 181 YETNNQETFGALDGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQD 240
Db 201 YETNNQETFGALDGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQD 260
QY 241 ALWOKLAKDIOVASNEILRDCPFHPGKYKVVNVSILYKTPCTKRFEMTLPPQOEIOGIG 300
Db 261 ALWOKLAKDIOVASNEILRDCPFHPGKYKVVNVSILYKTPCTKRFEMTLPPQOEIOGIG 320
QY 301 NYQOCHOSILELNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQE 360
Db 321 NYQOCHOSILELNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQE 380
QY 361 KVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIVLSLLQGYHFTADSWEHIFHI 420
Db 381 KVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIVLSLLQGYHFTADSWEHIFHI 440
QY 421 GKIQSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHST 456
Db 441 GKIQSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHST 476

RESULT 3

RAY70911

ID AAY70911 standard; protein; 476 AA.

AC AAY70911;

XX 17-AUG-2000 (first entry)

XX Human CD39-L4-1 protein construct.

DE Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic.

OS Homo sapiens.

OS Synthetic.

XX Key

XX Region 1. 37

XX Location/Qualifiers

XX /note= "Human CD39-L4 protein N-terminal end"

XX /note= "Cleavage site of leader sequence"

XX /note= "Human soluble CD39 protein"

XX W0200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

(IMMV) IMMUNEX CORP.

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

DR WPI; 2000-339644/29.

XX New soluble CD39 polypeptides having apyrase activity, useful for
inhibiting angiogenesis and treating unstable angina, myocardial
infarction, stroke, coronary artery disease or injury.

PS Claim 6; Page 89-91; 122pp; English.

XX The present sequence is a fusion protein construct CD39-L4-1, comprising
the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is
a secreted apyrase, belonging to the CD39 family. Soluble CD39 is
constructed by removing the N- and C-terminal transmembrane domains. It
retains the capacity to metabolise ATP and ADP at relevant concentrations
and the ability to block and reverse ADP-induced platelet activation and
recruitment, including platelet aggregation. Soluble CD39 polypeptides
are useful for inhibiting angiogenesis. It is useful for the treatment of
unstable angina, myocardial infarction, stroke, coronary artery disease
or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia,
embolism, platelet-associated ischaemic disorders including lung,
coronary and cerebral ischaemia, thrombotic disorders including coronary,
peripheral and cerebral artery thrombosis, intracardiac and venous
thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
for preventing thrombus formation or reformation, occlusion, reocclusion,
stenosis or restenosis of blood vessels or stroke

XX Sequence 476 AA;

Query Match 97.6%; Score 2373; DB 3; Length 476;

Best Local Similarity 97.6%; Pred. No. 8.2e-233;

Matches 445; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSHRNOQTWTFEGIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIYKWPAAKENDTGVVHQ 60
Db 21 VSHRNOQTWTFEGIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIYKWPAAKENDTGVVHQ 80
QY 61 VEECRVKGPGISKVFQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME 120
Db 81 VEECRVKGPGISKVFQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRME 140
QY 121 SEELADRLVDVVERSLNYPDFQGARITGOEGAYGWTITNYLLGKFSOKTRWFSIVP 180
Db 141 SEELADRLVDVVERSLNYPDFQGARITGOEGAYGWTITNYLLGKFSOKTRWFSIVP 200
QY 181 YETNNQETFGALDGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQD 240
Db 201 YETNNQETFGALDGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQD 260
QY 241 ALWOKLAKDIOVASNEILRDCPFHPGKYKVVNVSILYKTPCTKRFEMTLPPQOEIOGIG 300
Db 261 ALWOKLAKDIOVASNEILRDCPFHPGKYKVVNVSILYKTPCTKRFEMTLPPQOEIOGIG 320
QY 301 NYQOCHOSILELNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQE 360
Db 321 NYQOCHOSILELNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQE 380
QY 361 KVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIVLSLLQGYHFTADSWEHIFHI 420
Db 381 KVTMMKKFCAQPWEEIKTSYAGVKEKYLSEYCSGTIVLSLLQGYHFTADSWEHIFHI 440
QY 421 GKIQSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHST 456
Db 441 GKIQSDAGWTGLGYMLNLTNNIPAEQPLSTPLSHST 476

RESULT 4

AAY70888

ID AAY70888 standard; protein; 476 AA.

XX The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
CC pancreatic (AAW04339) ATPases have been partially sequenced. The
CC sequences have been found to be highly homologous to a human lymphoid
CC cell activation antigen designated CD39 (Maliszewski et al. (1994). J.
CC Immunol. : 3574-3583). The complete sequences of the ATPases types I and
CC II have not been obtained yet. Assuming that the CD39 gene product is an
CC ATPase type II, the use of CD39 in the reduction of platelet aggregation
CC and of thrombogenicity may be contemplated, as well as a process of
CC making ATPases using the CD39 sequence (AAT38516)
XX
SQ Sequence 510 AA;

Query Match : 94.4%; Score 2297; DB 2; Length 510;
Best Local Similarity 97.1%; Pred. No. 5.3e-225;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 12 GIFLSSMKPINVASSTLYGIVLDGSSHTSLIYKWPAAEKENDTGCVHVQVEECRVKPGI 71
Db 36 GLTONKALPENVK----YGVLDAGSSHTSLIYKWPAAEKENDTGCVHVQVEECRVKPGI 91

QY 72 SKFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLVDV 131
Db 92 SKFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLVDV 151

QY 132 VERSLSNYPDFQGARITITQEGAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDFQGARITITQEGAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 211

QY 192 LDLGASTQVTFVPQNTIESPDNALQRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIQ 251
Db 212 LDLGASTQVTFVPQNTIESPDNALQRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIQ 271

QY 252 VASNEILRDPFCFHPGKVKVNSDLYKTPCTKREMTLPFOQFEIQTGIGNYQOCHOSTLE 311
Db 272 VASNEILRDPFCFHPGKVKVNSDLYKTPCTKREMTLPFOQFEIQTGIGNYQOCHOSTLE 331

QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCA 391

QY 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWT 451

QY 432 LGYMLNTNMIPAEQPLSTPLSHST 456
Db 452 LGYMLNTNMIPAEQPLSTPLSHST 476

RESULT 6
AAW04264
ID AAW04264 standard; protein; 510 AA.
XX
AC AAW04264;
XX
DT 29-MAY-1997 (first entry)
XX
DE Human CD39 protein.
XX
KW Human; lymphocyte activation marker; gene therapy;
KW ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;
KW transplantation; endothelial cell; prosthetic device;
KW platelet aggregation; inhibition; intravascular.
XX
OS Homo sapiens.
XX
FN WO9630532-A1.
XX
PD 03-OCT-1996.
XX
PF 22-MAR-1996; 96WO-EP001270.
XX

PR 24-MAR-1995; 95US-00410371.
XX 12-FEB-1996; 96US-00600383.
PA (SANO) SANDOZ LTD.
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Bach FH, Robson S;
XX WPI; 1996-455377/45.
DR N-PSDB; AAT33966.
XX
PT Gene therapy of inflammatory or immunological stimulation of platelet
PT aggregation - using CD39 protein with ATP di:phosphohydrolase activity,
PT useful for preventing or alleviating thrombotic condition in mammalian
PT subject.
XX
PS Claim 3; Page 39; 65pp; English.
XX
CC Non-human transgenic or somatic recombinant mammals, whose cells contain
CC a heterologous DNA encoding a polypeptide (especially human CD39 protein)
CC having ATP-diphosphohydrolase activity under cellular activating
CC conditions is claimed. In particular the animal is a pig and its cells
CC (or tissues or organs) can be used for transplantation. DNA coding for
CC human CD39 is also useful for genetically modifying a mammalian cell to
CC render it less susceptible to an inflammatory or immunological stimulus
CC and platelet aggregation. The modified cells can be used to prevent or
CC alleviate a thrombotic condition. The present sequence is that of the
CC human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-
CC 3584
XX
SQ Sequence 510 AA;

Query Match : 94.4%; Score 2297; DB 2; Length 510;
Best Local Similarity 97.1%; Pred. No. 5.3e-225;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 12 GIFLSSMKPINVASSTLYGIVLDGSSHTSLIYKWPAAEKENDTGCVHVQVEECRVKPGI 71
Db 36 GLTONKALPENVK----YGVLDAGSSHTSLIYKWPAAEKENDTGCVHVQVEECRVKPGI 91

QY 72 SKFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLVDV 131
Db 92 SKFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLVDV 151

QY 132 VERSLSNYPDFQGARITITQEGAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDFQGARITITQEGAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 211

QY 192 LDLGASTQVTFVPQNTIESPDNALQRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIQ 251
Db 212 LDLGASTQVTFVPQNTIESPDNALQRLYKGDYNYVTHSFLCYGKDQALWQKLAKDIQ 271

QY 252 VASNEILRDPFCFHPGKVKVNSDLYKTPCTKREMTLPFOQFEIQTGIGNYQOCHOSTLE 311
Db 272 VASNEILRDPFCFHPGKVKVNSDLYKTPCTKREMTLPFOQFEIQTGIGNYQOCHOSTLE 331

QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCA 391

QY 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWT 451

QY 432 LGYMLNTNMIPAEQPLSTPLSHST 456
Db 452 LGYMLNTNMIPAEQPLSTPLSHST 476

RESULT 7
AAW09010
ID AAW09010 standard; protein; 510 AA.
XX

Query Match 94.4%; Score 2297; DB 4; Length 510;
Best Local Similarity 97.1%; Pred. No. 5.3e-225;

Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;	
Qy	12 GIPFLSSMKPYNVSASTLYGVLVDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGI 71
Dd	36 GLTONKALPENVK-----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGI 91
Qy	72 SKFQVKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
Dd	92 SKFQVKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 151
Qy	132 VERSLSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGA 191
Dd	152 VERSLSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGA 211
Qy	192 LDLGASTQVTFVQNTIESPDNALQFRLYGKDYNVYTHSPFLCYGKQDQALWQKLAKDIQ 251
Dd	212 LDLGASTQVTFVQNTIESPDNALQFRLYGKDYNVYTHSPFLCYGKQDQALWQKLAKDIQ 271
Qy	252 VASNEILRDPCHFGYKVKVNVSDLYKTPCTKREMTLPQOFEIOGIGNYQOCHOSILE 311
Dd	272 VASNEILRDPCHFGYKVKVNVSDLYKTPCTKREMTLPQOFEIOGIGNYQOCHOSILE 331
Qy	312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 371
Dd	332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy	372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHIKIQGSDAGWT 431
Dd	392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHIKIQGSDAGWT 451
Qy	432 LGYMLNLTNMIAPAEQPLSTPLSHST 456
Dd	452 LGYMLNLTNMIAPAEQPLSTPLSHST 476

RESULT 10	
ID	ADJ57262 standard; protein; 510 AA.
XX	ADJ57262;
AC	06-MAY-2004 (first entry)
XX	Human CD39 polypeptide.
XX	CD39; nucleoside diphosphate; thrombolytic; anticoagulant;
KW	cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;
KW	cardiac; antianginal; antiarteriosclerotic; gynaecological;
KW	cerebroprotective; cancer; human; apyrase; enzyme.
XX	Homo sapiens.
OS	
XX	Key Location/Qualifiers
PH	Domain 55..61
FT	/note = ACR1
FT	Domain 125..135
FT	/note = ACR2
FT	Domain 171..183
FT	/note = ACR3
FT	Domain 213..220
FT	/note = ACR4
FT	Domain 447..454
FT	/note = ACR5
XX	
PN	W02003070823-A2.
XX	
PD	28-AUG-2003.
XX	
PF	19-FEB-2003; 2003WO-US004845.
XX	
PR	20-FEB-2002; 2002US-0358303P.
XX	
PA	(GEO) GEN HOSPITAL CORP.

PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX	
PI	Elmaleh DR, Robson SC, Papisov MI;
XX	
DR	WPI; 2003-778966/73.
DR	N-PSDB; ADJ57261.
XX	
PT	New enzyme polymer conjugate used for treating abnormal levels of
PT	extracellular nucleotides or platelet aggregation, graft transplant,
PT	cardiovascular disease, cancer and sepsis.
XX	
PS	Claim 20; SEQ ID NO 2; 82pp; English.
XX	
CC	The invention relates to a conjugate (I) comprising an enzyme and a
CC	biodegradable polymer, where (i) enzymatic activity of the enzyme is
CC	higher relative to that of the enzyme in the absence of the biodegradable
CC	polymer, or (ii) the half life of the enzyme is longer than that of the
CC	enzyme in the absence of the polymer. The enzymatic activity (i) is at
CC	least 10 (preferably at least 100) times higher in the presence of the
CC	polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,
CC	preferably an apyrase, especially a soluble form of CD39 and catalyzes
CC	hydrolysis of nucleoside diphosphate. The conjugate can be used to treat
CC	diseases relating to abnormal levels of extracellular nucleotides or
CC	abnormal aggregation of platelets, particularly cardiovascular disease,
CC	cancer, sepsis or a disease related to graft transplant. (I) is also used
CC	for treating coronary artery disease or injury following myocardial
CC	infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,
CC	platelet associated ischaemic disorders including lung, coronary and
CC	cerebral ischaemia, reocclusion following thrombosis, thrombotic
CC	disorders, and thrombosis and coagulopathies associated with exposure to
CC	a foreign or injured tissue surface, in combination with angioplasty,
CC	carotid endarterectomy, anastomosis of vascular grafts and chronic
CC	cardiovascular devices. The present sequence represents a human CD39
CC	polypeptide.
XX	
SQ	Sequence 510 AA;
Query Match 94.4%; Score 2297; DB 7; Length 510;	
Best Local Similarity 97.1%; Pred. No. 5.3e-225;	
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;	
Qy	12 GIPFLSSMKPYNVSASTLYGVLVDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGI 71
Dd	36 GLTONKALPENVK-----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGI 91
Qy	72 SKFQVKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
Dd	92 SKFQVKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 151
Qy	132 VERSLSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGA 191
Dd	152 VERSLSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGA 211
Qy	192 LDLGASTQVTFVQNTIESPDNALQFRLYGKDYNVYTHSPFLCYGKQDQALWQKLAKDIQ 251
Dd	212 LDLGASTQVTFVQNTIESPDNALQFRLYGKDYNVYTHSPFLCYGKQDQALWQKLAKDIQ 271
Qy	252 VASNEILRDPCHFGYKVKVNVSDLYKTPCTKREMTLPQOFEIOGIGNYQOCHOSILE 311
Dd	272 VASNEILRDPCHFGYKVKVNVSDLYKTPCTKREMTLPQOFEIOGIGNYQOCHOSILE 331
Qy	312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 371
Dd	332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy	372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHIKIQGSDAGWT 431
Dd	392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHIKIQGSDAGWT 451
Qy	432 LGYMLNLTNMIAPAEQPLSTPLSHST 456
Dd	452 LGYMLNLTNMIAPAEQPLSTPLSHST 476

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RESULT 11
ADL24295
ID ADL24295 standard; protein; 510 AA.
XX
AC ADL24295;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human CD39.
XX
KW cardiovascular disease; IL-17; interleukin; IL-18; 4-LBB; CD30; OX40;
KW antagonist.
XX
OS Homo sapiens.
XX
PN WO2004019866-A2.
XX
PD 11-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-US026354.
XX
PR 28-AUG-2002; 2002US-0406418P.
XX
PR 12-AUG-2003; 2003US-0494457P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
PA Burton PB, Deisher TA;
XX
PI WPI; 2004-239107/22.
XX
DR N-P5DB; ADL24294.
XX
XX Use of IL-17, IL-18, 4-LBB, CD30 or OX40 antagonists, for treating a
XX cardiovascular disease, e.g. chronic immune myocarditis, congestive heart
XX failure, aneurysm, angina, embolism, restenosis, ischemia or
XX thrombocytopenic purpura.
XX
PS Disclosure; Page 133-134; 135pp; English.
XX
XX The present invention relates to a method of treating cardiovascular
XX disease in a subject, comprising administering an IL-17, IL-18, 4-LBB,
XX CD30 or OX40 antagonist. The IL-17, IL-18, 4-LBB, CD30 or OX40
XX antagonists are useful for treating cardiovascular disorders, e.g.
XX (chronic immune) myocarditis, congestive heart failure, aneurysms,
XX angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The
XX present sequence is a polypeptide used in the exemplification of the
XX invention.
XX
SQ Sequence 510 AA;

Query Match 94.4%; Score 2297; DB 8; Length 510;
Best Local Similarity 97.1%; Pred. No. 5,3e-225;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 12 GIFLSSMKPINVSASTLYGIVLDGSSHTSLYIKWPAEKENDTGCVHVQVEECRVKGGI 71
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 36 GLTONKALPENVK----YGVLDGSSHTSLYIKWPAEKENDTGCVHVQVEECRVKGGI 91
Qy 72 SKFVKVNEIGLYLTDCHMERAVIPRSQHOETPVYLGATAGMRLRMESEELADRVLDV 131
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 92 SKFVKVNEIGLYLTDCHMERAVIPRSQHOETPVYLGATAGMRLRMESEELADRVLDV 151
Qy 132 VERSLSNYPFDQAGRIITGQEGAYGWTITNYLLGKFSQKTRFWSIVPYETNNQETFGA 191
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 152 VERSLSNYPFDQAGRIITGQEGAYGWTITNYLLGKFSQKTRFWSIVPYETNNQETFGA 211
Qy 192 LDLGASTQVTFVQNGQITSPDNALQRLYKGQDYNVYTHSFLCYGKQDQALWKAKDIQ 251
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 212 LDLGASTQVTFVQNGQITSPDNALQRLYKGQDYNVYTHSFLCYGKQDQALWKAKDIQ 271
Qy 252 VASNEILLRDPCHFGYKXKVVNSDLKTPCTKREMTLPFOQFELQIGNYQQCHQSILE 311
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 272 VASNEILLRDPCHFGYKXKVVNSDLKTPCTKREMTLPFOQFELQIGNYQQCHQSILE 331
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Qy 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFMKFLNLTSEKVSQEKVTEMKKFCA 371
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFMKFLNLTSEKVSQEKVTEMKKFCA 391
Qy 372 QPWEIEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHHPIGIKQSDAGWT 431
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 392 QPWEIEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHHPIGIKQSDAGWT 451
Qy 432 LGYMLNLTNMIIPARQPLSTPLSHST 456
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dy 452 LGYMLNLTNMIIPARQPLSTPLSHST 476

RESULT 12
ADQ99453
ID ADQ99453 standard; protein; 510 AA.
XX
AC ADQ99453;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human CD39 protein.
XX
KW CD39-like protein; gene mapping; molecular weight marker;
KW food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW NTPase; human; enzyme.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 47..68
FT /note= "Apyrase region (ACR) I"
FT Region 124..142
FT /note= "Apyrase region (ACR) II"
FT Region 169..191
FT /note= "Apyrase region (ACR) III"
FT Region 207..228
FT /note= "Apyrase region (ACR) IV"
XX
XX US6759214-B1.
XX
XX 06-JUL-2004.
XX
XX 13-JUL-2001; 2001US-00908510.
XX
XX 29-JAN-1999; 99US-00240639.
XX
XX (NUVE-) NUVELO INC.
XX
XX Chadwick BP, Frischauf A;
XX
XX WPI; 2004-515395/49.
XX
XX New CD-39-like polypeptides and polynucleotides, useful in chromosome and
XX gene mapping, as molecular weight markers, as food supplements, or as
XX anti-thrombotic or anti-tissue graft rejection agents.
XX
XX Example; Fig 8; 104pp; English.
XX
XX The invention relates to novel CD39-like polypeptides (CD39-like
XX nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding
XX such polypeptides. CD39-like polynucleotides may be used as hybridisation
XX probes, PCR primers and in chromosome and gene mapping. Polypeptides of
XX the invention may be used as molecular weight markers, as food
XX supplements, as anti-thrombotic or anti-tissue graft rejection agents, or
XX for regulating ATP neurotransmission in smooth muscle, peripheral ganglia
XX or brain. Sequences of the invention are useful in modulating ecto-ATPase
XX activity and for identifying compounds that modulate ecto-ATPase
XX activity. The present sequence is human CD39 protein, a member of the
XX CD39-like protein family. Note: This sequence is stated to be the same as
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Search completed: March 7, 2005, 13:13:07
Job time : 76.6034 secs

72 SKFVQKNEIGIYITDCMERAREVIPSQHQETPVVLGATAGMRLRMSEELADRLVD 131
 92 SKFVQKNEIGIYITDCMERAREVIPSQHQETPVVLGATAGMRLRMSEELADRLVD 151
 122 VEPDSINVPDPEOCARIITGORECAYGAWITINYLKGFOSKTRFWSIVPYETNNQETFGA 191

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 7, 2005, 13:23:03 ; Search time 53.496 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-4_COPY_21_476
Perfect score: 2432
Sequence: 1 VSHRNQQTWFGIFLSMKXP.....NLTNMPABQPLSLSHST 456

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues
Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				%		Query		Match		Length		DB		ID		Description	
Result No.	Score	Match	Length	DB	ID	Description											
1	2430	99.9	476	9	US-09-835-147-4	Sequence 4, Appli											
2	2373	97.6	476	9	US-09-835-147-3	Sequence 3, Appli											
3	2297	94.4	502	13	US-10-092-063-38	Sequence 38, Appli											
4	2297	94.4	510	9	US-09-835-147-2	Sequence 2, Appli											
5	2297	94.4	510	9	US-09-374-586-1	Sequence 1, Appli											
6	2297	94.4	510	10	US-09-781-796B-1	Sequence 1, Appli											
7	2297	94.4	510	16	US-10-646-308-30	Sequence 30, Appli											
8	2297	94.3	439	9	US-09-374-586-2	Sequence 2, Appli											
9	2294	94.3	454	9	US-09-835-147-6	Sequence 6, Appli											
10	2294	94.3	463	9	US-09-835-147-30	Sequence 30, Appli											
11	2294	94.3	464	9	US-09-835-147-27	Sequence 27, Appli											
12	2294	94.3	473	9	US-09-835-147-29	Sequence 29, Appli											
13	2294	94.3	474	9	US-09-835-147-28	Sequence 28, Appli											

14	2294	94.3	478	9	US-09-835-147-8	Sequence 8, Appli
15	2294	94.3	487	9	US-09-835-147-26	Sequence 26, Appli
16	994	40.9	495	9	US-09-823-356-4	Sequence 4, Appli
17	892.5	36.7	529	9	US-09-923-304-4	Sequence 4, Appli
18	891.5	36.7	458	13	US-10-052-586-496	Sequence 496, App
19	891.5	36.7	458	14	US-10-174-590-496	Sequence 496, App
20	891.5	36.7	458	14	US-10-176-758-496	Sequence 496, App
21	891.5	36.7	458	14	US-10-175-737-496	Sequence 496, App
22	891.5	36.7	458	14	US-10-174-581-496	Sequence 496, App
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27	891.5	36.7	458	14	US-10-173-706-496	Sequence 496, App
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30	891.5	36.7	458	14	US-10-176-482-496	Sequence 496, App
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32	891.5	36.7	458	14	US-10-176-913-496	Sequence 496, App
33	891.5	36.7	458	14	US-10-180-552-496	Sequence 496, App
34	891.5	36.7	458	14	US-10-180-557-496	Sequence 496, App
35	891.5	36.7	458	14	US-10-173-700-496	Sequence 496, App
36	891.5	36.7	458	14	US-10-174-572-496	Sequence 496, App
37	891.5	36.7	458	14	US-10-174-579-496	Sequence 496, App
38	891.5	36.7	458	14	US-10-174-588-496	Sequence 496, App
39	891.5	36.7	458	14	US-10-175-739-496	Sequence 496, App
40	891.5	36.7	458	14	US-10-175-740-496	Sequence 496, App
41	891.5	36.7	458	14	US-10-175-743-496	Sequence 496, App
42	891.5	36.7	458	14	US-10-176-488-496	Sequence 496, App
43	891.5	36.7	458	14	US-10-176-492-496	Sequence 496, App
44	891.5	36.7	458	14	US-10-176-747-496	Sequence 496, App
45	891.5	36.7	458	14	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
; US-09-835-147-4

Query Match 99.9%; Score 2430; DB 9; Length 476;

Best Local Similarity 100.0%; Pred. No. 3.6e-215; Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db 81 VBECRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMELLRME 140	
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QY 241 ALWOKLAKDIOVASNEILRDPCHPGYKVVNVSDDLKTPCTKRFEMTLPPQOFEIOGIG 300	
Db 261 ALWOKLAKDIOVASNEILRDPCHPGYKVVNVSDDLKTPCTKRFEMTLPPQOFEIOGIG 320	
QY 301 NYQOCHOSILELFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQE 360	
Db 321 NYQOCHOSILELFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQE 380	
QY 361 KVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIF 420	
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QY 421 GKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHST 456	
Db 441 GKIQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHST 476	
RESULT 2	
US-09-835-147-3	
; Sequence 3, Application US/09835147	
; Patent No. US2002000277A1	
; GENERAL INFORMATION:	
; APPLICANT: Maliszewski, Charles R.	
; APPLICANT: Gayle III, Richard B.	
; APPLICANT: Price, Virginia L.	
; APPLICANT: Gimpe, Steven D.	
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment	
; FILE REFERENCE: 2879-US	
; CURRENT APPLICATION NUMBER: US/09/835,147	
; CURRENT FILING DATE: 2001-04-13	
; PRIOR APPLICATION NUMBER: US 60/104,585	
; PRIOR FILING DATE: 1998-10-16	
; PRIOR APPLICATION NUMBER: US 60/107,466	
; PRIOR FILING DATE: 1998-11-06	
; PRIOR APPLICATION NUMBER: US 60/149,010	
; PRIOR FILING DATE: 1999-08-13	
; PRIOR APPLICATION NUMBER: PCT/US99/22955	
; PRIOR FILING DATE: 1999-10-13	
; NUMBER OF SEQ ID NOS: 31	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 3	
; LENGTH: 476	
; TYPE: PRT	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: Description of Artificial Sequence: Fusion	
; OTHER INFORMATION: construct of human CD39	
US-09-835-147-3	
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Best Local Similarity 97.6%; Pred. No. 6.6e-210; Indels 0; Gaps 0;	
Matches 445; Conservative 2; Mismatches 9; Indels 0; Gaps 0;	
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DB 152 VERSLSNYPDFQAGRIITGQEBGAGWTINVLGKFSQKTRWFSIVPYETNNQTFGA 211
QY 192 LDLGASTQVTFVPPQNQTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWKLAKDIQ 251
DB 212 LDLGASTQVTFVPPQNQTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWKLAKDIQ 271
QY 252 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILE 311
DB 272 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILE 331
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DB 332 LFNSTYCPYSCAFNGIFLPPLOQDFGAFSAFYFVWKFNLNLTSEKVSQSKVTMMKKFCA 391
QY 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQSGDAGWT 431
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QY 432 LGYMLNLTNNMIPAEQPLSTPLSHST 456
DB 452 LGYMLNLTNNMIPAEQPLSTPLSHST 476

RESULT 4
US-09-835-147-2 ;
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match 94.4%; Score 2297; DB 9; Length 510;
Best Local Similarity 97.1%; Pred. No. 7.5e-203;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
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DB 36 GLUTQNALPENVK----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVEBCRVKPGI 91
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DB 332 LFNSTYCPYSCAFNGIFLPPLOQDFGAFSAFYFVWKFNLNLTSEKVSQSKVTMMKKFCA 391
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QY 432 LGYMLNLTNNMIPAEQPLSTPLSHST 456
DB 452 LGYMLNLTNNMIPAEQPLSTPLSHST 476

RESULT 5
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match 94.4%; Score 2297; DB 9; Length 510;
Best Local Similarity 97.1%; Pred. No. 7.5e-203;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
QY 12 GIFLSSMXPINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEBCRVKPGI 71
DB 36 GLUTQNALPENVK----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVEBCRVKPGI 91
QY 72 SKFVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDV 131
DB 92 SKFVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDV 151
QY 132 VERSLSNYPDFQAGRIITGQEBGAGWTINVLGKFSQKTRWFSIVPYETNNQTFGA 191
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QY 192 LDLGASTQVTFVPPQNQTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWKLAKDIQ 251
DB 212 LDLGASTQVTFVPPQNQTIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWKLAKDIQ 271
QY 252 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILE 311
DB 272 VASNEILRDPCHPHGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILE 331
QY 312 LFNSTYCPYSCAFNGIFLPPLOQDFGAFSAFYFVWKFNLNLTSEKVSQSKVTMMKKFCA 371
DB 332 LFNSTYCPYSCAFNGIFLPPLOQDFGAFSAFYFVWKFNLNLTSEKVSQSKVTMMKKFCA 391
QY 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQSGDAGWT 431
DB 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQSGDAGWT 451

QY 432 LGYMLNLTNMPAEQPLSTPLSHST 456
Db 452 LGYMLNLTNMPAEQPLSTPLSHST 476.

RESULT 6
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SWIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; FILE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 94.4%; Score 2297; DB 10; Length 510;
Best Local Similarity 97.1%; Pred. No. 7.5e-203;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 12 GIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 71
Db 36 GLTONKALPENVK----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 91
QY 72 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
Db 92 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 151
QY 132 VERSLSNYPDPFOGARIITGOEAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDPFOGARIITGOEAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
QY 192 LDLGASTQVTFVFNQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQ 251
Db 212 LDLGASTQVTFVFNQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQ 271
QY 252 VASNEILRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILE 311
Db 272 VASNEILRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILE 331
QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 391
QY 372 QPWEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 451
QY 432 LGYMLNLTNMPAEQPLSTPLSHST 456
Db 452 LGYMLNLTNMPAEQPLSTPLSHST 476

RESULT 7
US-10-646-308-30

; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 94.4%; Score 2297; DB 16; Length 510;
Best Local Similarity 97.1%; Pred. No. 7.5e-203;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
QY 12 GIFLSSMKXPINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 71
Db 36 GLTONKALPENVK----YGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 91
QY 72 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 131
Db 92 SKFVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDV 151
QY 132 VERSLSNYPDPFOGARIITGOEAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDPFOGARIITGOEAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
QY 192 LDLGASTQVTFVFNQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQ 251
Db 212 LDLGASTQVTFVFNQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQ 271
QY 252 VASNEILRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILE 311
Db 272 VASNEILRDCPFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQOCHOSILE 331
QY 312 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCA 391
QY 372 QPWEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 451
QY 432 LGYMLNLTNMPAEQPLSTPLSHST 456
Db 452 LGYMLNLTNMPAEQPLSTPLSHST 476

RESULT 8
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439

QY	9	WFEIPLGSMXPIINVSASTL-----YGVLDAGSSHTSLIYKWPAAKENDTGVVHVEE	63
Db	14	WVPG---STGAPTSTQNKALPENVKYIGVLDAGSSHTSLIYKWPAAKENDTGVVHVEE	70
QY	64	CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEE	123
Db	71	CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEE	130
QY	124	LADRVLDDVVERSLNYPDFQAGARIITGOEGAYGMITINYLKGFSQKTRWFSIVPVET	183
Db	131	LADRVLDDVVERSLNYPDFQAGARIITGOEGAYGMITINYLKGFSQKTRWFSIVPVET	190
QY	184	NQOETFGALDLGGASTQVTFVQNTIESPDNALQRLYKGDYNYVTHSFCLYCGKQDALW	243
Db	191	NNQETFGALDLGGASTQVTFVQNTIESPDNALQRLYKGDYNYVTHSFCLYCGKQDALW	250
QY	244	OKLAKDIOVASNEILRDCPFHPCYKVVNVSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQ	303
Db	251	OKLAKDIOVASNEILRDCPFHPCYKVVNVSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQ	310
QY	304	QCHOSILELNTSYCPYSCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVT	363
Db	311	QCHOSILELNTSYCPYSCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVT	370
QY	364	EMMKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGKI	423
Db	371	EMMKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGKI	430
QY	424	QGS DAGWTGLYMLNLTNMPAEQPLSTPLSHST	456
Db	431	QGS DAGWTGLYMLNLTNMPAEQPLSTPLSHST	463
RESULT 11			
US-09-835-147-27			
; Sequence 27, Application US/09835147			
; Patent No. US2002000277A1			
; GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; CURRENT FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 27			
; TYPE: PRT			
; LENGTH: 464			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-27			
Query Match 94.3%; Score 2294; DB 9; Length 464;			
Best Local Similarity 98.6%; Pred. No. 1.2e-202;			
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;			
US-09-835-147-27			
QY	20	PINVSASTLYGVLDAGSSHTSLIYKWPAAKENDTGVVHVEECRVKPGISKFKVQKN	79
Db	32	PENVK-----YGVLDAGSSHTSLIYKWPAAKENDTGVVHVEECRVKPGISKFKVQKN	87
RESULT 12			
US-09-835-147-29			
; Sequence 29, Application US/09835147			
; Patent No. US2002000277A1			
; GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; CURRENT FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 29			
; TYPE: PRT			
; LENGTH: 473			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-29			
Query Match 94.3%; Score 2294; DB 9; Length 473;			
Best Local Similarity 98.6%; Pred. No. 1.3e-202;			
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;			
US-09-835-147-29			
QY	20	PINVSASTLYGVLDAGSSHTSLIYKWPAAKENDTGVVHVEECRVKPGISKFKVQKN	79
Db	41	PENVK-----YGVLDAGSSHTSLIYKWPAAKENDTGVVHVEECRVKPGISKFKVQKN	96
QY	80	EIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDDVVERSLNY	139
Db	97	EIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDDVVERSLNY	156

QY 140 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 199
|
|
|
Db 157 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 216
|
|
|
QY 200 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 259
|
|
|
Db 217 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 276
|
|
|
QY 260 DPCFHPGYKVVNVSDLYKTPCTKRPMTLPFQOFIQQIGNYQQCHQSILELFTNTSYCP 319
|
|
|
Db 277 DPCFHPGYKVVNVSDLYKTPCTKRPMTLPFQOFIQQIGNYQQCHQSILELFTNTSYCP 336
|
|
|
QY 320 YSCAFNGIPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 379
|
|
|
Db 337 YSCAFNGIPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 396
|
|
|
QY 380 SYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLNLT 439
|
|
|
Db 397 SYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLNLT 456
|
|
|
QY 440 NMIPAEQPLSTPLSHST 456
|
|
|
Db 457 NMIPAEQPLSTPLSHST 473
|
|
|

RESULT 13
US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 94.3%; Score 2294; DB 9; Length 474;
Best Local Similarity 98.8%; Pred. No. 1.3e-202;
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 20 PINVASLTGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKPVQKN 79
|
|
|
Db 42 PENVK---YGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKPVQKN 97
|
|
|
QY 80 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSLSN 139
|
|
|
Db 98 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSLSN 157
|
|
|
QY 140 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 199
|
|
|
Db 158 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 217
|
|
|

QY 200 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 259
|
|
|
Db 218 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 277
|
|
|
QY 260 DPCFHPGYKVVNVSDLYKTPCTKRPMTLPFQOFIQQIGNYQQCHQSILELFTNTSYCP 319
|
|
|
Db 278 DPCFHPGYKVVNVSDLYKTPCTKRPMTLPFQOFIQQIGNYQQCHQSILELFTNTSYCP 337
|
|
|
QY 320 YSCAFNGIPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 379
|
|
|
Db 338 YSCAFNGIPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT 397
|
|
|
QY 380 SYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLNLT 439
|
|
|
Db 398 SYAGVKEKLYSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLNLT 457
|
|
|
QY 440 NMIPAEQPLSTPLSHST 456
|
|
|
Db 458 NMIPAEQPLSTPLSHST 474
|
|
|

RESULT 14
US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match 94.3%; Score 2294; DB 9; Length 478;
Best Local Similarity 98.6%; Pred. No. 1.3e-202;
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 20 PINVASLTGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKPVQKN 79
|
|
|
Db 46 PENVK---YGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKPVQKN 101
|
|
|
QY 80 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSLSN 139
|
|
|
Db 102 EIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVERSLSN 161
|
|
|
QY 140 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 199
|
|
|
Db 162 PFDFOGARIITQEGAGYGTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAST 221
|
|
|
QY 200 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 259
|
|
|
Db 222 QVTFVPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALWQKLAKDIOVASNEILR 281
|
|
|

Qy

260

DPCFHPGKVVVNSDLKYTPCTKRFEMTLPPQOFIQTGIGNYQOCHOSILELFNTSYCP

319

Db

282

DPCFHPGKVVVNSDLKYTPCTKRFEMTLPPQOFIQTGIGNYQOCHOSILELFNTSYCP

341

Qy

320

YSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT

379

Db

342

YSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKT

401

Qy

380

SVAGVKEKYLSEYCFSGTYYLSLLQGYHFTADSWEHIFIGKIQSDAGWTLGYMLNLT

439

Db

402

SVAGVKEKYLSEYCFSGTYYLSLLQGYHFTADSWEHIFIGKIQSDAGWTLGYMLNLT

461

Qy

440

NMIPAEQPLSTPLSHST

456

Db

462

NMIPAEQPLSTPLSHST

478

Search completed: March 7, 2005, 14:12:43

Job time : 59.496 secs

RESULT 15

US-09-835-147-26

; Sequence 26, Application US/09835147

; Patent No. US2002002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 487

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39

US-09-835-147-26

Query Match

Best Local Similarity

Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

94.3%; Score 2294; DB 9; Length 487;

98.6%; Pred. No. 1.3e-202;

Qy

20

PINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRVKPGISKFVKQVN

79

Db

55

PENVK-----YGVLDAGSSHTSLYIKWPAEKENDTGTVHQBECRVKPGISKFVKQVN

110

Qy

80

BIGYILTCMERAREVTPRSQHOETPVYLGATAGMRLRMESSELDADRLDLDVVERSLSNY

139

Db

111

BIGYILTCMERAREVTPRSQHOETPVYLGATAGMRLRMESSELDADRLDLDVVERSLSNY

170

Qy

140

PFDFOGARIITQGEAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAST

199

Db

171

PFDFOGARIITQGEAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGAST

230

Qy

200

QVTFVPQNOTTIESPDNALQFRLYKGDYNYVTHSFLCYGKQDALWKLAKDQIVASNEILR

259

Db

231

QVTFVPQNOTTIESPDNALQFRLYKGDYNYVTHSFLCYGKQDALWKLAKDQIVASNEILR

290

Qy

260

DPCFHPGKVVVNSDLKYTPCTKRFEMTLPPQOFIQTGIGNYQOCHOSILELFNTSYCP

319

Db

291

DPCFHPGKVVVNSDLKYTPCTKRFEMTLPPQOFIQTGIGNYQOCHOSILELFNTSYCP

350

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2297	94.4	502	4	US-09-557-800C-55	Sequence 55, Appl
2	2297	94.4	502	4	US-09-370-622A-38	Sequence 38, Appl
3	2297	94.4	510	3	US-08-930-921-1	Sequence 1, Appl
4	2297	94.4	510	4	US-09-781-796C-1	Sequence 1, Appl
5	892.5	36.7	529	3	US-09-240-639-4	Sequence 4, Appl
6	892.5	36.7	529	4	US-09-908-510A-4	Sequence 4, Appl
7	892.5	36.7	529	4	US-09-905-744B-4	Sequence 4, Appl
8	892.5	36.7	529	4	US-10-107-660-4	Sequence 4, Appl
9	892.5	36.7	529	4	US-10-107-576-4	Sequence 4, Appl
10	892.5	36.7	529	4	US-09-905-732B-4	Sequence 4, Appl
11	892.5	36.7	529	4	US-09-923-304-4	Sequence 4, Appl
12	892.5	36.7	529	4	US-09-949-016-6049	Sequence 4, Appl
13	892.5	36.7	529	4	US-09-905-743B-4	Sequence 4, Appl
14	892.5	36.7	556	4	US-09-949-016-11328	Sequence 11328, A
15	854	35.1	479	4	US-09-949-016-11559	Sequence 11559, A
16	798	32.8	153	3	US-09-240-639-13	Sequence 13, Appl
17	798	32.8	153	4	US-09-908-510A-13	Sequence 13, Appl
18	798	32.8	153	4	US-09-905-744B-13	Sequence 13, Appl
19	798	32.8	153	4	US-10-107-660-13	Sequence 13, Appl
20	798	32.8	153	4	US-10-107-576-13	Sequence 13, Appl
21	798	32.8	153	4	US-09-905-732B-13	Sequence 13, Appl
22	798	32.8	153	4	US-09-905-743B-13	Sequence 13, Appl
23	796.5	32.8	282	4	US-09-949-016-7977	Sequence 7977, Ap
24	595	24.5	154	3	US-09-240-639-14	Sequence 14, Appl
25	595	24.5	154	4	US-09-908-510A-14	Sequence 14, Appl
26	595	24.5	154	4	US-09-905-744B-14	Sequence 14, Appl
27	595	24.5	154	4	US-10-107-660-14	Sequence 14, Appl

Db 152 VERSLSNYPDFQCARIIITQOEGAGYVITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
Qy 192 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 251
Db 212 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 271
Qy 252 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 311
Db 272 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 331
Qy 312 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 451
Qy 432 LGYMLNLTNMTIPABOPLSTPLSHST 456
Db 452 LGYMLNLTNMTIPABOPLSTPLSHST 476
RESULT 2
US-09-370-625A-38
; Sequence 38, Application US/09370625A
; Patent No. 660032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-38
Query Match 94.4%; Score 2297; DB 4; Length 502;
Best Local Similarity 97.1%; Pred. No. 7.2e-238;
Matches 432; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
Qy 12 GIFLSMXPINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGTVHGVVEECRVKGP 71
Db 36 GLTONKALPENVK---YGVLDAGSSHTSLYIKWPAEKENDTGTVHGVVEECRVKGP 91
Qy 72 SKFVQKNEIGIYLTDCMERAREVIPSQOETPVYLGATAGMRLRMESEELADRLDV 131
Db 92 SKFVQKNEIGIYLTDCMERAREVIPSQOETPVYLGATAGMRLRMESEELADRLDV 151
Qy 132 VERSLSNYPDFQCARIIITQOEGAGYVITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDFQCARIIITQOEGAGYVITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
Qy 192 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 251
Db 212 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 271
Qy 252 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 311
Db 272 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 331
Qy 312 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 451
Qy 432 LGYMLNLTNMTIPABOPLSTPLSHST 456
Db 452 LGYMLNLTNMTIPABOPLSTPLSHST 476

Qy 312 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 451
Qy 432 LGYMLNLTNMTIPABOPLSTPLSHST 456
Db 452 LGYMLNLTNMTIPABOPLSTPLSHST 476
RESULT 3
US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; CURRENT FILING DATE: 1998-01-02
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-08-930-921-1
Query Match 94.4%; Score 2297; DB 3; Length 510;
Best Local Similarity 97.1%; Pred. No. 7.4e-238;
Matches 432; Conservative 7; Mismatches 7; Indels 4; Gaps 1;
Qy 12 GIFLSMXPINVSASTLYGIVLDAGSSHTSLYIKWPAEKENDTGTVHGVVEECRVKGP 71
Db 36 GLTONKALPENVK---YGVLDAGSSHTSLYIKWPAEKENDTGTVHGVVEECRVKGP 91
Qy 72 SKFVQKNEIGIYLTDCMERAREVIPSQOETPVYLGATAGMRLRMESEELADRLDV 131
Db 92 SKFVQKNEIGIYLTDCMERAREVIPSQOETPVYLGATAGMRLRMESEELADRLDV 151
Qy 132 VERSLSNYPDFQCARIIITQOEGAGYVITINLLGKFSQKTRWFSIVPYETNNQETFGA 191
Db 152 VERSLSNYPDFQCARIIITQOEGAGYVITINLLGKFSQKTRWFSIVPYETNNQETFGA 211
Qy 192 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 251
Db 212 LDLGASTQVTFVPOQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQALWOKLAKDIO 271
Qy 252 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 311
Db 272 VASNEILLRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILE 331
Qy 312 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 371
Db 332 LFNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMMKKFCA 391
Qy 372 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 431
Db 392 QPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWT 451
Qy 432 LGYMLNLTNMTIPABOPLSTPLSHST 456
Db 452 LGYMLNLTNMTIPABOPLSTPLSHST 476

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:

	Query Match	36.7%	Score 892.5	DB 3	Length 529
	Best Local Similarity	41.7%	Pred. No. 9.5e-87		
	Matches 177	Conservative	76	Mismatches 164	Indels 7
	Gaps				
Qy	29	YGIVLDAGSHTSLYIKWPAEKENDTGVVHQVVEECRVKGGIGSKFVKQVNEIGIYITDC	88		
Db	57	YGIVLDAGSRTTYYVQWPAEKENTGVVQIFKCSKGSIGSIYGNNDQVPAEEC	116		
Qy	89	MEAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARI	148		
Db	117	MQVKGVQPSHLGSGTPIHLGATAGMRLLRLQNETAANEVLIESIQSYFKSQPPDFRGAQI	176		
Qy	149	ITQSGEGAGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDLGCASTQVTFVFPNQ	208		
Db	177	ISQSGEGVGIWTANYILMGNLFLEKNLWHMWV--HPHGVEITGALDLGCASTQISFVAGEK	234		
Qy	209	TIISPONALQFRLYGKDYNVYTHSFICYGKQDQALWQKLAKDIQVA-SNEILRDCPFHPGY	267		

```

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

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[illegible]

QY 385 KEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGKIQSDAGWTGLGYMLNTNMIPA 444
Db 414 DEVARSYCFGSANYIYHLFVNGYKFTETWQIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473
QY 445 EQPL 448
Db 474 ESPL 477

RESULT 9

US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4

Query Match 36.7%; Score 892.5; DB 4; Length 529;
Best Local Similarity 41.7%; Pred. No. 9.5e-87;
Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

QY 29 YGIVLDAGSSHTSLYIKWPAEKENDTGWVHVVEECRVKPGISGKFKVQKVNIEIGYLTDC 88
Db 57 YGIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKCSVKSGISGYGNPDVPRAFEEC 116
QY 89 MERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVERSLNSYPPDFOGARI 148
Db 117 MQVKGVQPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKSQPPDFRGAQI 176
QY 149 ITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGASTQVTFVPOQ 208
Db 177 ISGQEGVYGVITANYLNGNLEKNLWMMV--HPHGVETTTGALDLGASTQISFVAGEK 234
QY 209 TIESPDNALQRLYKGVNVTHTSFLCYGKQDQALWQKLADIOVA-SNEILRDCPFHPGY 267
Db 235 MDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLLQNSPTKQHLTNPCYPRDY 294
QY 268 KKVNVSDLYKTPCT--KRFEWTLPPQOFETQIGIGNYQQCHQSILELFTNTSYC-PYSQCA 324
Db 295 SISTMGHVFDSLCTVDORPESYNPDVITFEGTDPGLCKEKVASIFDFKACHDQETCS 354
QY 325 FNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQWPBEEIKTSYAGV 384
Db 355 FDGVYQPKIGPFAFAGFYTTASALNL-SGSFSLDTFNSSTWNFCSQNSQLPILLPKP 413
QY 385 KEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGKIQSDAGWTGLGYMLNTNMIPA 444
Db 414 DEVARSYCFGSANYIYHLFVNGYKFTETWQIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473
QY 445 EQPL 448
Db 474 ESPL 477

RESULT 10

US-09-905-732B-4
; Sequence 4, Application US/09905732B
; Patent No. 6787328

; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-732B-4

Query Match 36.7%; Score 892.5; DB 4; Length 529;
Best Local Similarity 41.7%; Pred. No. 9.5e-87;
Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

QY 29 YGIVLDAGSSHTSLYIKWPAEKENDTGWVHVVEECRVKPGISGKFKVQKVNIEIGYLTDC 88
Db 57 YGIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKCSVKSGISGYGNPDVPRAFEEC 116
QY 89 MERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVERSLNSYPPDFOGARI 148
Db 117 MQVKGVQPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKSQPPDFRGAQI 176
QY 149 ITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGASTQVTFVPOQ 208
Db 177 ISGQEGVYGVITANYLNGNLEKNLWMMV--HPHGVETTTGALDLGASTQISFVAGEK 234
QY 209 TIESPDNALQRLYKGVNVTHTSFLCYGKQDQALWQKLADIOVA-SNEILRDCPFHPGY 267
Db 235 MDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKFLAMLLQNSPTKQHLTNPCYPRDY 294
QY 268 KKVNVSDLYKTPCT--KRFEWTLPPQOFETQIGIGNYQQCHQSILELFTNTSYC-PYSQCA 324
Db 295 SISTMGHVFDSLCTVDORPESYNPDVITFEGTDPGLCKEKVASIFDFKACHDQETCS 354
QY 325 FNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQWPBEEIKTSYAGV 384
Db 355 FDGVYQPKIGPFAFAGFYTTASALNL-SGSFSLDTFNSSTWNFCSQNSQLPILLPKP 413
QY 385 KEKYLSEYCFSGTYILSLLOQYHFTADSWHEHIFGKIQSDAGWTGLGYMLNTNMIPA 444
Db 414 DEVARSYCFGSANYIYHLFVNGYKFTETWQIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473
QY 445 EQPL 448
Db 474 ESPL 477

RESULT 11

US-09-923-304-4
; Sequence 4, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:

; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UFGC:658US
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-4

Query Match 36.7%; Score 892.5; DB 4; Length 529;
 Best Local Similarity 41.7%; Pred. No. 9.5e-87;
 Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

QY 29 YGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGIGSKFVKQKNEIGIYLTDC 88
 DB 57 YGIVLDAGSSRTTYYVQWPAEKENNTGVVSTFKCSVKSGSISSYGNPNQDVPVRAPEEC 116

QY 89 MERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLNYPDFOGARI 148
 DB 117 MQVKGVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKSQPFDPRGAQI 176

QY 149 ITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVPOQ 208
 DB 177 ISGQEGVYGWITANYLMGNFLEKLMHMYV--HPHGVETTGALDGLGASTQISFVAGEK 234

QY 209 TIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIOVA-SNEILRDPCHPGY 267
 DB 235 MDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKFLAMLLQNSPTKNHLTNPCYPRDY 294

QY 268 KKVNVSDLYKTPCT--KRFEWTLFPQOFEIQGIGNYQOCHQSILELFTSYC-PYSQCA 324
 DB 295 SISFTMGHVFDSLCTVDQRPESYNPNVDITTEGTGDPSLCKEKVASIFDFKACHDQETCS 354

QY 325 FNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGV 384
 DB 355 FDGVYQPKIGFPVAFAGFYTTASALNL-SGSFSLDTFNSSWTWFCSONWSQLPLLPKF 413

QY 385 KEKYLSEYCFSGTYILSLLLQYHFTADSWEHIFIGIKQSDAGWTLYMLNLTNMPA 444
 DB 414 DEVYARSYCFSSANYIYHLFVNGYKFTETWPIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473

QY 445 EOPL 448
 DB 474 ESPL 477

RESULT 12
 US-09-949-016-6049
 ; Sequence 6049, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6049
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6049

Query Match 36.7%; Score 892.5; DB 4; Length 529;
 Best Local Similarity 41.7%; Pred. No. 9.5e-87;
 Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

QY 29 YGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGIGSKFVKQKNEIGIYLTDC 88
 DB 57 YGIVLDAGSSRTTYYVQWPAEKENNTGVVSTFKCSVKSGSISSYGNPNQDVPVRAPEEC 116

QY 89 MERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLNYPDFOGARI 148
 DB 117 MQVKGVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKSQPFDPRGAQI 176

QY 149 ITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVPOQ 208
 DB 177 ISGQEGVYGWITANYLMGNFLEKLMHMYV--HPHGVETTGALDGLGASTQISFVAGEK 234

QY 209 TIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIOVA-SNEILRDPCHPGY 267
 DB 235 MDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKFLAMLLQNSPTKNHLTNPCYPRDY 294

QY 268 KKVNVSDLYKTPCT--KRFEWTLFPQOFEIQGIGNYQOCHQSILELFTSYC-PYSQCA 324
 DB 295 SISFTMGHVFDSLCTVDQRPESYNPNVDITTEGTGDPSLCKEKVASIFDFKACHDQETCS 354

QY 325 FNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGV 384
 DB 355 FDGVYQPKIGFPVAFAGFYTTASALNL-SGSFSLDTFNSSWTWFCSONWSQLPLLPKF 413

QY 385 KEKYLSEYCFSGTYILSLLLQYHFTADSWEHIFIGIKQSDAGWTLYMLNLTNMPA 444
 DB 414 DEVYARSYCFSSANYIYHLFVNGYKFTETWPIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473

QY 445 EOPL 448
 DB 474 ESPL 477

RESULT 13
 US-09-905-743B-4
 ; Sequence 4, Application US/09905743B
 ; Patent No. 6828423
 ; GENERAL INFORMATION:
 ; APPLICANT: Chadwick, Brian Paul
 ; APPLICANT: Frischauf, Anna Maria
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
 ; TITLE OF INVENTION: ACIDS
 ; FILE REFERENCE: 28110/36120C
 ; CURRENT APPLICATION NUMBER: US/09/905,743B
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: 09/240,639
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-905-743B-4

Query Match 36.7%; Score 892.5; DB 4; Length 529;
 Best Local Similarity 41.7%; Pred. No. 9.5e-87;
 Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

QY 29 YGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGIGSKFVKQKNEIGIYLTDC 88
 DB 57 YGIVLDAGSSRTTYYVQWPAEKENNTGVVSTFKCSVKSGSISSYGNPNQDVPVRAPEEC 116

QY 89 MERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLNYPDFOGARI 148
 DB 117 MQVKGVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKSQPFDPRGAQI 176

QY 149 ITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVPOQ 208
 DB 177 ISGQEGVYGWITANYLMGNFLEKLMHMYV--HPHGVETTGALDGLGASTQISFVAGEK 234

QY 209 TIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIOVA-SNEILRDPCHPGY 267
 DB 235 MDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKFLAMLLQNSPTKNHLTNPCYPRDY 294

QY 268 KKVNVSDLYKTPCT--KRFEWTLFPQOFEIQGIGNYQOCHQSILELFTSYC-PYSQCA 324
 DB 295 SISFTMGHVFDSLCTVDQRPESYNPNVDITTEGTGDPSLCKEKVASIFDFKACHDQETCS 354

QY 325 FNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEIKTSYAGV 384

```
Db 355 FDGYQPKIGPFAVAFYTTASALNL-SGSFSLDTFNSSTWNCQNSQLPILLPKF 413
Qy 385 KEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNLTNMPA 444
Db 414 DEVYARSCFSANIYIHLFVNGYKFTETWQIHFEKEVGNSSIAWSLGYMLSLTNQIPA 473
Qy 445 EOPL 448
Db 474 ESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 36.7%; Score 892.5; DB 4; Length 556;
Best Local Similarity 41.7%; Pred. No. 1e-86;
Matches 177; Conservative 76; Mismatches 164; Indels 7; Gaps 5;

Qy 29 YGIVLDAGSSHTSLYIYKPAEKENDTGVVHQVBECKVKGFGISKFKVQKNEIGIYLTDC 88
Db 84 YGIVLDAGSSRTTVVYQWPAEKENNTGWSQTFKCSYKSGISYGNPNQDVPRAFECC 143
Qy 89 MERAREVIPSQHOETPVYLGATAGMRLRMESSELADRLVDVVERSLNYPDFPQGARI 148
Db 144 MQKVGQVPSHLGSPHILGATAGMRLRLQNETAANEVLESIQSYFKSQPFDFRGAQI 203
Qy 149 ITGQEGAYGWITINYLKGSQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVPOQ 208
Db 204 ISGQEGVYGVITANYLGNFLEKNLHMV--HPHGVETTTGALDGLGASTQISFVAGEK 261
Qy 209 TIESPDNALQRLYKGDYVNYTHSFLCYGKQALWQKADIQVA-SNEILRDPCHFGY 267
Db 262 MDLNTSDIMQVSLGYVYVTLTHSFQCYGRNEAEKFLAMLLQNSPTKNHLTNPCYPRD 321
Qy 268 KKVNVSDLYKTPTCT--KRFEWTLPPQOFELQIGNTYQOCHQSILELNTSYC-PYSQCA 324
Db 322 SISTMGHVFSLCTVDORPESYNPNVDVITEGTDPSLCKEKVASIFDFKACHDQETCS 381
Qy 325 FNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPMEEIKTSYAGV 384
Db 382 FDGYQPKIGPFAVAFYTTASALNL-SGSFSLDTFNSSTWNCQNSQLPILLPKF 440
Qy 385 KEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGKIQGSDAGWTGLGYMLNLTNMPA 444
Db 441 DEVYARSCFSANIYIHLFVNGYKFTETWQIHFEKEVGNSSIAWSLGYMLSLTNQIPA 500
Qy 445 EOPL 448
Db 501 ESPL 504
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```
RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 35.1%; Score 854; DB 4; Length 479;
Best Local Similarity 41.7%; Pred. No. 1.1e-82;
Matches 180; Conservative 66; Mismatches 132; Indels 54; Gaps 9;

Qy 29 YGIVLDAGSSHTSLYIYKPAEKENDTGVVHQVBECKVKGFGISKFKVQKNEIGIYLTDC 88
Db 47 YGIVLDAGSSHTSMFIYKWPADKENDTGIVQGHSSCDVPGGGISSYADNPDSGASQSLVGC 106
Qy 89 MERAREVIPSQHOETPVYLGATAGMRLRMESSELADRLVDVVERSLNYPDFPQGARI 148
Db 107 LEQALQDVPKEXHAGTFLYLGATAGMRLNLNTPASTSVLMAYVTHLTQYPPDFRGAIR 166
Qy 149 ITGQEGAYGWITINYLIG--KFSQKTRWFSIVPYETNNQETFGALDGLGASTQVTFVP 205
Db 167 LSGQEGVGVWNTANYLLENFIKYGVWGRW-----RPRKGTLCAMDGLGASTQITP-- 218
Qy 206 QNQTIESPDNA--LQFLRYGKDYVNYTHSFLCYGKQALWQKADIQVASNEILRDPCE 263
Db 219 -ETTSPEADRASEVQLHLHYGQHYRVYTHSFLCYGRDQVQLRLASALQTHGFH---PCW 273
Qy 264 HPGYKVVNVSDLYKTPTCTKRFEMTLPPQOF-----EQIGINYQOCHQSILELNTSY 317
Db 274 PRGFSTQVLLGDVYQSPT----MAQRPNFNSSARVSLSGSDPHLCRDLVSLGFSFSS 329
Qy 318 CPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFL--NLTSEKVSQEKVTEMKKFCAQPMEE 375
Db 330 CPFSRCFNGVQFPVAGNFVAFSAFFYVDVFLTSMGLPVATLQQLQLEAAAVNVCNQTA 389
Qy 376 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGKIQGSDAGWTGLGYM 435
Db 390 Q-----QJLSRGYGFDERAFGCVIFQKKAADTAVGMLGYM 425
Qy 436 LNLTNMIPASQP 447
Db 426 LNLTNLIPADPP 437

Search completed: March 7, 2005, 13:27:56
Job time : 20.4328 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 13.5783 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: us-09-835-147a-27_copy_25_464
Perfect score: 2352
Sequence: 1 ATONKALPENVKYGVLDAG.....NLTNMPAEQPLSTPLSHST 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	99.8	510	2	I56242
2	505	21.5	483	2	D86276
3	469.5	20.0	405	2	E86276
4	453	19.3	630	2	S50463
5	416	17.7	572	2	T40856
6	406.5	17.3	516	2	G84442
7	402.5	17.1	485	2	T34147
8	394.5	16.8	508	2	C86276
9	383.5	16.3	557	2	T16696
10	381.5	16.2	556	2	T39109
11	374	15.9	455	2	S48859
12	334	14.2	454	2	JC4616
13	332	14.1	1052	2	T04339
14	328.5	14.0	479	2	T23508
15	320.5	13.6	518	2	A40732
16	167	7.1	628	2	A55421
17	103	4.4	369	2	S77299
18	101.5	4.3	716	2	T21516
19	100	4.3	307	2	T27332
20	99	4.2	1951	2	B43963
21	98.5	4.2	590	2	A81411
22	98.5	4.2	797	2	D86247
23	98.5	4.2	989	2	B84532
24	98.5	4.2	1509	2	B99985
25	98	4.2	371	2	T05213
26	98	4.2	665	2	T18979
27	98	4.2	3848	2	T17414
28	97.5	4.1	392	2	A36738
29	97.5	4.1	461	2	G91228

30 97.5 4.1 461 2 F86075 probable permease
31 97 4.1 494 2 T03774 probable histidine
32 96 4.1 883 2 B85725 probable fimbrial
33 96 4.1 1028 2 I51173 myosin I beta - bu
34 96 4.1 1415 2 A72369 (R)-2-hydroxygluta
35 95.5 4.1 468 2 H65192 hypothetical 51.7
36 95.5 4.1 591 2 F89770 hypothetical prote
37 95.5 4.1 1900 2 AG2391 serine/threonine k
38 95 4.0 288 1 B48583 Mg2+ transporth h
39 95 4.0 451 2 G69859 Mgt+ transporth h
40 95 4.0 564 2 S15962 hypothetical prote
41 95 4.0 927 2 T43110 lactacin 481/lacto
42 93 4.0 466 2 JC6525 processing peptida
43 92.5 3.9 404 2 T21251 hypothetical prote
44 92.5 3.9 556 2 A90715 probable dnaK prot
45 92.5 3.9 556 2 H64799 probable dnaK-type

ALIGNMENTS

RESULT 1
I56242
lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56242
R:Maliszewski, C.R.; DeLessepe, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;
J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A:Reference number: I56242; MUID:95015846; PMID:7930580
A:Accession: I56242
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: UNIPROT:P49961; GB:S73813; MID:g765255; PIDN:AAB32152.1; PID:g765255
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 99.8%; Score 2348; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.2e-183;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFYQK	61
Db	38	TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFYQK	97
Qy	62	VNEIGIYLTDCMERAREVIRSRQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL	121
Db	98	VNEIGIYLTDCMERAREVIRSRQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL	157
Qy	122	NYPPDFQGARITIQEESGAYGWIITVLLGKFSQKTRWFSIVPVETNNQETFGALDLGGA	181
Db	158	NYPPDFQGARITIQEESGAYGWIITVLLGKFSQKTRWFSIVPVETNNQETFGALDLGGA	217
Qy	182	STQVTFVFPQNTIESPDNALQFLRYLGDYNNYTHSFICYGKQDALQWKLAKDIQVASNEI	241
Db	218	STQVTFVFPQNTIESPDNALQFLRYLGDYNNYTHSFICYGKQDALQWKLAKDIQVASNEI	277
Qy	242	LRDPCFHPGKVVNVSDLYKTPCTKRFEMTLPQQOEIQQIGNYQQCHQSILELFTSY	301
Db	278	LRDPCFHPGKVVNVSDLYKTPCTKRFEMTLPQQOEIQQIGNYQQCHQSILELFTSY	337
Qy	302	CPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKYTEMMKFKCAQPWEEI	361
Db	338	CPYSQCAFNGIFLPLQDGFAGFAFYVMKFLNLTSEKVSQEKYTEMMKFKCAQPWEEI	397
Qy	362	KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIKIQGSDAGWTLYMLN	421
Db	398	KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIKIQGSDAGWTLYMLN	457
Qy	422	LTNMPAEQPLSTPLSHST	440
Db	458	LTNMPAEQPLSTPLSHST	476

anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 20.0%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 2.4e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

QY 53 PGISKFQVKVNEIGVLTDCMERAREVPRSOHOETPVYLGATAGMRLRMESEELADRV 112
DB 29 PGLSSYADNPEGASVSVTKLVEFAKRIIPGKLKSDIRLMATAGWRLLDVVPQE---QI 85
QY 113 LDVVERSLSNYPDFQ3---ARIITGOEGAYGMITINYLKGFPSQKTRWFSIVPYETNQ 170
DB 86 LDVTRVRLRSSGFKQDEWATVISGTDEGIYAWVANHALGSLG-----GDPL 133
QY 171 ETGALDLGGASTVTFVQNTIESPDNALQPLRYGK-DYNNVYTHSFILCYGKDOA---L 226
DB 134 KTTGIVELGASQVTFVPSEHV---PPFSRTISYGNVSYIYSHFLDFGQDAEDKL 190
QY 227 WOKLAKDIOVASNE-ILRDPCHPGYKVVNVSDDLKTPCTK-----RFEWTLPF 275
DB 191 LESLQNSVAASTGDGIVEDCTPKGY-----IYDTHSQDSSGFLSESKFASL-- 240
QY 276 QQFEIQIGNYQOCHOSILELP--NTSYCPYSOCANGLFPLPLOGDFGAFSAFYVMKF 333
DB 241 ---QVQAAGDFTKRSATLAMLQEGKENCAYKHCISGSTTTPNIQGSFLATENFHTSKF 297
QY 334 LNTSEKVSQEKVTEWM---KFCAPQWBEIKTSYAGVKEKYLSEYCFSGTILSLLLQG 390
DB 298 FGL-GEK---EWSEMLAKRGFCGEWSKLKKEYPPTKDKYLHRYCFSSAYIISMLHDS 353
QY 391 YHFTADSWEIHFIKTI--QGS DAGWTLG-YMLN 421
DB 354 LGVALDD-ERIKYASKAGKENIPLDMALGAFILN 386

RESULT 4
S50463
hypothetical protein YER005w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dieterich, F.S.
A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005
C:Genetics:
A:Gene: SGD:YND1; MIPS:YER005w
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.3%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 20.0%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 2.4e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

QY 53 PGISKFQVKVNEIGVLTDCMERAREVPRSOHOETPVYLGATAGMRLRMESEELADRV 112
DB 29 PGLSSYADNPEGASVSVTKLVEFAKRIIPGKLKSDIRLMATAGWRLLDVVPQE---QI 85
QY 113 LDVVERSLSNYPDFQ3---ARIITGOEGAYGMITINYLKGFPSQKTRWFSIVPYETNQ 170
DB 86 LDVTRVRLRSSGFKQDEWATVISGTDEGIYAWVANHALGSLG-----GDPL 133
QY 171 ETGALDLGGASTVTFVQNTIESPDNALQPLRYGK-DYNNVYTHSFILCYGKDOA---L 226
DB 134 KTTGIVELGASQVTFVPSEHV---PPFSRTISYGNVSYIYSHFLDFGQDAEDKL 190
QY 227 WOKLAKDIOVASNE-ILRDPCHPGYKVVNVSDDLKTPCTK-----RFEWTLPF 275
DB 191 LESLQNSVAASTGDGIVEDCTPKGY-----IYDTHSQDSSGFLSESKFASL-- 240
QY 276 QQFEIQIGNYQOCHOSILELP--NTSYCPYSOCANGLFPLPLOGDFGAFSAFYVMKF 333
DB 241 ---QVQAAGDFTKRSATLAMLQEGKENCAYKHCISGSTTTPNIQGSFLATENFHTSKF 297
QY 334 LNTSEKVSQEKVTEWM---KFCAPQWBEIKTSYAGVKEKYLSEYCFSGTILSLLLQG 390
DB 298 FGL-GEK---EWSEMLAKRGFCGEWSKLKKEYPPTKDKYLHRYCFSSAYIISMLHDS 353
QY 391 YHFTADSWEIHFIKTI--QGS DAGWTLG-YMLN 421
DB 354 LGVALDD-ERIKYASKAGKENIPLDMALGAFILN 386

RESULT 4
S50463
hypothetical protein YER005w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dieterich, F.S.
A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005
C:Genetics:
A:Gene: SGD:YND1; MIPS:YER005w
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.3%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

Qy	10	NVRGIVLDAGSSHTSLYIKWP-----ARKENDTV-----VHQVECRVK-GPGI 55
Db	7	NDREGIVLDAGSSGSRIRHFWQDFTESLLHATNQDSQILOSPVRIHOEKDWTFLNPGCL 66
Qy	56	SKFVQKXNE-IGIYLTDCMERAREVIPSQHQETPVVLGATAGMRLLRWESBELADRLVD 114
Db	67	SSFEEKKPDQAYKSHIKPLDPAKNIIPESHWSGCVFQIATAGMRL-----PDQIOSSIID 123
Qy	115	VVERSLGNYPPDF-----QGARIITGOEBGAYGMITINYLLGKFSQKTRMFSIVPYETN 168
Db	124	GLCQGL-KHPAEFLVEDCSAQIQVIDGETEGLYGLNLNYLGHENDYNP-----EVS 175
Qy	169	NOETFGALDLCGASTOVTTFVQNQ-----TIESPDNALQFLRYCKDYNNVTH 215
Db	176	DHFTFGFMDMGASTQIAFAPHDGSEIARHRDDIATIFLRSVNGDLQ-----KWDVFS 229
Qy	216	SFLCVGQDQALWQKLAKDIOVA-----SNEILRDPCHFPGYKVVNVSDLYKT 263
Db	230	TWLGFGANQARRVYLQALINTLPENTNDYENDDFSTRNLNDPCMPRG-----SSTDPE 281
Qy	264	PCTKRFEMLPQFOFEI OGIGNYQOCHOSILE-LFNTSYCPYSQCAFNGIFLPPLOQGP- 321
Db	282	----EFKDTI----FHAGSGNYEOCTKSIYPLLLKNMPCDDPECLFNGVHAPRI--DFA 331
Qy	322	----GAPSAFYVMKPLNLTSKVSQSKVTETMMKKFCAQWEEI-----KTSYAGVKEK 371
Db	332	NDKFIGTSEYWTANDVFKLGE-YNPKFSKSLREFCNSWNTQILANSKDKVYNSIPEEN 390
Qy	372	YLSBYCPSGTYILSLLLQY---HFTADSWEHIIH-----FIGIKQSGDAGWTLGYML 420
Db	391	FLKDACPKGNVNLNTHGFDWPRIDVA-ENVNDRPLFOSVEKVEEBELSTGLRIL 447

RESIN, T 5

RESOUR 5
 T40856
 probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40856
 R:Ramsberger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: 221952
 A:Accession: T40856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-572 <RAM>
 A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN000068; SPDB:
 A:Experimental source: strain 972n-; cosmid c11E10
 C:Genetics:
 A:Gene: SPDB:SPCC11E10.05c
 A:Map position: 3

	Query Match	17.7%;	Score 416;	DB 2;	Length 572;
	Best Local Similarity	27.3%;	Pred. No. 9e-26;		
	Matches 131;	Conservative 69;	Mismatches 156;	Indels 124;	Gaps 19
Qy	12 KYGIIVLDAGSHTSIYIYKVAEKEN-----DTGVVHVQEERCKVGPGISKRV	59	: : : : :		
Db	4 KYGIFADSGSSGRLLIYSWDYDTSLSLSDKKVKKLPLIETGIGDGKKWSLKVPQGISSEA	63	: : : : :		
Qy	60 QKVNEIG-IYITDCMERAREVIPRSQHQTTPVYLGCATAGMRLLRMESELADRVLDDVER	118	: : : : :		
Db	64 NNPXHGKKHLKELDFAAHAIPKDVBKETPVFLSATAGMRLLLGYDAQ---NKILSHACR	120	: : : : :		
Qy	119 SL-SNYPPDF---QGARIITGOEGAGCWITINYLKGFSOKTRWFISIVPYETNNQETF	173	: : : : :		
Db	121 YIKKNYPDIPNCNSIRVIDGKAEGMWGLATNYLLKTLEBK-----DTSTV	168	: : : : :		
Qy	174 GALDLGGASTQVTP-VPONQITESPD-----NALQFLRYKDNVYTHSFCLCYCK	222	: : : : :		
Db	169 GFIDMGGSASVGIAPFELPPSQLKNYKXSISTVHIGIQNGOQL-----EKPLFTVTWLGFA	223	: : : : :		
Qy	223 DQALLQWKLAQIOVASNEI---LRDPCEPHPGYKVVNVSDLYTKTCTKRFEMLTFPQQPE	279	: : : : :		

224	NEAYRYLGLLIESKGVNLTSDPCSLRG-----RTYDIDGIE	263
280	IQIGINYQQCHQSILELPNTSY-CPYSCAFNGIFLPLOQDGFASAFYFMKFLNLT	338
264	FAGTGDILKQCLKLTLYNLINKDKPCMPDNFDGISIPPV--DF-ANTEFVGVSFEWYTTN	320
339	EKVSQ-----EKVTENMKKFCQAPWEEI-----KTSYAGVKEKYLSFYCFSGTY	382
321	DVFDMGGSYHPPNPFYKKVDE---YCGTEWETMLSRLYNKELTPTSDENKLEKLCFKASW	376
383	ILSLLLQG-----YHPTADSWEIHTFCTKIOGSDAGWTGLGYML	420
377	ALANYLHGFDVPKNTSSDAKGLSVIPAYHSPFTSLE-----KIERTFVSWTGLQVL	430

RESULT 6

RESULT 6
G84442
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84442
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <SPT>
A;Cross-references: UNIPROT:O80612; GB:AEO02093, NID:G3461821; PIDN:AAC32915.1; GSPDB:G
C;Genetics:
A;Gene: ACG202970
A;Map position: 2
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	17.3%	Score	406.5	DB 2	Length	516			
Best Local Similarity	27.5%	Pred. No.	4.6e-25						
Matches	117	Conservative	68	Mismatches	187	Indels	53	Gaps	13
Qy	10	NVKGVILDAGSSHTSLYIKWPAEKENDTGVHVQVECRVK-GPGISKFKVQKNEIGY	68						
Db	65	SLRYSVVIDGGSTGTRIHVFGYRIESGKPVFEFRGANYASLKLHPLGSADFADDDPGASVS	124						
Qy	69	LTDQWERAREVIPSQHOETPVYLGATAGMRLLRWSEELADRLVDVVERSL--SNYPFD	126						
Db	125	LTELVEFAKRPVPGKMIEFVRLMATAGMRLLELPQVE---KILGVARRVLSKSGFLFR	181						
Qy	127	FOGARIITGOEBGAYGITINYLKGFQSQTRWFSIVPYETNNQBTFGALDIGGASTQVT	186						
Db	182	DEWASVSGSDEGVYAMVANFALGSLG-----GDPLKTTGIVELGGASAQVT	229						
Qy	187	FVPQNTIESPDNALQPRLYGKDVNNYTHSPCLYCKDOA----LW-QKLAKD-----IQVAS	238						
Db	230	FVSSEPM--PPEFRTISFGNVTVNLYSHSPHFQONAAHDKLMSGLLSRDHNSAVEPTR	287						
Qy	239	NEILLRDCPFHPGKKVNVSDLYKTPCTKREMTLPQOQFEIQGIGNYQQCHQSILELFN	298						
Db	288	EKIPTDPCAPKGYNLNDANTQKLSGLLAEERSLSDSP-----QAGNYSQCRSAALTIIQ	342						
Qy	299	TSYCPYSQCAFNGIYFLPPLQDGFAGFAFYVMKFLNLTSEKVSOEKYTEMMKFKCAOPW	358						
Db	343	DG-----NGRILIIAG----FSLFPLGL-----GEKAWLSNMISAGERFCGEDW	383						
Qy	359	EIKTSYAGVKKEYLSYCFSGVTYLSLLQGYHFTADSWHHIFGIKQSSDAGWTGLY	418						
Db	384	SKLRVKPDSLHEEDLLRYCFSSAVIVSLLDHTGLPI added -BRIGYANQAGDIPLDWALCA	442						
Qy	419	MLNLT	423						
Db	443	FIQOT	447						

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: C86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:G5080800; PIDN:AAD39310.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated

A;Accession: T34147
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-485 <BRA>
A;Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C33H5.14
A;Introns: 22/1; 83/1; 120/2; 167/3; 269/3; 399/3
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.8%; Score 394.5; DB 2; Length 508;
Best Local Similarity 28.2%; Pred. No. 4.3e-24;
Matches 123; Conservative 71; Mismatches 171; Indels 71; Gaps 20;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISKFVQKVEIGYIY 68
DB 63 SLHYSVIIDGSSGTRVHVGVRIESGKPVDFGGEENYASLKLSPGLSAYADNPEGVSES 122
QY 69 LTDCMERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQ 128
DB 123 VTELVEFAKRVHKGKLSKSDIRLMATAGRLLELPVQE-QILDVTRVLESSGDFP- 178
QY 129 GARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNN-QETFGALDGLG-----GA 181
DB 179 -----RDWASVISILENFQDLMKVYMLGILLMRSV 211
QY 182 STQVTFVQNTTESDNALQFLYK-DYVNTHTSFLCYGKQALWQKLAKDI-QVASN 239
DB 212 RLEVTFV---STELVPSFSTRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
QY 240 E-----ILRDCPCHPGYKVVNV-SDLYKTPCTK-RFEMTLFQOFEIQIGNYQOCHSI 293
DB 268 STQGIIVPDCIPKGVILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
QY 294 LELF--NTSYCPYSQCAFNGIFLPPQDGFASAFVFMKFLNLTSEKVSQEKVTEMM- 350
DB 321 FAMLQEBKGTCKYKRSIGSIFTPNQQSGSLATENFHTSKFFGL-GEK---EWLSEML 376
QY 351 --KKFCAQPEEIKTSYAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIGKIQ 408
DB 377 AGREFCGEESKLVKVKYPTFDENLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
QY 409 GSD--AGWTILG-YMLN 421
DB 436 EEDPLDVALGAFILN 451

Query Match 17.1%; Score 402.5; DB 2; Length 485;
Best Local Similarity 26.7%; Pred. No. 8.9e-25;
Matches 116; Conservative 69; Mismatches 187; Indels 63; Gaps 15;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGV---VHVEECRVK-GPGISKFVQKVEI 65
DB 22 NIKYGVICDAGSSGTRFVYTLKPLSGGLTIDTLIHESPEVWVKVTPGLSSFGDKPEQV 81
QY 66 GYLTDCHERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPF 125
DB 82 VEYLPFLRFABEHIPIYQOLGETDLIFATAGMRLLEPAQDAIKNLQNLKSVTALRV 141
QY 126 DFOGARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLGASTQV 185
DB 142 SDSNRIIDGAWEGIYIAVNYILGRFDKE-----NDKVGIMDMGASVQI 189
QY 186 TFPVQNTIESPD--NALQFLYKGD-----YNYVTHSFLCYGKQALWQKLAKDIOVA 237
DB 190 APEIANEK-ESYNGGVNVEINLSTETNEDYKIYITFLGYGANEGL-KKYENSLVYS 247
QY 238 SNEILLRDCPCHPGYKVVNVSDLYKTPCTKRFEMTLFQOFEIQIGNYQOCHOSILFL 297
DB 248 GNS--NDSCSPRLNRLIG-----EFTVNGTGEWDVCLAQVSLI 285
QY 298 NTS---YCPYSQCAFNGIFLPPQ---GDFGAFSAFYFMKFLNLTSEKVSQEKVTEMMK 351
DB 286 GDKAQPSQCNPTCFRLNVIAPSVNLSTVQLYGSEYVYVTSNFGSGGE-YHYQKFTDEV 344
QY 352 KFCAPQWEI-----KTSVAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIG 405
DB 345 KYCQKDWNDIQGFKRNEPNADIERLGTNCFCFAAVTSLVLDG--FNVDTKHLFQSVL 402
QY 406 KIQSDAGWTILGVL 420
DB 403 KIAGEEMQWALGAML 417

RESULT 9
Ti6696
Hypothetical protein R07E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: Ti6696
R;Miller, N.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid R07E4.
A;Reference number: Z18561
A;Accession: Ti6696
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-557 <MIL>
A;Cross-references: EMBL:U39652; NID:G1049390; PID:G1049394; PIDN:AAA80403.1; CESP:R07E4.4
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:R07E4.4
A;Introns: 39/1; 67/1; 145/2; 192/3; 244/3; 317/3; 451/3; 488/2

Query Match 16.3%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.8e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISKFVQKVEIGYIY 68
DB 63 SLHYSVIIDGSSGTRVHVGVRIESGKPVDFGGEENYASLKLSPGLSAYADNPEGVSES 122
QY 69 LTDCMERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQ 128
DB 123 VTELVEFAKRVHKGKLSKSDIRLMATAGRLLELPVQE-QILDVTRVLESSGDFP- 178
QY 129 GARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNN-QETFGALDGLG-----GA 181
DB 179 -----RDWASVISILENFQDLMKVYMLGILLMRSV 211
QY 182 STQVTFVQNTTESDNALQFLYK-DYVNTHTSFLCYGKQALWQKLAKDI-QVASN 239
DB 212 RLEVTFV---STELVPSFSTRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
QY 240 E-----ILRDCPCHPGYKVVNV-SDLYKTPCTK-RFEMTLFQOFEIQIGNYQOCHSI 293
DB 268 STQGIIVPDCIPKGVILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
QY 294 LELF--NTSYCPYSQCAFNGIFLPPQDGFASAFVFMKFLNLTSEKVSQEKVTEMM- 350
DB 321 FAMLQEBKGTCKYKRSIGSIFTPNQQSGSLATENFHTSKFFGL-GEK---EWLSEML 376
QY 351 --KKFCAQPEEIKTSYAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIGKIQ 408
DB 377 AGREFCGEESKLVKVKYPTFDENLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
QY 409 GSD--AGWTILG-YMLN 421
DB 436 EEDPLDVALGAFILN 451

RESULT 8
C86276
7A19.33 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86276
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Query Match 16.3%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.8e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISKFVQKVEIGYIY 68
DB 63 SLHYSVIIDGSSGTRVHVGVRIESGKPVDFGGEENYASLKLSPGLSAYADNPEGVSES 122
QY 69 LTDCMERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQ 128
DB 123 VTELVEFAKRVHKGKLSKSDIRLMATAGRLLELPVQE-QILDVTRVLESSGDFP- 178
QY 129 GARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNN-QETFGALDGLG-----GA 181
DB 179 -----RDWASVISILENFQDLMKVYMLGILLMRSV 211
QY 182 STQVTFVQNTTESDNALQFLYK-DYVNTHTSFLCYGKQALWQKLAKDI-QVASN 239
DB 212 RLEVTFV---STELVPSFSTRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
QY 240 E-----ILRDCPCHPGYKVVNV-SDLYKTPCTK-RFEMTLFQOFEIQIGNYQOCHSI 293
DB 268 STQGIIVPDCIPKGVILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
QY 294 LELF--NTSYCPYSQCAFNGIFLPPQDGFASAFVFMKFLNLTSEKVSQEKVTEMM- 350
DB 321 FAMLQEBKGTCKYKRSIGSIFTPNQQSGSLATENFHTSKFFGL-GEK---EWLSEML 376
QY 351 --KKFCAQPEEIKTSYAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIGKIQ 408
DB 377 AGREFCGEESKLVKVKYPTFDENLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
QY 409 GSD--AGWTILG-YMLN 421
DB 436 EEDPLDVALGAFILN 451

Query Match 16.3%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.8e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISKFVQKVEIGYIY 68
DB 63 SLHYSVIIDGSSGTRVHVGVRIESGKPVDFGGEENYASLKLSPGLSAYADNPEGVSES 122
QY 69 LTDCMERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQ 128
DB 123 VTELVEFAKRVHKGKLSKSDIRLMATAGRLLELPVQE-QILDVTRVLESSGDFP- 178
QY 129 GARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNN-QETFGALDGLG-----GA 181
DB 179 -----RDWASVISILENFQDLMKVYMLGILLMRSV 211
QY 182 STQVTFVQNTTESDNALQFLYK-DYVNTHTSFLCYGKQALWQKLAKDI-QVASN 239
DB 212 RLEVTFV---STELVPSFSTRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
QY 240 E-----ILRDCPCHPGYKVVNV-SDLYKTPCTK-RFEMTLFQOFEIQIGNYQOCHSI 293
DB 268 STQGIIVPDCIPKGVILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
QY 294 LELF--NTSYCPYSQCAFNGIFLPPQDGFASAFVFMKFLNLTSEKVSQEKVTEMM- 350
DB 321 FAMLQEBKGTCKYKRSIGSIFTPNQQSGSLATENFHTSKFFGL-GEK---EWLSEML 376
QY 351 --KKFCAQPEEIKTSYAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIGKIQ 408
DB 377 AGREFCGEESKLVKVKYPTFDENLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
QY 409 GSD--AGWTILG-YMLN 421
DB 436 EEDPLDVALGAFILN 451

Query Match 16.3%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 3.8e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;
QY 10 NVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVK-GPGISKFVQKVEIGYIY 68
DB 63 SLHYSVIIDGSSGTRVHVGVRIESGKPVDFGGEENYASLKLSPGLSAYADNPEGVSES 122
QY 69 LTDCMERAREVIPSQHOETPVVLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQ 128
DB 123 VTELVEFAKRVHKGKLSKSDIRLMATAGRLLELPVQE-QILDVTRVLESSGDFP- 178
QY 129 GARIITQOEGAYGWITINYLKGFQSKTRWFSIVPYETNN-QETFGALDGLG-----GA 181
DB 179 -----RDWASVISILENFQDLMKVYMLGILLMRSV 211
QY 182 STQVTFVQNTTESDNALQFLYK-DYVNTHTSFLCYGKQALWQKLAKDI-QVASN 239
DB 212 RLEVTFV---STELVPSFSTRTLAYGNVSNLYSHSFLDFGQD-AAQEKLSSELYNSAAN 267
QY 240 E-----ILRDCPCHPGYKVVNV-SDLYKTPCTK-RFEMTLFQOFEIQIGNYQOCHSI 293
DB 268 STQGIIVPDCIPKGVILETNLQKDLPGFLADKGTATL-----QAAGNFSECRSAA 320
QY 294 LELF--NTSYCPYSQCAFNGIFLPPQDGFASAFVFMKFLNLTSEKVSQEKVTEMM- 350
DB 321 FAMLQEBKGTCKYKRSIGSIFTPNQQSGSLATENFHTSKFFGL-GEK---EWLSEML 376
QY 351 --KKFCAQPEEIKTSYAGVKEKVSFCFSGVYVILSLQLQYHFTADSWEHIFHIGKIQ 408
DB 377 AGREFCGEESKLVKVKYPTFDENLLRYCFSSAYIISMLHDSLGVALDD-ERIKYASKAG 435
QY 409 GSD--AGWTILG-YMLN 421
DB 436 EEDPLDVALGAFILN 451

Query Match	15.9%;	Score 374;	DB 2;	Length 455;
Best Local Similarity	25.6%;	Pred. No. 1.7e-22;		
Matches 116;	Conservative 80;	Mismatches 169;	Indels 88;	Gaps 18
Qy	13	YGIVLDAGSGHTSLYIYKVPAAEKENDTGVVH---	QVEBCRVKPGGISKFQVKVNEIGIYL	69
Db	44	YAVVFDAGSTGSRIHVVHF---	NQNLDDLHIGKVEYNNKTTTCLSSYANPEQAAKSL	99
Qy	70	TDCHERAREVIPSQHQETPVYLCATAGMRLRMSEELADRVLDVDPVRSLSN--YPPDFQ	128	
Db	100	IPLEQREDVVPDDLQPKTPVRLGATAGRLUNGDAE---	KIQSVRDMLSNRSTFTNVQ	156
Qy	129	--GARIITQEGEGAYGMITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVT	186	
Db	157	PDVAHSIIDGTQEGSYLWTVNYALGNLGGK-----	YTKTVGVVIDLGGSGVQMA	204
Qy	187	FVPQNQTIESPDNAL-----	QFRLYGKDYNVYTHSFCLVCYGKDOALWOKLAKDIOVAS	238

[illegible]


```

A;Map position: 5L
C;Function:
A;Description: hydrolase
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F;10-24/Domain: transmembrane #status predicted <TM>
F;41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          13.6%; Score 320.5; DB 2; Length 518;
Best Local Similarity 26.8%; Pred. No. 4.6e-18;
Matches 121; Conservative 70; Mismatches 188; Indels 73; Gaps 20;

Qy 9  ENVKYGIVL DAGSSHTSLXYIKYPAEKENDTVGVHVQVECKRVGPGISKVFQKVNEIGI- 67
Db 89 EEHKYVIMIDAGSTGSRVHIYKFDVCTSPPTLL--DEKFDMLPEGLSSF--DTDSVGAA 143
Qy 68 -YITDCWERAREVIPSQHOETPVYLGATAGMBLL- RMESEELADRLVDVVERSLSNYPF 125
Db 144 NSLDPLLLKVMNVYPIKARSCCTPAVKATAGLLGLDGAASKILLSAVRDHLEK--DYPF 200
Qy 126 ---DFOGARIITQGEBCAYGWIITVYLLGKFSOKTRWFSIVPYETNNQE--TGCALDLGG 180
Db 201 PVVEGDGVSTMGDEEGVFAMITNTYLLGNIG-----ANGPKLPTAAVFDLGG 248
Qy 181 ASTQVTFVPO---NOTIESPDNALQRLYGYKYNVYTHSFLCYG-----KQQAALWOKL 230
Db 249 GSTQIVFEPTFPINEKXWDGEHKFPDLKFGDENTLTQFSLHGLGKEGRKNVNSVLVENA 308
Qy 231 AKDIQVASNE-----ILRDFCPHPGYKKVNVNSDLYKTPCTKRFEMTLPFQQFEIQGIG- 284
Db 309 LKDGKILKGNATKTHQLSSFLPP---KVNAATNEKVTLESK-----ETVITDIFGP 356
Qy 285 ---NYQOCHQSILELFN-TSYCYPSYQAFNGIFLPP-----QGFPGASAFYFVMKFL 334
Db 357 DEPSGAQCRFLTDEILNKDAQCCSPCSFNGVHQPSLVRTFKESNDIYIFESFYDRTRPL 416
Qy 335 NLTSEKVSQKVTMMKKFC--AQPEEIKTSVAGVKEKYLSE--YCFSGTYIILSLILQG 390
Db 417 GMPLSTLNE-LNDLARIYCKGETWNSVFSGIAGSLDELESDSHFCLDUSFQVSLHTG 475
Qy 391 YHPTADSWEHIFHGKIQSGDAGWTLGYMLN 422
Db 476 YDIPLQ--RELRTGKKIANKEIGWCLGASLPL 505

Search completed: March 7, 2005, 13:24:59
Job time : 15.5783 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 61.641 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: us-09-835-147a-27_copy_25_464

Perfect score: 2352

Sequence: 1 ATQNKALPENKYGIVLDAG.....NLTNMIPAEQPLSTPLSHST 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	99.8	510	1 ENP1_HUMAN	P49961 homo sapien
2	1835	78.0	510	1 ENP1_MOUSE	P55772 mus musculus
3	1835	78.0	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1830	77.8	510	2 Q92106	Q921q6 mus musculus
5	1818	77.3	372	2 Q86V3	Q86vr3 homo sapien
6	1794.5	76.3	511	1 ENP1_RAT	P97687 rattus norv
7	1715	72.9	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1690.5	71.9	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	66.9	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1450	61.6	508	2 Q6DF81	Q6dfs1 xenopus tro
11	1418	60.3	508	2 Q6GP74	Q6gp74 xenopus lae
12	1366.5	55.5	492	2 Q8DC46	Q8dc46 brachydanio
13	1046	44.5	497	2 Q6UQ22	Q6uq22 mus musculus
14	1004	42.7	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	42.4	493	2 Q90X66	Q90x66 gallus gall
16	974	41.4	454	2 Q6ZM69	Q6zm69 brachydanio
17	971.5	41.3	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	41.0	495	1 ENP2_MOUSE	O35026 mus musculus
19	964.5	41.0	495	2 Q921R1	Q921r1 mus musculus
20	961	40.9	455	2 Q7T014	Q7t014 brachydanio
21	953	40.5	494	1 ENP2_CHICK	P79784 gallus gall
22	937.5	39.9	502	2 Q66L64	Q66l64 brachydanio
23	936	39.8	526	2 Q6GN44	Q6gna4 xenopus lae
24	933	39.7	500	2 Q6NV19	Q6nv19 xenopus tro
25	913.5	38.8	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	38.7	529	1 ENP3_HUMAN	Q75355 homo sapien
27	907.5	38.6	495	1 ENP2_HUMAN	Q9y513 homo sapien
28	906.5	38.5	458	2 Q6UVZ0	Q6uvz0 homo sapien
29	902.5	38.4	529	2 Q6BFW6	Q6bfw6 m mus muscu
30	854	36.3	453	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	35.1	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	28.0	544	2	Q7YTA4	Q7yta4 schistosoma
33	620.5	26.4	300	2	Q8K0L2	Q8k0l2 mus musculus
34	596.5	25.4	209	2	Q8UVX9	Q8uvx9 torpedo mar
35	505	21.5	483	2	Q9XI62	Q9xi62 arabidopsis
36	504	21.4	488	2	Q6NQ48	Q6nq48 arabidopsis
37	491	20.9	503	2	Q94AP8	Q94ap8 arabidopsis
38	491	20.9	503	2	Q8H1D8	Q8h1d8 arabidopsis
39	485	20.6	537	2	Q6Z543	Q6z543 oryza sativ
40	483	20.5	634	2	Q6FRC2	Q6frc2 candida gla
41	482.5	20.5	336	2	Q8CCV2	Q8ccv2 mus musculus
42	471.5	20.0	555	2	Q94E22	Q94ez2 arabidopsis
43	469.5	20.0	405	2	Q9M9T7	Q9m9t7 arabidopsis
44	466	19.8	611	2	Q6DH30	Q6dh30 brachydanio
45	465.5	19.8	555	2	Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1

ID	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
AC	P49961: Q9UQ09; Q9Y3Q9;			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)			
DE	(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell			
DE	activation antigen) (Ecto-apyrase) (CD39 antigen).			
GN	Name=ENTPD1; Synonyms=CD39;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J.,			
RA	Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,			
RA	Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;			
RT	"The CD39 lymphoid cell activation antigen. Molecular cloning and			
RT	structural characterization.";			
RL	J. Immunol. 153:3574-3583(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	TISSUE=Umbilical vein;			
RA	MEDLINE=97149443; PubMed=896251;			
RA	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K.,			
RA	Millan M., Hancock W.W., Bach F.H.;			
RT	"Loss of ATP diphosphohydrolase activity with endothelial cell			
RT	activation.";			
RL	J. Exp. Med. 185:153-163(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).			
RC	TISSUE=Placenta;			
RX	MEDLINE=99332083; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;			
RA	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,			
RA	Titani K., Fujimura Y., Narita N.;			
RT	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I			
RT	and II.";			
RL	FEBS Lett. 453:335-340(1999).			
RN	[4]			
RP	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96096723; PubMed=8529670;			
RA	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;			
RT	"Purification and properties of human placental ATP			
RT	diphosphohydrolase.";			
RL	Eur. J. Biochem. 234:66-74(1995).			
RN	[5]			
RP	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND			
RC	399-405 (ISOFORM PLACENTAL I).			
RC	TISSUE=Placenta;			

FT	CARBOHYD	73	73	N-linked (GlcNAc...)	(Potential).
FT	CARBOHYD	226	226	N-linked (GlcNAc...)	(Potential).
FT	CARBOHYD	291	291	N-linked (GlcNAc...)	(Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc...)	(Potential).
FT	CARBOHYD	428	428	N-linked (GlcNAc...)	(Potential).
FT	CARBOHYD	457	457	N-linked (GlcNAc...)	(Potential).
SQ	SEQUENCE	510 AA;	5720S MW; 8E6A6113D2E13930 CRC64;		

Query Match		78.0%;	Score 1835;	DB 1;	Length 510;
Best Local Similarity		76.4%;	Pred. No. 2.5e-136;		
Matches	337;	Conservative	45;	Mismatches	55;
				Indels	4;
Gaps	3;				

QY	2	TQNKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVBCRVKPGIGSFVQK	61
Db	38	TQNKLPLPENVKYGIVLDAGSSHTNLVIKKWPAEKENDTGVVQQLEECQVKGPGISKYAQK	97
QY	62	VNEIGIYLTDCHERABEVIPRSQHETPVYLGATAGMRLLRMESEELADVLVDVERLS	121
Db	98	TDEIGAYLAECHNELSTELIPTSKHHGTTPVYLGATAGMRLLRMESEQADEVLAAVSTSLK	157
QY	122	NYPPFFOQARIITGOBEGAYGITINLLGKFSQKTRFPSIVFYETNNOBTFGALDLGGA	181
Db	158	SYPPFFOQAKILITGOBEGAYGITINLLGRFTQEQSWLSLIS-DSQKETFGALDLGGA	216
QY	182	STQVTVPNQNTIESPDNALQFLRYKDXNVYTHSPFLCYGKDQALMQKLAKDIQVASNEI	241
Db	217	STQITFPVNQNTIESPENSIFRLYGEDTVTVTHSPFLCYGKDQALMQKLAKDIQVSSGGV	276
QY	242	LSDPCFHQYKVVNVSIDLYKTCTCRPEMTLPFQOFELQIGIGNYQQCHQSILELENTSY	301
Db	277	LKDPFCFNPGYEKVNVSELGYPTCTCRFEKKLPFDQFRIGTGTDYBQCHQSILELFNNSH	336
QY	302	CYPSCAFNGIELPPLQGDFGAFSAFYFWKFLNLTSEK--VSQEKVTEHMKKFCAOPWE	359
Db	337	CYPSCAFNGVFLPPLHGSGFAFSAPFYWMDPKVKAKNSVISQEKXTEITKNFCCKSWE	396
QY	360	EIKTSYAGVKEKYLEYCFSGTYIIISLLQGHYHTADSWEHIHFICKIQGSDDAGWTLYGM	419
Db	397	ETKTSYPSVKEKYLEYCFSGAYILS-LLOQYNFTDSSWEQIHFMGIKIDS NAGWTLYGM	455
QY	420	LNLTNMIPAEOPLSTPLSHST	440
Db	456	LNLTNMIPAEOPLSPPLPHST	476

RESULT 3	
QC8DV7	PRELIMINARY;
ID	QC8DV7
AC	O8CDV7
DT	01-NAR-2003 (TrEMBLrel. 23, Created)
DT	01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:492151C05 product:cotnucleoside triphosphate diphosphohydrolase 1, full insert sequence.
DE	Name=Entpd1;
OS	Mus musculus (Mouse);
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Testis;
RC	MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RC	Carninci P.; Hayaehizaki Y.;
RA	"High-efficiency full-length cDNA cloning."
RT	Meth. Enzymol. 303:19-44(1999).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Testis;
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA	RIKEN FANTOM Consortium;
RT	"Functional annotation of a full-length mouse cDNA collection."

SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Cochlea; DOI=10.1016/S0169-328X(99)00244-2;
 RX MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
 RA Vlatkovic S.M., Housley G.B., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 termination of purinergic transmission.";
 RL Brain Res. Mol. Brain Res. 73:85-92(1999).
 RN [3]
 RP SEQUENCE OF 432-511 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=9031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
 RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 rat brain.";
 RL Neuropharmacology 36:1189-1200(1997).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
 kidney, liver, muscle, thymus, lung and spleen.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 CC
 DR EMBL; U81295; AAC53195.1; -;
 DR EMBL; Y15685; CAA75730.1; -;
 DR RGD; 69265; Entrez.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 FT DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 511 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 332 332 F -> L (in Ref. 2).
 SQ SEQUENCE 511 AA; 57408 MW; 4CC123D3B644C193 CRC64;
 Query Match 76.3%; Score 1794.5; DB 1; Length 511;
 Best Local Similarity 74.4%; Pred. NO. 4e-133;
 Matches 328; Conservative 51; Mismatches 59; Indels 3; Gaps 3;
 QY 2 TONKALPENKYGIVLDAGSHTSILYIKVPAEKENDGVVHVEECVKGPGISKPVOK 61
 DB 38 THNKLPLPENKYGIVLDAGSHNTLIYIKVPAEKENDGVVOLLLEECQVKGPGISKVAK 97
 QY 62 VNEIGIYLDQWERAREYIPRSQHOTPVYLGATAGMELLRMESEELADRLVDVVERSL 121
 DB 98 TDEIAAYLAECWKNSTERIPASKQHTPVYLGATAGMELLRMESEELADRLVDVVERSL 157
 QY 122 NYPDFQAGRIITGQEGAYGNTINYLKFGSKQTRWFSIVPVETNNQETFGALDLGGA 181
 DB 158 SYPDFQAGRIITGQEGAYGNTINYLKFGSKQTRWFSIVPVETNNQETFGALDLGGS 216

QY 182 STQVTFVQNTLESNDNALQRLYKDYVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 241
 DB 217 STQVTFVPLNQLSEAPETSQRLYGTDTYVYTHSFLCYGKQDQALWOKLAKDIOVSSGGI 276
 QY 242 LRDCFFHPGKVVVNSDLVKTCTKRFEMTLPQOFEIQIGNYQOCHOSILELFNTSY 301
 DB 277 LKDFCFYPGYKVVVNSLYGTCTKRFEMTLPQOFEIQIGNYQOCHOSILELFNTSY 336
 QY 302 CPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFL-NLTSEKY-SOEKVTMMKFCAPQWE 359
 DB 337 CPYSQCAFNGIFLPPLOGDFGAFSAFYVMDFPKKMANDSVSOEKMTEITKPFCSKPWE 396
 QY 360 EIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFGIQSDAGWTILGYM 419
 DB 397 EVKASYPTVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFGIQSDAGWTILGYM 456
 QY 420 LNLNMIAPAEQPLSTPLSHST 440
 DB 457 LNLNMIAPAEQPLSTPLSHST 477
 RESULT 7
 ENPI_PIG ID ENPI_PIG STANDARD; PRT; 510 AA.
 AC Q9MYU4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
 activation antigen) (Ecto-apyrase) (CD39 antigen).
 GN Name=ENTPD1; Synonyms=CD39;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic endothelium;
 RX MEDLINE=20325090; PubMed=10866813;
 RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O.,
 RA Sevigny J.;
 RT "Distribution, cloning, and characterization of porcine nucleoside
 triphosphate diphosphohydrolase-1.";
 RL Eur. J. Biochem. 267:4106-4114(2000).
 RN [2]
 RP SEQUENCE OF 202-220.
 RC TISSUE=Pancreas;
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 nucleotides to regulate purinergic neurotransmission. Could also
 be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Highest expression found in vascular
 endothelium, smooth muscle, spleen and lung.
 CC -!- PTM: Cleaved into two polypeptides that seem to stay together by
 noncovalent interactions.
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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ENBL; AJ133746; CAB95871.1; -;			Ectonucleoside triphosphate
Interpro; IPR000407; GDAI_CD39_NTPase.			diphosphohydrolase 1.
Pfam; PF01150; GDAI_CD39; 1.			Ectonucleoside triphosphate
PROSITE; PS01238; GDAI_CD39_NTPASE; 1.			diphosphohydrolase 1 27 kDa subunit.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;			Ectonucleoside triphosphate
Magnesium; Transmembrane.			diphosphohydrolase 1 54 kDa subunit.
CHAIN 1 510			Cytoplasmic (Potential).
FT FT			Potential.
FT CHAIN 1 201			Extracellular (Potential).
FT FT			Potential.
FT CHAIN 202 510			Potential.
FT FT			Cytoplasmic (Potential).
FT DOMAIN 1 16			N-linked (GlcNAc. . .) (Potential).
FT TRANSMEM 17 37			N-linked (GlcNAc. . .) (Potential).
FT DOMAIN 38 477			N-linked (GlcNAc. . .) (Potential).
FT TRANSMEM 478 498			N-linked (GlcNAc. . .) (Potential).
FT DOMAIN 499 510			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1 73 73			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 245 245			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 274 274			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 291 291			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 333 333			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 370 370			N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 457 457			N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 203 203			G -> S (in Ref. 2).
SQ SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;			

Query Match	72.9%	Score 1715;	DB 1;	Length 510;
Best Local Similarity	70.7%	Pred. No. 7.5e-127;		
Matches 311;	Conservative 63;	Mismatches 64;	Indels 2;	Gaps 2;

Qy	2	TQNKALPENVKYGI	VL	DAGSHSTSLY	Y	KWPAEKENDTGV	VH	QVECRVKG	PG	ISKVFQK	61
Db	38	TQNKPLPENVKFI	VL	DAGSHSTSLY	Y	KWPAEKENDTGV	V	QVEECKLKG	PG	ISEPAKK	97
Qy	62	VNRIGTYLTPCME	RAREVI	PRSHOETPV	YL	GATAGMRLLR	MESEEL	ADRVLDV	V	VERSL	121
Db	98	LGHIDIYLEACME	REARTV	PKSQAETPV	YL	GATAGMRLLR	MKNENLA	SKILSTV	ARE	SIT	157
Qy	122	NYPDFDQAGARI	ITGOEBAG	WITIN	YLL	LQKFSQKTW	FSIVPV	YETNNQ	ETFG	ALD	181
Db	158	RYPDFDQAGARI	ITGOEBAG	WITIN	YLL	DKFIQSGW	FNLPKR	KGDTQ	ETYG	ALD	217
Qy	182	STOVTVPONQ	TETSP	DNALQ	FLY	KDYNVYTH	SFLCYG	KDQALW	KLAKD	IQV	241
Db	218	STOITVPQ	QNVLES	PENTL	HFRLY	KGXSVYTH	SFLCYG	KDQALL	OKLTK	DLK	276
Qy	242	LRDPCFHPG	YKVVV	SDLYK	TPCKTR	FEMTLP	FQOQFEI	QIGNY	QOCHOS	ILE	301
Db	277	IHEPCFHS	GYYRR	MNVSH	LYEAP	CTRREF	LSLPP	PELEI	QGTG	DQKQ	336
Qy	302	CPYSQCAFNGI	FIP	LPLOGD	FGAS	AFYFV	WKFLN	LTSEK	V	-QBK	360
Db	337	CPYSRCSF	DGVFLP	LPQD	PAFSA	FYVNG	FLNLT	SEEGS	FQ	SKVTS	396
Qy	361	IKTSYAGV	KEKYLSEY	CFSG	TYTIL	SLLQGV	HFTADS	WEH	THF	IGK	420
Db	397	LQMYFGD	VEKYLSEY	CFSG	TYTIL	SLLSGV	HFTAE	TWKNI	HFH	MKG	456
Qy	421	NLTNMI	PAEQ	LP	STPL	SHST	440				
Db	457	NLTNMI	PSE	PS	TR	LSHST	476				

RESULT 8					
ENP1_BOVIN					
ID	ENP1_BOVIN	STANDARD;	PRT;	513 AA.	
AC	O18956;				
DT	16-OCT-2001	(Rel. 40, Created)			

16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (CD39 antigen) (Ecto-apyrase).
Name=ENTPDI; Synonyms=CD39;
Bos taurus (Bovine).
OS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC
Bovinae; Bos.
ON
NCBI_TaxID=9913;
OX
[1]
SEQUENCE FROM N.A.
RN
TISSUE=Aortic endothelium;
RP
Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RA
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL
[2]
SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RN
TISSUE=Aorta;
RP
MEDLINE=97115958; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RX
Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA
Beaudoin A.R., Bach F.H., Robson S.C.;
RA
Identification and characterization of CD39/vascular ATP
RT
diphosphohydrolase.";
RT
J. Biol. Chem. 271:33116-33122 (1996).
RC
-!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC
nucleotides to regulate purinergic neurotransmission. Could also
CC
be implicated in the prevention of platelet aggregation.
CC
Hydrolyzes ATP and ADP equally well.
CC
-!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC
-!- COFACTOR: Requires calcium and magnesium.
CC
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
-!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

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or send an email to license@isb-sib.ch).

EMBL; AF005940; AAB62382.1; --	
InterPro; IPR000407; GDAI_CD39_NTPase.	
Pfam; PF01150; GDAI_CD39; 1.	
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.	
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;	
KW Magnesium; Transmembrane.	
DOMAIN	1 16
TRANSMEM	17 37
FT POTENTIAL.	
DOMAIN	38 481
TRANSMEM	482 502
FT POTENTIAL.	
DOMAIN	503 513
FT CYTOPLASMIC (Potential).	
CARBOHYD	73 73
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	227 227
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	245 245
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	307 307
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	336 336
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	373 373
FT N-linked (GlcNac. .) (Potential).	
CARBOHYD	460 460
FT N-linked (GlcNac. .) (Potential).	
CONFLICT	97 97
FT K -> N (in Ref. 2).	
CONFLICT	101 103
FT INV -> CGF (in Ref. 2).	
CONFLICT	464 464
FT K -> V (in Ref. 2).	
SEQUENCE	513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;

	Query Match	71.9%	Score 1690.5	DB 1	Length 513
	Best Local Similarity	69.8%	Pred. No. 6.5e-125		
	Matches 309	Conservative 64	Mismatches 65	Indels 5	Gaps 3
QY	2	TQNKALPENVKYGI	VLDAGSSHTSYLYIKWPAEKNDTGVWVHQVECRVKGFGISKFVQK	61	
Db	38	TQNKALPENVKFGI	VLDAGSSHTSYLYIKWPAEKNDTGVWVQIIESNVKFGISGFQAKK	97	


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QY 62 VNEIGIYLTDCMREAREVIPSQHOETPVYLGATAGMELLMESEELADRVLDVVERSL 121
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 98 VNEINVLYTACMERAKQVIPSIOHWETPVYLGATAGMELLMESEELADRVLDVVERSL 157

QY 122 NYPDFQCARITGQEGAGYMTITNYLLGKPSQKTRWFSIVPVETNNQETFGALDLGGA 181
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 158 EYPDFQCARITGQEGAGYMTITNYLLGKPSQKTRWFSIVPVETNNQETFGALDLGGA 217

QY 182 STQTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLADQVASEI 241
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 218 STQTFVQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLADQVASEI 276

QY 242 LRDPFCFPGYKVVNVSLYTPCTKREMT---LPFOQFIQIGNYQOCHOSILEFN 298
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 277 IHEPCFHSRYWRKIKWVNLGFCFKRHELNSSFFPLVDIIRGAGNFQRCRIIQLFN 336

QY 299 TSYCPYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEK-VSQEKVTEMMKKFCAQP 357
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 337 TSYCPYSCSFGNVLPLHGFQGAFAFYVMBEFLNLTSESVSVEQLTEKLEFCAQR 396

QY 358 WBEIKTSVAGVKEKYLSEYCSGTYVLSLLQGHFTADSWHEHIFIGKIQSGDAGWTLG 417
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 397 WEEVQNFGEVKEKYLSEYCSGTYVLSLLQGHFTADSWHEHIFIGKIQSGDAGWTLG 456

QY 418 YMLNLTNMPAEOPLSTPLSHST 440
RL |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 457 YMLNLTNMPAEOPLSTPLSHST 479

RESULT 9
Q8CEB1 PRELIMINARY; PRT; 420 AA.
ID Q8CEB1
AC Q8CEB1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mus musculus; 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732419M16 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence. (Fragment).
GN Name=Entpd;
OS Mus musculus. (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
(2)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
(3)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
(4)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
(5)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
(6)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1;
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:apyrase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
FT NON_TER.
SQ SEQUENCE 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
Query Match 66.9%; Score 1574; DB 2; Length 420;
Best Local Similarity 74.5%; Pred. No. 8.1e-116;
Matches 289; Conservative 42; Mismatches 53; Indels 4; Gaps 3;
QY 55 ISKFKVQKNEIGIYLTDCMREAREVIPSQHOETPVYLGATAGMELLMESEELADRVLD 114
DB 1 ISKYAQKTDEIGAYLAECMELSTELIPTSKHHQTPVYLGATAGMELLMESEELADRVLD 60
QY 115 VVERSLSNYPDFQCARITGQEGAGYMTITNYLLGKPSQKTRWFSIVPVETNNQETFG 174
DB 61 AVSTLSKSPYDFQCARITGQEGAGYMTITNYLLGKPSQKTRWFSIVPVETNNQETFG 119
QY 175 ALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAD 234
DB 120 ALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAD 179
QY 235 QVASENILLRDPCHPHGKVVNVSLYTPCTKREMT---LPFOQFIQIGNYQOCHOSIL 294
DB 180 QVSSGVLKDPFCFPGYKVVNVSLYTPCTKREMT---LPFOQFIQIGNYQOCHOSIL 239
QY 295 ELFNSTVCPYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEK-VSQEKVTEMMKK 352
DB 240 ELFNSTVCPYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEK-VSQEKVTEMMKK 299
QY 352 FCAQFWBEIKTSVAGVKEKYLSEYCSGTYVLSLLQGHFTADSWHEHIFIGKIQSGDAG 412
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Db 300 FGCSKWEETKTSYPSVKSEKYLSEYCFSGAYILS-LLQGYNFTGSSWEQIHFMGKIKDSNA 358
 QY 413 GWTGLGYMLNTNMIPAEQPLSTPLSHST 440
 Db 359 GWTGLGYMLNTNMIPAEQPLSTPLPHST 386

RESULT 10
 Q6DFS1
 ID ID PRELIMINARY; PRT; 508 AA.
 AC O6DFS1;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Entpd1-prov provin.
 GN Name-entpd1-prov;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC076662; AAH76662.1; -
 DR GO; GO:0015787; F:hydrolase activity; IEA.
 DR InterPro; IPR00407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39.1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 61.6%; Score 1450; DB 2; Length 508;
 Best Local Similarity 60.2%; Pred. No. 6.5e-106;
 Matches 263; Conservative 75; Mismatches 97; Indels 2; Gaps 2

QY 3 QNKALPENVKYGIIVLDAGSSHTSYIVYKWPAAKENDTGVVHVEECRVKVGPGISKEVQKV 62
 Db 39 QNKPLPKNIKGIIVLDAGSSHTSYIYEWPAKENDTGVVQVQINECKVEGNGLISSYGHPE 98
 QY 63 NEIGIYLTDCMERAREVIPSRSQHOETPPYVLGATAGMELLRMESEELADRVLVDIVERSLSN 122
 Db 99 LKAGLSLQCKWAKARQVPEKQRETTPYVLGATAGMELLRLTWTAAEEVLSSVENTLAS 158
 QY 123 YPFDFOGARIITGOEGAYGHITINYLKFPKSQKTRWFSIVPVTNNQETFGALDILGGAS 182
 Db 159 PFPDFOGARIITGOEGAYGHITINYLGNFIODSGWFKVIP-NFKPTETSGALDILGGAS 217

Qy	183	TQVTFVQNOTIESPDNALQFRLYKGYNVVYTHSFLCYGKQOALWQKIAQIVASNEIL	244
Db	218	TQITFFSKRE-IESQENSLHFLRYKGYSDIYTHSFLCYGKQALRLQIANGIKDATDSL	276
Qy	243	RDCFCFHGYKVVNVSDLYTKPTCKRFEWTLFPQOFETQIGIYQOQCHQSIILELPTSVC	302
Db	277	LDPFCNFGYRRNASTNDLYISPCLSKURIPAPSTLDIRGTGNVQLCKRNQVAIFNRTHC	336
Qy	303	PYSQAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKXCAQPWBBIK	362
Db	337	TYSHCSFNGVFPQSLDGTGFAFSAYFYVMNPLNLTNEQMSLDKVKETVERHCSRPDWEVK	396
Qy	363	TSVAGVKEKYLSEYCFSGTWTLSLLLOGYHFTADSWERHIFGIKIQSDAGWTLGYMLNL	422
Db	397	KDPFKIKYKYLSEYCFSGTWTILNLLYGYGFSSFNWDIRFLGKIKQSDAGWTLGYMLNL	456
Qy	423	TNMIPAEQPLSTPLSHS	439
Db	457	TNMIPAEPLSYPPLSHA	473
RESULT 11			
Qy	606P74	PRELIMINARY;	PRT; 508 AA.
AC	Q6GP74;		
DT	05-JUN-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DE	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	MGC80631	protein.	
GN	Name=MGC80631;		
OS	Xenopus laevis	(African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Schein J.E.,		
RA	Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;		
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,		
RA	Richardson P.;		
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus		
RT	initiative."		
RL	Dev. Dyn. 225:384-391(2002).		
RN	[3]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RC	TISSUE=Spleen;		
RA	Klein S., Gerhard D.S.;		

[illegible]

FT diphasophydrolase.";
 RL J. Biol. Chem. 273:16043-16049(1998).
 RN [2]
 RP SEQUENCE OF 1-17.
 RC TISSUE=Stomach;
 RX MEDLINE=9742428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
 RA Lewis-Carl S., Kirley T.L.;
 RA "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
 RT gizzard and stomach. Purification and N-terminal sequence of the
 RT stomach ecto-apyrase.";
 RL J. Biol. Chem. 272:23645-23652(1997).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF041355; AAC26491.1; -
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39_1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Magnesium; Transmembrane.
 FT DOMAIN 1 7 Cytoplasmic (Potential).
 FT TRANSMEM 8 28 Potential.
 FT DOMAIN 29 463 Extracellular (Potential).
 FT TRANSMEM 464 486 Potential.
 FT DOMAIN 487 493 Potential.
 FT CARBOHYD 65 65 Cytoplasmic (Potential).
 FT CARBOHYD 79 79 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 133 133 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 223 223 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 234 234 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 267 267 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 324 324 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 330 330 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 372 372 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 382 382 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 445 445 N-linked (GlcNAc. .) (Potential).
 FT CONFLICT 16 16 C -> W (in Ref. 2).
 FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
 SQ SEQUENCE 493 AA; 54034 MW; F14FP4C3AA2F3603 CRC64;

 Query Match 42.7%; Score 1004; DB 1; Length 493;
 Best Local Similarity 45.7%; Pred. No. 1.1e-70;
 Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

 QY 7 LPENVKYGVLNAGSSHTSLIYIKWPAEKENDGVVHVEECRVKPGISKFKVQKYNELG 66
 DB 35 LPPTGTYKGLVFDAGSTHTALIVYQWPAEKENGTVGVQVESCITVNGSGISSYADDPAG 94

 QY 67 IYLTDCMERAREVIPSQHOETPVYLGATAGMRELLRMESEELADRVLVDVVERSLSNYPFD 126
 DB 95 ASLKPCLDKAWAIVPEQQWQPTTYLGATAGMRELLRSEQNSKRAEQVFAEVSKAIRFPVD 154

 QY 127 FQGARITQEGAYGNITNYLLG---KPSQKTRWFSIVPYETNNQETFGALDLGGAST 183
 DB 155 FRGAQILITNGEESFGWITVNYLLETLLIKFSAGKW-----BHPQNTVEVLGALDLGGAST 209

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 71.8785 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147a-27_COPY_25_464

Perfect score: 2352
Sequence: 1 ATQNKALPENVKYGIVLADG.....NLTNMIPAEQPLSTPLSHST 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2352	100.0	464	3	Aay70922 Human sol
2	2352	100.0	464	3	Aay70899 Protein e
3	2349	99.9	454	3	Aay70913 Human sol
4	2349	99.9	454	3	Aay70890 Protein e
5	2349	99.9	463	3	Aay70925 Human sol
6	2349	99.9	463	3	Aay70902 Protein e
7	2349	99.9	473	3	Aay70924 Human sol
8	2349	99.9	473	3	Aay70901 Protein e
9	2349	99.9	474	3	Aay70923 Human sol
10	2349	99.9	474	3	Aay70900 Protein e
11	2349	99.9	476	3	Aay70911 Human CD3
12	2349	99.9	476	3	Aay70888 Protein e
13	2349	99.9	478	3	Aay70914 Human sol
14	2349	99.9	478	3	Aay70891 Protein e
15	2348	99.8	439	4	Aab71918 Soluble h
16	2348	99.8	487	3	Aay70921 Human sol
17	2348	99.8	487	3	Aay70898 Protein e
18	2348	99.8	510	2	Aaw04334 Human lym
19	2348	99.8	510	2	Aaw04264 Human CD3
20	2348	99.8	510	3	Aay70910 Human sol
21	2348	99.8	510	4	Aay70887 Human sol
22	2348	99.8	510	4	Aab71917 Human CD3
23	2348	99.8	510	7	AdJ57262 Human CD3
24	2348	99.8	510	8	AdL24295 Human CD3
25	2348	99.8	510	8	Adq99453 Human CD3

26	2348	99.8	510	8	ADR69210	Human CD3
27	2348	99.8	510	8	ADR69042	Human CD3
28	2348	99.8	510	8	ADs17924	Human CD3
29	2348	99.8	510	8	ABO84674	Human can
30	2348	99.8	510	8	ADR87821	Human CD3
31	2348	99.8	511	8	ADK60421	Angiogene
32	2348	99.8	511	8	ADK60722	Angiogene
33	2348	99.8	511	8	ADP73345	CD39 lymph
34	2348	99.8	517	7	ADN95839	Human BEC
35	2348	99.8	517	8	ADK60221	Angiogene
36	2348	99.8	517	8	ADK60522	Angiogene
37	2348	99.8	517	8	ADP73145	Angiogene
38	2348	99.8	522	8	ABO84672	Human can
39	2294	97.5	476	3	AAy70912	Human CD3
40	2294	97.5	476	3	AAy70889	Protein e
41	2294	97.5	529	8	ABM83376	Human dia
42	2136	90.8	503	8	ABM83377	Human dia
43	1969	83.7	402	8	ABO84671	Human can
44	1841	78.3	377	7	AD162735	Human apo
45	1118	47.5	311	8	ABO84673	Human can

ALIGNMENTS

RESULT 1	
AAAY70922	
ID	AAAY70922 standard; protein; 464 AA.
XX	
AC	AAAY70922;
XX	
DT	17-AUG-2000 (first entry)
XX	
DE	Human soluble CD39 fusion protein construct, pIL2LTrim1.
XX	
KW	Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
Key	Location/Qualifiers
Peptide	1..24
FT	/label= Leader peptide
FT	/note= "Derived from human interleukin 2 (hIL2)"
FT	
FT	Cleavage-site
FT	24..25
FT	/note= "Cleavage site of leader sequence"
FT	
FT	Protein
FT	26..464
FT	/note= "Human soluble CD39 protein"
XX	
XX	
PN	WO200023459-A1.
XX	
PD	27-APR-2000.
XX	
PF	13-OCT-1999; 99WO-US022955.
XX	
XX	
PR	16-OCT-1998; 98US-0104585P.
PR	06-NOV-1998; 98US-0107468P.
XX	
PR	13-AUG-1999; 99US-0149010P.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX	
DR	WPI; 2000-339644/29.
XX	
PT	New soluble CD39 polypeptides having apyrase activity, useful for

Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiac; cerebroprotective; arteriosclerosis; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; pIL2Trim1 variant.

Homo sapiens.
Synthetic.

Key Location/Qualifiers
Cleavage-site 24..25
Protein 26..464
/note= "soluble portion of CD39"

WO200023094-A2.
27-APR-2000.
13-OCT-1999; 99WO-US023641.
16-OCT-1998; 98US-0104585P.
06-NOV-1998; 98US-0107466P.
13-AUG-1999; 99US-0149010P.
(IMMUNEX) IMMUNEX CORP.
(CORR) CORNELL RES FOUND INC.
Maliszewski CR, Gayle RB, Marcus AJ;
WPI; 2000-339518/29.
Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.

Example 11; Page 111-112; 118pp; English.

The present sequence is the protein encoded by Trim1 construct. pIL2Trim1 variant was constructed by removing the human IL2 residues from solCD39 fusion construct. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Query Match 100.0%; Score 2352; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 2.7e-232;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATONKALPENKYGIVLDAGSHTSLYIKWPAEKENDTGVVHVVECRVKGPGISKFPVQ 60
25 ATONKALPENKYGIVLDAGSHTSLYIKWPAEKENDTGVVHVVECRVKGPGISKFPVQ 84
61 KVNIEGILYITDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRVLDVVERSL 120

Query Match 100.0%; Score 2352; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 2.7e-232;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATONKALPENKYGIVLDAGSHTSLYIKWPAEKENDTGVVHVVECRVKGPGISKFPVQ 60
25 ATONKALPENKYGIVLDAGSHTSLYIKWPAEKENDTGVVHVVECRVKGPGISKFPVQ 84
61 KVNIEGILYITDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRVLDVVERSL 120
85 KVNIEGILYITDCMERAREVIPSQHQETPVYLGATAGMRLMESEELADRVLDVVERSL 144
121 SNYPFDQGARITGQEGAYGWITINLLGKFSOKTRWFSIVPYETNNQETFGALDGG 180
145 SNYPFDQGARITGQEGAYGWITINLLGKFSOKTRWFSIVPYETNNQETFGALDGG 204
181 ASQVTFVQNTQIESPDNALQRLYGKDYNNVTHSFLCYGKQDQALWOKLAKDIQVASNE 240
205 ASQVTFVQNTQIESPDNALQRLYGKDYNNVTHSFLCYGKQDQALWOKLAKDIQVASNE 264
241 ILRDPCHFPGYKKVNVNSDLYKTPCTKRFEMTLPFQCFIQQIGNYQCHQSIILELFNTS 300
265 ILRDPCHFPGYKKVNVNSDLYKTPCTKRFEMTLPFQCFIQQIGNYQCHQSIILELFNTS 324
301 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 360
325 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 384
361 IKTSYAGKVKSEYCFSTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTLYGML 420
385 IKTSYAGKVKSEYCFSTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTLYGML 444
421 NLTNMIPAEQPLSTPLSHST 440
445 NLTNMIPAEQPLSTPLSHST 464

RESULT 2
AA70899 standard; protein; 464 AA.
AA70899;
17-AUG-2000 (first entry)
Protein encoded by Trim 1 construct.

Db 85 KNEIGIVLTCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 144
 QY 121 SNYPDFQAGARIITQOEGEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180
 Db 145 SNYPDFQAGARIITQOEGEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 204
 QY 161 ASTQVTFVQNTQTESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALMOKLAKDIQVASNE 240
 Db 205 ASTQVTFVQNTQTESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALMOKLAKDIQVASNE 264
 QY 241 ILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPEQOFEIOGIGNYQOCHOSIILEFNLS 300
 Db 265 ILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPEQOFEIOGIGNYQOCHOSIILEFNLS 324
 QY 301 YCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 360
 Db 325 YCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 384
 QY 361 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQSDAGWTLGYML 420
 Db 385 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQSDAGWTLGYML 444
 QY 421 NLTMNIPAEQPLSTPLSHST 440
 Db 445 NLTMNIPAEQPLSTPLSHST 464

RESULT 3
 AAY70913
 ID AAY70913 standard; protein; 454 AA.
 XX
 AC AAY70913;
 DT 17-AUG-2000 (first entry)
 XX
 DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.
 XX
 KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
 KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Protein
 FT 1..15
 FT /label= Mature human interleukin_2
 FT /note= "N-terminal region"
 FT Protein
 FT 16..454
 FT /note= "Human soluble CD39 protein"
 XX
 FN WO200023459-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-05022955.
 XX
 PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX
 DR WPI; 2000-339644/29.
 DR N-PSDB; AAD00206.
 XX

PT New soluble CD39 polypeptides having apyrase activity, useful for
 PT inhibiting angiogenesis and treating unstable angina, myocardial
 PT infarction, stroke, coronary artery disease or injury.
 XX
 PS Claim 6a; Page 95-97; 122pp; English.
 XX
 CC The present sequence is a fusion construct, comprising the N-terminal
 CC amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
 CC region, that has apyrase activity. This results in high levels of solCD39
 CC expression and activity in the transfected cells. Soluble CD39 is
 CC constructed by removing the N- and C-terminal transmembrane domains. It
 CC retains the capacity to metabolise ATP and ADP at relevant concentrations
 CC and the ability to block and reverse ADP-induced platelet activation and
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC are useful for inhibiting angiogenesis. It is useful for the treatment of
 CC unstable angina, myocardial infarction, stroke, coronary artery disease
 CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
 CC embolism, platelet-associated ischaemic disorders including lung, coronary,
 CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
 CC peripheral and cerebral artery thrombosis, intracardiac and venous
 CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
 CC for preventing thrombus formation or reformation, occlusion, reocclusion,
 CC stenosis or restenosis of blood vessels or stroke
 XX
 SQ Sequence 454 AA;
 Query Match 99.9%; Score 2349; DB 3; Length 454;
 Best Local Similarity 99.8%; Pred. No. 5.4e-232;
 Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPVQ 60
 Db :|||||
 15 STQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKFPVQ 74
 QY 61 KVNIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 120
 Db :|||||
 75 KVNIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 134
 QY 121 SNYPDFQAGARIITQOEGEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180
 Db :|||||
 135 SNYPDFQAGARIITQOEGEGAYGWTINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 194
 QY 181 ASTQVTFVQNTQTESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALMOKLAKDIQVASNE 240
 Db :|||||
 195 ASTQVTFVQNTQTESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALMOKLAKDIQVASNE 254
 QY 241 ILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPEQOFEIOGIGNYQOCHOSIILEFNLS 300
 Db :|||||
 255 ILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPEQOFEIOGIGNYQOCHOSIILEFNLS 314
 QY 301 YCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 360
 Db :|||||
 315 YCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMKMKFCAQPWEE 374
 QY 361 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQSDAGWTLGYML 420
 Db :|||||
 375 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFGIKIQSDAGWTLGYML 434
 QY 421 NLTMNIPAEQPLSTPLSHST 440
 Db :|||||
 435 NLTMNIPAEQPLSTPLSHST 454
 RESULT 4
 AAY70890
 ID AAY70890 standard; protein; 454 AA.
 XX
 AC AAY70890;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by fusion construct of human soluble CD39 cDNA-1.
 XX

XX	Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Protein	1..15
FT		/label= Mature human interleukin_2
FT		/note= "N-terminal region"
FT	Protein	16..454
FT		/note= "Human soluble CD39 protein"
XX	WO200023094-A2.	
XX	27-APR-2000.	
XX	13-OCT-1999;	99WO-US023641.
XX	16-OCT-1998;	98US-0104585P.
PR	06-NOV-1998;	98US-0107466P.
PR	13-AUG-1999;	99US-0149010P.
XX	(IMMV) IMMUNEX CORP.	
PA	(CORR) CORNELL RES FOUND INC.	
XX	Maliszewski CR, Gayle RB, Marcus AJ;	
XX	WPI; 2000-339518/29.	
DR	N-PSDB; AAD00201.	
XX	Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.	
PT	polyPeptides.	
XX	Claim 6; Page 95-97; 118pp; English.	
XX	The present sequence is the protein encoded by a fusion construct of sol (soluble)CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke	
XX	Sequence 454 AA;	
SQ	Query Match	99.9%; Score 2349; DB 3; Length 454;
	Best Local Similarity	99.8%; Pred. No. 5.4e-232;
	Matches 439; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATQKALPENVKYGVLDAGSSHTSLYIKWPAEKNDTGVRHQVECRVKGGISKFVQ 60	
Db	15 STQKALPENVKYGVLDAGSSHTSLYIKWPAEKNDTGVRHQVECRVKGGISKFVQ 74	
Qy	61 KYNEIGVLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 120	
Db	75 KYNEIGVLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 134	
Qy	121 SNYPDFQCARITGOEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGG 180	
Db	135 SNYPDFQCARITGOEGAYGMITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGG 194	
Qy	181 ASTQVTFVQNOTIESPDNALQFRLYGKDYNYVTHSEFLCYGKDQALWOKLAKDIOVASNE 240	
Db	195 ASTQVTFVQNOTIESPDNALQFRLYGKDYNYVTHSEFLCYGKDQALWOKLAKDIOVASNE 254	
Qy	241 ILRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPTQFQEIQIGNYQQCHQSILELFNTS 300	
Db	255 ILRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPTQFQEIQIGNYQQCHQSILELFNTS 314	
Qy	301 YCPYSQCAFNGIFLPPLQDGFAGFAFYFVMKFLNLTSEKVSQEKVTEMMKFCQAPWEE 360	
Db	315 YCPYSQCAFNGIFLPPLQDGFAGFAFYFVMKFLNLTSEKVSQEKVTEMMKFCQAPWEE 374	
Qy	361 IKTSYAGVKEKYLSEYCFSGSTVILSLLOGYHFTADSWEHIHFPGIKQSDAGWTILGYML 420	
Db	375 IKTSYAGVKEKYLSEYCFSGSTVILSLLOGYHFTADSWEHIHFPGIKQSDAGWTILGYML 434	
Qy	421 NLTNMIPAEQPLSTPLSHST 440	
Db	435 NLTNMIPAEQPLSTPLSHST 454	
RESULT 5		
AAAY70925		
ID	AAAY70925 standard; protein; 463 AA.	
XX	AC	AAAY70925;
XX	DT	17-AUG-2000 (first entry)
XX	DB	Human soluble CD39 fusion protein construct, IgkappaLsolCD39.
XX	KW	Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; antiarteriosclerotic; antianginal; cerebroprotective; antiarteriosclerotic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig; immunoglobulin kappa.
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label= Leader peptide
FT		/note= "Derived from human immunoglobulin Ig kappa"
FT	Cleavage-site	20..21
FT		/note= "Cleavage site of leader sequence"
FT	Region	21..24
FT		/note= "Residues derived from human interleukin 2 (IL2)"
FT	Protein	25..463
FT		/note= "Human soluble CD39 protein"
XX	PN	WO200023459-A1.
XX	PD	27-APR-2000.
XX	PF	13-OCT-1999;
XX	PF	13-OCT-1999;
PR	16-OCT-1998;	98US-0104585P.
PR	06-NOV-1998;	98US-0107466P.
PR	13-AUG-1999;	99US-0149010P.

XX (IMMV) IMMUNEX CORP.
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 116-118; 122pp; English.
XX
XX The present sequence is the fusion protein construct, IgkappaSolCD39.
CC This construct comprises of the leader peptide from human immunoglobulin
CC IG kappa, linked to the soluble CD39 (solCD39) protein region by few
CC residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase
CC activity and is constructed by removing the N- and C-terminal
CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
CC at relevant concentrations and the ability to block and reverse ADP-
CC induced platelet activation and recruitment, including for inhibiting
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
CC myocardial infarction, coronary artery disease or injury, embolism,
CC atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-
CC associated ischaemic disorders including lung, coronary and cerebral
CC ischaemia, thrombotic disorders including coronary, peripheral and
CC cerebral artery thrombosis, intracardiac and venous thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
SQ Sequence 463 AA;

Query Match 99.9%; Score 2349; DB 3; Length 463;
Best Local Similarity 99.8%; Pred. No. 5.6e-232;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATQNKALPENVKYIGVLDAGSSHTSLYIKKPAEKENDTGVVHVVEECRVKPGIGSKFVQ 60
Db |
24 STQNKALPENVKYIGVLDAGSSHTSLYIKKPAEKENDTGVVHVVEECRVKPGIGSKFVQ 83
QY 61 KVNIEIGVLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 120
Db |
84 KVNIEIGVLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 143
QY 121 SNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRFWSIVPYETNNQTFGALDLGG 180
Db |
144 SNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRFWSIVPYETNNQTFGALDLGG 203
QY 181 ASTQVTFVQNOTTIESPDNALQFRLYGKDVNYVTHSFLCYGKQDALWOKLAKDIQVASNE 240
Db |
204 ASTQVTFVQNOTTIESPDNALQFRLYGKDVNYVTHSFLCYGKQDALWOKLAKDIQVASNE 263
QY 241 ILRDPCHFPGYKVVNVSDLYKTPCTKRFENTLFPQFQEIQIGNYQQCHOSILELFNTS 300
Db |
264 ILRDPCHFPGYKVVNVSDLYKTPCTKRFENTLFPQFQEIQIGNYQQCHOSILELFNTS 323
QY 301 YCPYSQCAFNGIFLPLQDGFAGSAFYVWKFLNLTSEKVSQEKVTEMMKKFCAQPWEE 360
Db |
324 YCPYSQCAFNGIFLPLQDGFAGSAFYVWKFLNLTSEKVSQEKVTEMMKKFCAQPWEE 383
QY 361 IKTSVAGVKEKYLSEYCFSGYVYLSLLQGVHFTADSWEHFTGKIQGSDAGWTLGMYL 420
Db |
384 IKTSVAGVKEKYLSEYCFSGYVYLSLLQGVHFTADSWEHFTGKIQGSDAGWTLGMYL 443
QY 421 NLTNMIPAEQLSTPLSHST 440
Db |
444 NLTNMIPAEQLSTPLSHST 463

RESULT 6

AAV70902
ID AAY70902 standard; protein; 463 AA.
XX
XX AAY70902;
XX
XX 17-AUG-2000 (first entry)
XX
DE Protein encoded by IgkappaSolCD39 construct.
XX
XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticosagulant;
KW coronary ischaemia; vascular occlusion; IgkappaSolCD39 construct.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Igkappa leader sequence"
FT Cleavage-site 20..21
FT Region 21..24
FT /note= "Derived from IL-2"
FT Region 25..463
FT /note= "Soluble portion of CD39"
FT Region 25..32
FT /note= "Derived from solCD39"
XX
XX WO2000023094-A2.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US023641.
XX
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Maliszewski CR, Gayle RB, Marcus AJ;
PI
XX WPI; 2000-339518/29.
DR
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39
PT polypeptides.
XX
XX Claim 6; Page 116-118; 118pp; English.
XX
XX The present sequence is the protein encoded by IgkappaSolCD39 construct.
CC This is used for transient expression of solubleSolCD39 in recombinant
CC cells for determining enzymatic activity and platelet inhibitory activity
CC for each protein product. SolCD39 is used in the treatment of unstable
CC angina, myocardial infarction, stroke, coronary artery disease or injury,
CC atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism,
CC platelet-associated ischaemic disorder including lung ischaemia, coronary
CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke

QY 421 NLTNMIPAEQPLSTPLSHST 440
Db 454 NLTNMIPAEQPLSTPLSHST 473

RESULT 8

AAV70901
ID AAV70901 standard; protein; 473 AA.

AC AAV70901;

DT 17-AUG-2000 (first entry)

DE Protein encoded by Trim 4 construct.

KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pIL2Trim4 variant.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Cleavage-site 26..27

FT Protein 35..473

FT /note= "Soluble portion of CD39"

XX WO200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

PA (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39
PT polypeptides.

PS Example 11; Page 114-116; 118pp; English.

XX The present sequence is the protein encoded by Trim4 construct. pIL2Trim4
CC variant was constructed by removing the human IL2 residues from solCD39
CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
CC human IL2 to the solCD39 coding region results in high levels of both
CC expression and activity in the supernatants of transfected cells. SolCD39
CC is used in the treatment of unstable angina, myocardial infarction,
CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
CC disorder including lung ischaemia, coronary ischaemia and cerebral
CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
CC Soluble CD39 is also useful for preventing thrombus formation or

CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke

SQ Sequence 473 AA;

Query Match 99.9%; Score 2349; DB 3; Length 473;

Best Local Similarity 99.8%; Pred. No. 5.7e-232;

Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKFVQ 60

Db 34 STQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKFVQ 93

QY 61 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 120

Db 94 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 153

QY 121 SNYPDFQGARIIITQEGEGAYGWITINYLKGFQSKTRWFSIVFYETNNQETFGALDLGG 180

Db 154 SNYPDFQGARIIITQEGEGAYGWITINYLKGFQSKTRWFSIVFYETNNQETFGALDLGG 213

QY 181 ASTQVTFVPOQTIESPDNALQFRLYKQDYNVYTHSFLCYGKQDALWQKLAKDIQVASNE 240

Db 214 ASTQVTFVPOQTIESPDNALQFRLYKQDYNVYTHSFLCYGKQDALWQKLAKDIQVASNE 273

QY 241 ILRDPCHFPGYKVVVSDLYKTPCTKRFEMLTLPFQFQFEIQGIGNYQQCHQSILLEFNPS 300

Db 274 ILRDPCHFPGYKVVVSDLYKTPCTKRFEMLTLPFQFQFEIQGIGNYQQCHQSILLEFNPS 333

QY 301 YCPYSQCAFNGIFLPLPQDGFAPSAFYFMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 360

Db 334 YCPYSQCAFNGIFLPLPQDGFAPSAFYFMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 393

QY 361 IKTSYAGVKKYLSEYCFSGTYILSLLLQGVHFTADSWEHIHFHGKIQGSDAGWTGLGYML 420

Db 394 IKTSYAGVKKYLSEYCFSGTYILSLLLQGVHFTADSWEHIHFHGKIQGSDAGWTGLGYML 453

QY 421 NLTNMIPAEQPLSTPLSHST 440

Db 454 NLTNMIPAEQPLSTPLSHST 473

RESULT 9

AAV70923

ID AAV70923 standard; protein; 474 AA.

XX AC AAV70923;

XX DT 17-AUG-2000 (first entry)

XX Human soluble CD39 fusion protein construct, pIL2LTrim3.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..24

FT /label= Leader peptide

FT /note= "Derived from human interleukin 2 (hIL2)"

FT Cleavage-site 24..25

FT /note= "Cleavage site of leader sequence"

FT Protein 36..474

FT /note= "Human soluble CD39 protein"

XX

CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
CC Soluble CD39 is also useful for preventing thrombus formation or
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke
XX
SQ Sequence 474 AA;

Query Match 99.9%; Score 2349; DB 3; Length 474;
Best Local Similarity 99.8%; Pred. No. 5.8e-232;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQ 60
DB 35 STQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQ 94

QY 61 KVEIGIYLTDCMERAREVPRSQHETPVYLGATAGMRLLRMESEELADRLVDVVERSL 120
DB 95 KVEIGIYLTDCMERAREVPRSQHETPVYLGATAGMRLLRMESEELADRLVDVVERSL 154

QY 121 SNYPDFQGARIIITQOEGAGYWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDGG 180
DB 155 SNYPDFQGARIIITQOEGAGYWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDGG 214

QY 181 ASTQVTFVPQNTTIESPDNALQFRLYKQDYNVYTHSFYCYGKQDQALWOKLADIQVASNE 240
DB 215 ASTQVTFVPQNTTIESPDNALQFRLYKQDYNVYTHSFYCYGKQDQALWOKLADIQVASNE 274

QY 241 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQOFEIOGIGNYQCHOSILELFNTS 300
DB 275 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQOFEIOGIGNYQCHOSILELFNTS 334

QY 301 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 360
DB 335 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 394

QY 361 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYML 420
DB 395 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYML 454

QY 421 NLTNMIPAEQPLSTPLSHST 440
DB 455 NLTNMIPAEQPLSTPLSHST 474

RESULT 11
AA70911
ID AA70911 standard; protein; 476 AA.
XX AC AA70911;
XX DT 17-AUG-2000 (first entry)
XX DE Human CD39-L4-1 protein construct.
XX
KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preecclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiatic; vasotropic; thrombolytic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT Region 1..37
FT /note= "Human CD39-L4 protein N-terminal end"
FT Cleavage-site 20..21
FT /note= "Cleavage site of leader sequence"
FT Region 38..476
FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX (IMMV) IMMUNEX CORP.
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 89-91; 122pp; English.
XX
XX The present sequence is a fusion protein construct CD39-L4-1, comprising
XX the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is
XX a secreted apyrase, belonging to the CD39 family. Soluble CD39 is
XX constructed by removing the N- and C-terminal transmembrane domains. It
XX retains the capacity to metabolise ATP and ADP at relevant concentrations
XX and the ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular occlusion, preecclampsia,
XX embolism, platelet-associated ischaemic disorders including lung,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis, intracardiac and venous
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 476 AA;

Query Match 99.9%; Score 2349; DB 3; Length 476;
Best Local Similarity 99.8%; Pred. No. 5.8e-232;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQ 60
DB 37 STQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQ 96

QY 61 KVEIGIYLTDCMERAREVPRSQHETPVYLGATAGMRLLRMESEELADRLVDVVERSL 120
DB 97 KVEIGIYLTDCMERAREVPRSQHETPVYLGATAGMRLLRMESEELADRLVDVVERSL 156

QY 121 SNYPDFQGARIIITQOEGAGYWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDGG 180
DB 157 SNYPDFQGARIIITQOEGAGYWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDGG 216

QY 181 ASTQVTFVPQNTTIESPDNALQFRLYKQDYNVYTHSFYCYGKQDQALWOKLADIQVASNE 240
DB 217 ASTQVTFVPQNTTIESPDNALQFRLYKQDYNVYTHSFYCYGKQDQALWOKLADIQVASNE 276

QY 241 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQOFEIOGIGNYQCHOSILELFNTS 300
DB 277 ILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPPQOFEIOGIGNYQCHOSILELFNTS 336

QY 301 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 360
DB 337 YCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 396

QY 361 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYML 420
DB 395 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFTKIQGSDAGWTGLGYML 454

Db397 IKTSYAGVKEKYLSEYCFSGTYIISLLQLQGVHFTADSWEHIFGIKIQSGDAGWTGLGYML 456

Qy421 NLTNMIPAEQPLSTPLSHST 440

Db457 NLTNMIPAEQPLSTPLSHST 476

RESULT 12

AAAY70888

AAAY70888 standard; protein; 476 AA.

XX

ACAAAY70888;

XX

DT17-AUG-2000 (first entry)

XX

DEProtein encoded by CD39-L4-1 construct.

XX

DESoluble CD39; ADP-induced platelet activation; platelet aggregation;

KWunstable angina; myocardial infarction; stroke; coronary artery disease;

KWatherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;

KWplatelet-associated ischaemic disorder; lung ischaemia; thrombolytic;

KWcerebral ischaemia; thrombotic disorder; coronary artery thrombosis;

KWcerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;

KWperipheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;

KWPE; Pulmonary embolism; transient ischaemic attack; thrombus formation;

KWocclusion; reocclusion; stenosis; restenosis; antianginal; cardiatic;

KWcerabroprotective; antiarteriosclerotic; vasotropic; anticoagulant;

KWcoronary ischaemia; vascular occlusion.

XX

OSHomo sapiens.

OSSynthetic.

XX

XXKey

XXLocation/Qualifiers

XXRegion1..37

FT/note= "Derived from CD39-L4"

FTCleavage-site

FTRegion20..21

FT/note= "Soluble portion of CD39"

FT

XXWO200023094-A2.

XX

XX27-APR-2000.

XX

XX13-OCT-1999; 99WO-US023641.

XX

XX16-OCT-1998; 98US-0104588P.

XX

XX06-NOV-1998; 98US-0107466P.

XX

XX13-AUG-1999; 99US-0149010P.

XX

XX(IMMV) IMMUNEX CORP.

XX(CORR) CORNELL RES FOUND INC.

XX

XXMaliszewski CR, Gayle RB, Marcus AJ;

XX

XXWPI; 2000-338518/29.

XX

XXInhibiting platelet activation and recruitment, useful for treating a

PTmammal suffering from unstable angina, myocardial infarction, stroke,

FTcoronary artery disease or injury, comprises administering soluble CD39

FTpolypeptides.

XX

XXClaim 6; Page 89-91; 118pp; English.

XX

XXThe present sequence is a fusion construct of human soluble CD39 encoded

CCby CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the

CCCD39 family. The fusion construct is used for the expression and activity

CCof soluble CD39 in CHO (chinese hamster ovary) cells. Soluble CD39

CCretains the capacity of wildtype CD39 to metabolise ATP and ADP at

CCphysiologically relevant concentrations as well as the ability to block

CCand reverse ADP-induced platelet activation and recruitment including

CCplatelet aggregation. This is used in the treatment of unstable angina,

CCmyocardial infarction, stroke, coronary artery disease or injury,

CCatherosclerosis, peripheral vascular occlusion, preeclampsia, embolism,

CCplatelet-associated ischaemic disorder including lung ischaemia, coronary

CCischaemia and cerebral ischaemia, thrombotic disorder including coronary

CCartery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,

CCperipheral artery thrombosis, venous thrombosis, thrombosis,

CCcoagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),

CCtransient ischaemic attack. Soluble CD39 is also useful for preventing

CCthrombus formation or reformation, occlusion, reocclusion, stenosis or

CCrestenosis of blood vessels or stroke

XX

XXSequence 476 AA;

XX

XXQuery Match99.9%; Score 2349; DB 3; Length 476;

XXBest Local Similarity99.8%; Pred. No. 5.8e-232;

XXMatches 439; Conservative1; Mismatches0; Indels0; Gaps0;

XX

Qy1ATONKALPENVKYGIIVLDAGSSHTSIYIKVPAEKENDTGVVHVEECRVKFGISKFVQ 60

Db37STONKALPENVKYGIIVLDAGSSHTSIYIKVPAEKENDTGVVHVEECRVKFGISKFVQ 96

Qy61KNEIGIYLTDGCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVVERSL 120

Db97KNEIGIYLTDGCMERAREVIPSQHOETPVYLGATAGMELLRMESEELADRVLDVVVERSL 156

Qy121SNYPFDFQAGARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180

Db157SNYPFDFQAGARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 216

Qy181ASTQVTFVPQNTIESPDNALQPLRYGKDYNNVYTHSFCLYCKDQALWQKLDIQVASNE 240

Db217ASTQVTFVPQNTIESPDNALQPLRYGKDYNNVYTHSFCLYCKDQALWQKLDIQVASNE 276

Qy241ILRDPGFHPGKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQQCHQSILELFWNIS 300

Db277ILRDPGFHPGKVKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQQCHQSILELFWNIS 336

Qy301YCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFLNLTSEKVSQEKYTEMMKFCQAPWEE 360

Db337YCPYSQCAFNGIFLPLQDGFAGSAFYFVWKFLNLTSEKVSQEKYTEMMKFCQAPWEE 396

Qy361IKTSYAGVKEKYLSEYCFSGTYIISLLQLQGVHFTADSWEHIFGIKIQSGDAGWTGLGYML 420

Db397IKTSYAGVKEKYLSEYCFSGTYIISLLQLQGVHFTADSWEHIFGIKIQSGDAGWTGLGYML 456

Qy421NLTNMIPAEQPLSTPLSHST 440

Db457NLTNMIPAEQPLSTPLSHST 476

XX

XXRESULT 13

XXAAAY70914

XXIDAAAY70914 standard; protein; 478 AA.

XX

XXACAAAY70914;

XX

XXDT17-AUG-2000 (first entry)

XX

XXDEHuman soluble CD39 fusion protein construct, pIL2solCD39.

XX

XXSoluble CD39; solCD39; human; apyrase activity; platelet activation;

KWunstable angina; myocardial infarction; stroke; coronary artery disease;

KWatherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;

KWplatelet-associated ischaemic disorder; thrombotic disorder; reocclusion;

KWcoagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

KWthrombus formation; occlusion; stenosis; restenosis; angiogenesis;

KWantianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;

KWcardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX

XXHomo sapiens.

XXSynthetic.

XX

XXKey

XXLocation/Qualifiers

XXRegion1..24

FT/label= Leader_peptide

FT

FT Protein /note= "Derived from human interleukin 2 (hIL2)"
FT 25. .36
FT /label= Mature human interleukin 2
FT /note= "Derived from N-terminal end of human IL2"
FT 37. .39
FT /note= "Linker"
FT 40. .478
FT /note= "Human soluble CD39 protein"
XX WO200023459-A1.
XX
XX 27-APR-2000;
XX 13-OCT-1999; 99WO-US022955.
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
PA (IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX N-PSDB; AAD00207.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX
XX Disclosure; Page 99-101; 12pp; English.
XX
XX The present sequence is a fusion construct pIL2solCD39, comprising the
CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region.
CC having apyrase activity. This produces high levels of solCD39 expression
CC and activity in the transfected cells. Soluble CD39 is constructed by
CC removing the N- and C-terminal transmembrane domains. It retains the
CC capacity to metabolize ATP and ADP at relevant concentrations and the
CC ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
CC embolism, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX
SQ Sequence 478 AA;

Query Match 99.9%; Score 2349; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 5.8e-232;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATONKALPENVKYGLVDAGSHSTSLYIKKPAEKENDTGVVHVVEECRVKGPISKRVQ 60
DB 39 STONKALPENVKYGLVDAGSHSTSLYIKKPAEKENDTGVVHVVEECRVKGPISKRVQ 98
QY 61 KVNIEIGYLTDCMERAREVIPSQHQETPVVLGATAGNRLRMESEELADRLVDVRS 120
DB 99 KVNIEIGYLTDCMERAREVIPSQHQETPVVLGATAGNRLRMESEELADRLVDVRS 158
QY 121 SNYPDFOGARIITGOBEGAGWITINYLKFKSQKTRFWFSIVPYETNNQTFGALDGG 180
DB 159 SNYPDFOGARIITGOBEGAGWITINYLKFKSQKTRFWFSIVPYETNNQTFGALDGG 218
QY 181 ASTQVTFVPQNTTSPDNALQFLRYGKDYNNVYTHSFLCYKQDQALWOKLAKDIQVASNE 240
DB 219 ASTQVTFVPQNTTSPDNALQFLRYGKDYNNVYTHSFLCYKQDQALWOKLAKDIQVASNE 278

QY 241 ILRDPCHPGYKVKVNVSDLYKTCTKRFEMTLFPQFQFQIGNYQCHQSILELFNTS 300
DB 279 ILRDPCHPGYKVKVNVSDLYKTCTKRFEMTLFPQFQFQIGNYQCHQSILELFNTS 338
QY 301 YCPYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEE 360
DB 339 YCPYSQCAFNGIFLPLPQDGFAGFSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEE 398
QY 361 KTSYAGVKKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIKIGQSDAGWTLGYML 420
DB 399 KTSYAGVKKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIKIGQSDAGWTLGYML 458
QY 421 NLTMNIPAEQPLSTPLSHST 440
DB 459 NLTMNIPAEQPLSTPLSHST 478
XX
XX RESULT 14
XX AAY70891
XX ID AAY70891 standard; protein; 478 AA.
XX AC AAY70891;
XX XX
XX DT 17-AUG-2000 (first entry)
XX XX
XX Protein encoded by pIL2sol CD39.
XX Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticosagulant;
KW coronary ischaemia; vascular occlusion.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1. .24 /note= "hIL2 leader sequence"
XX Protein 25. .36 /note= "Mature human IL2"
XX Region 37. .39 /note= "Linker"
XX Protein 40. .478 /note= "SolCD39 protein"
XX
XX WO200023094-A2.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US023641.
XX
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX (IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
XX N-PSDB; AAD00202.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,

PT	coronary artery disease or injury, comprises administering soluble CD39	OS	Homo sapiens.
PT	polypeptides.	XX	
XX		PN	WO200111949-A1.
XX		XX	
PS	Disclosure; Page 99-101; 118pp; English.	PD	22-FEB-2001.
XX		XX	
CC	The present sequence is protein encoded by the coding region of	XX	
CC	pil2solCD39, a fusion construct encoding sol(soluble)CD39 having apyrase	PF	11-AUG-2000; 2000WO-US022060.
CC	activity. Fusion of 12 amino acids from the N-terminus of mature human	XX	
CC	IL2 to the solCD39 coding region results in high levels of both	XX	
CC	expression and activity in the supernatants of transfected cells. This is	PR	13-AUG-1999; 99US-00374586.
CC	used in the treatment of unstable angina, myocardial infarction, stroke,	XX	
CC	coronary artery disease or injury, atherosclerosis, peripheral vascular	XX	
CC	occlusion, pre-eclampsia, embolism, platelet-associated ischaemic disorder	PA	(UYCO) UNIV COLUMBIA NEW YORK.
CC	including lung ischaemia, coronary ischaemia and cerebral ischaemia, a	PI	Pinsky DJ;
CC	thrombotic disorder including coronary artery thrombosis, cerebral artery	XX	
CC	thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous	DR	WPI; 2001-202805/20.
CC	thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),	XX	
CC	pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also	XX	
CC	useful for preventing thrombus formation or reformation, occlusion,	PT	Treating stroke in a subject susceptible to intracranial hemorrhaging and
CC	reocclusion, stenosis or restenosis of blood vessels or stroke	PT	an ischemic disorder, involves administering a CD39 polypeptide which
XX		PT	inhibits ADP-mediated platelet aggregation or leukocyte accumulation.
SQ	Sequence 478 AA;	XX	
		XX	Claim 3; Page 14; 118pp; English.
		CC	The present sequence is the active fragment of human CD39. CD39 or its
		CC	active fragment may be administered to treat or prevent stroke in a
		CC	subject susceptible to intracranial haemorrhaging or an ischaemic
		CC	disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
		CC	or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
		CC	subject. CD39 or its active fragment is useful for treating or preventing
		CC	stroke, thrombotic disorders and ischaemic disorders such as peripheral
		CC	vascular disorder, pulmonary embolus, venous thrombosis, myocardial
		CC	infarction, transient ischaemic attack, unstable angina, reversible
		CC	ischaemic neurological deficit and sickle cell anaemia. It is also useful
		CC	for treating or preventing a stroke disorder in a subject undergoing
		CC	heart surgery, lung surgery, spinal surgery, brain surgery, vascular
		CC	surgery, abdominal surgery, or organ transplantation surgery
		XX	
		SQ	Sequence 439 AA;
			Query Match 99.8%; Score 2348; DB 4; Length 439;
			Best Local Similarity 100.0%; Pred. No. 6.5e-232;
			Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKPVQ 60	Qy	2 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKPVQ 61
Db	39 STONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKPVQ 98	Db	1 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKPVQ 60
Qy	61 KVEIGIVLTCMERAREVIPSQHOETPVYLGATAGNRLRMESEELADRVLDVVERSL 120	Qy	62 VNEIGIVLTCMERAREVIPSQHOETPVYLGATAGNRLRMESEELADRVLDVVERSL 121
Db	99 KVEIGIVLTCMERAREVIPSQHOETPVYLGATAGNRLRMESEELADRVLDVVERSL 158	Db	61 VNEIGIVLTCMERAREVIPSQHOETPVYLGATAGNRLRMESEELADRVLDVVERSL 120
Qy	121 SNYPDFQGARITITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 180	Qy	122 NYPDFQGARITITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 181
Db	159 SNYPDFQGARITITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 218	Db	121 NYPDFQGARITITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 180
Qy	181 ASTQVTFVPQNTIESPDNALQFRLYGKDYNNYTHSFCLCYGKDQALWOKLAKDIQVASNE 240	Qy	182 STQVTFVPQNTIESPDNALQFRLYGKDYNNYTHSFCLCYGKDQALWOKLAKDIQVASNEI 241
Db	219 ASTQVTFVPQNTIESPDNALQFRLYGKDYNNYTHSFCLCYGKDQALWOKLAKDIQVASNE 278	Db	181 STQVTFVPQNTIESPDNALQFRLYGKDYNNYTHSFCLCYGKDQALWOKLAKDIQVASNEI 240
Qy	241 ILRDCPFHFGYKXVNVSDLYKTPCTKPEMTLPQOFEIQIGNYQCHOSILELFNTS 300	Qy	242 LRDCPFHFGYKXVNVSDLYKTPCTKPEMTLPQOFEIQIGNYQCHOSILELFNTS 301
Db	279 ILRDCPFHFGYKXVNVSDLYKTPCTKPEMTLPQOFEIQIGNYQCHOSILELFNTS 338	Db	241 LRDCPFHFGYKXVNVSDLYKTPCTKPEMTLPQOFEIQIGNYQCHOSILELFNTS 300
Qy	301 YCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 360	Qy	302 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 361
Db	339 YCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 398	Db	301 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 360
Qy	361 IKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGLGYML 420	Qy	362 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGLGYMLN 421
Db	399 IKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGLGYML 458	Db	361 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGLGYMLN 420
Qy	421 NLTNMIPAEQPLSTPLSHST 440	Qy	422 LTNMIPAEQPLSTPLSHST 440
Db	459 NLTNMIPAEQPLSTPLSHST 478	Db	421 LTNMIPAEQPLSTPLSHST 439
			RESULT 15
			AAB71918
XX	AAB71918 standard; protein; 439 AA.	XX	
AC		AC	
XX		XX	
XX		XX	
DT	09-MAY-2001 (first entry)	XX	
XX		XX	
DE	Soluble human CD39 polypeptide.	XX	
XX		XX	
KW	Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;	XX	
KW	stroke; thrombotic disorder; ischaemic disorder.	XX	
XX		XX	

Search completed: March 7, 2005, 13:13:08
Job time : 72.9896 secs

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Result No.	Query			Description		
	Score	Match	ID	DB	Length	ID
1	2352	100.0	464	9	US-09-835-147-27	Sequence 27, Appl
2	2349	99.9	454	9	US-09-835-147-6	Sequence 6, Appl
3	2349	99.9	463	9	US-09-835-147-30	Sequence 30, Appl
4	2349	99.9	473	9	US-09-835-147-29	Sequence 29, Appl
5	2349	99.9	474	9	US-09-835-147-28	Sequence 28, Appl
6	2349	99.9	476	9	US-09-835-147-3	Sequence 3, Appl
7	2349	99.9	478	9	US-09-835-147-8	Sequence 8, Appl
8	2348	99.8	439	9	US-09-374-586-2	Sequence 2, Appl
9	2348	99.8	487	9	US-09-835-147-26	Sequence 26, Appl
10	2348	99.8	502	13	US-10-092-063-38	Sequence 38, Appl
11	2348	99.8	510	9	US-09-835-147-2	Sequence 2, Appl
12	2348	99.8	510	9	US-09-374-586-1	Sequence 1, Appl
13	2348	99.8	510	10	US-09-781-796B-1	Sequence 1, Appl

QY	1	ATONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	60
Db	25	ATONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	84
QY	61	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	120
Db	85	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	144
QY	121	SNYPDFQGARITGOEGAGYMWITINYLKGFQSKTRWFSIVPYETNNQTFGALDLGG	180
Db	145	SNYPDFQGARITGOEGAGYMWITINYLKGFQSKTRWFSIVPYETNNQTFGALDLGG	204
QY	181	ASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWOKLAKDIQVASNE	240
Db	205	ASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWOKLAKDIQVASNE	264
QY	241	ILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFNTS	300
Db	265	ILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFNTS	324
QY	301	YCPYSQCAFNGIFLPPLOGDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE	360
Db	325	YCPYSQCAFNGIFLPPLOGDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE	384
QY	361	IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWTLGYML	420
Db	385	IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWTLGYML	444
QY	421	NLTNMPAEQPLSTPLSHST	440
Db	445	NLTNMPAEQPLSTPLSHST	464
RESULT 2			
US-09-835-147-6			
; Sequence 6, Application US/09835147			
; Patent No. US20020002277A1			
GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 6			
; LENGTH: 454			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-6			
Query Match 99.9%; Score 2349; DB 9; Length 454;			
Best Local Similarity 99.8%; Pred. No. 8.9e-210;			
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
US-09-835-147-6			
QY	1	ATONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	60
Db	15	STONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	74

QY	61	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	120
Db	75	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	134
QY	121	SNYPDFQGARITGOEGAGYMWITINYLKGFQSKTRWFSIVPYETNNQTFGALDLGG	180
Db	135	SNYPDFQGARITGOEGAGYMWITINYLKGFQSKTRWFSIVPYETNNQTFGALDLGG	194
QY	181	ASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWOKLAKDIQVASNE	240
Db	195	ASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWOKLAKDIQVASNE	254
QY	241	ILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFNTS	300
Db	255	ILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIOGIGNYQOCHQSILELFNTS	314
QY	301	YCPYSQCAFNGIFLPPLOGDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE	360
Db	315	YCPYSQCAFNGIFLPPLOGDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE	374
QY	361	IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWTLGYML	420
Db	375	IKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKIQSDAGWTLGYML	434
QY	421	NLTNMPAEQPLSTPLSHST	440
Db	435	NLTNMPAEQPLSTPLSHST	454
RESULT 3			
US-09-835-147-30			
; Sequence 30, Application US/09835147			
; Patent No. US20020002277A1			
GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 30			
; LENGTH: 463			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-30			
Query Match 99.9%; Score 2349; DB 9; Length 463;			
Best Local Similarity 99.8%; Pred. No. 9.1e-210;			
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	60
Db	24	STONKALPENVKYIGVILDAGSSHTSLYIYKWPAAKENDTGVVHVQVEECRVKPGISKVFQ	83
QY	61	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	120
Db	84	KNEIGIYLTDTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	143

QY 121 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180
DB 144 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 203
QY 181 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 240
DB 204 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 263
QY 241 ILRDPCHFPGYKVVNVSDLYKTPCTKRPFWMLPFOQFEIIGIGNYQOCHQSIILELFNTS 300
DB 264 ILRDPCHFPGYKVVNVSDLYKTPCTKRPFWMLPFOQFEIIGIGNYQOCHQSIILELFNTS 323
QY 301 YCPYSQCAFNGIFLPPLQDGFAGFSAFYFVWKFNLNTSEKVSQEKVTENMKKFCAPWEE 360
DB 324 YCPYSQCAFNGIFLPPLQDGFAGFSAFYFVWKFNLNTSEKVSQEKVTENMKKFCAPWEE 383
QY 361 IKTSVAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIHFHFIKIQSGDAGWTLYYML 420
DB 384 IKTSVAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIHFHFIKIQSGDAGWTLYYML 443
QY 421 NLTNMIPAEQPLSTPLSHST 440
DB 444 NLTNMIPAEQPLSTPLSHST 463

RESULT 4

US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 99.9%; Score 2349; DB 9; Length 473;
Best Local Similarity 99.8%; Pred. No. 9.4e-210;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATONKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFPVQ 60
DB 34 STONKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFPVQ 93
QY 61 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVVERSL 120
DB 94 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVVERSL 153
QY 121 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180
DB 154 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 213

QY 181 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 240
DB 214 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 273
QY 241 ILRDPCHFPGYKVVNVSDLYKTPCTKRPFWMLPFOQFEIIGIGNYQOCHQSIILELFNTS 300
DB 274 ILRDPCHFPGYKVVNVSDLYKTPCTKRPFWMLPFOQFEIIGIGNYQOCHQSIILELFNTS 333
QY 301 YCPYSQCAFNGIFLPPLQDGFAGFSAFYFVWKFNLNTSEKVSQEKVTENMKKFCAPWEE 360
DB 334 YCPYSQCAFNGIFLPPLQDGFAGFSAFYFVWKFNLNTSEKVSQEKVTENMKKFCAPWEE 393
QY 361 IKTSVAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIHFHFIKIQSGDAGWTLYYML 420
DB 394 IKTSVAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIHFHFIKIQSGDAGWTLYYML 453
QY 421 NLTNMIPAEQPLSTPLSHST 440
DB 454 NLTNMIPAEQPLSTPLSHST 473
RESULT 5
US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 99.9%; Score 2349; DB 9; Length 474;
Best Local Similarity 99.8%; Pred. No. 9.5e-210;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATONKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFPVQ 60
DB 35 STONKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFPVQ 94
QY 61 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVVERSL 120
DB 95 KVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRVLDVVVERSL 154
QY 121 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 180
DB 155 SNYPDFQARIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGG 214
QY 181 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 240
DB 215 ASTQVTFVPOQNTIESPQNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNE 274


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QY 241 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 300
Db 275 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 334
QY 301 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 360
Db 335 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 394
QY 361 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIGSDAGWTLGYML 420
Db 395 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIGSDAGWTLGYML 454
QY 421 NLTNMIPAEQPLSTPLSHST 440
Db 455 NLTNMIPAEQPLSTPLSHST 474

RESULT 6
US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 476
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-3

Query Match 99.9%; Score 2349; DB 9; Length 476;
Best Local Similarity 99.8%; Pred. No. 9.5e-210;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATONKALPENVKYGIIVLDAGSSHTSLYIYKWPAREKENDTGVVHQBECRVKGPISKFVQ 60
Db 37 STQNKALPENVKYGIIVLDAGSSHTSLYIYKWPAREKENDTGVVHQBECRVKGPISKFVQ 96
QY 61 KNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 120
Db 97 KNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 156
QY 121 SNYPDFQGARITIQEERAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 180
Db 157 SNYPDFQGARITIQEERAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 216
QY 181 ASTQVTFVPQNTIESPDNALQFLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIOVASNE 240
Db 217 ASTQVTFVPQNTIESPDNALQFLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIOVASNE 276
QY 241 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 300
Db 277 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 336
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QY 301 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 360
Db 337 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 396
QY 361 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIGSDAGWTLGYML 420
Db 397 IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIGSDAGWTLGYML 456
QY 421 NLTNMIPAEQPLSTPLSHST 440
Db 457 NLTNMIPAEQPLSTPLSHST 476

RESULT 7
US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-8

Query Match 99.9%; Score 2349; DB 9; Length 478;
Best Local Similarity 99.8%; Pred. No. 9.6e-210;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATONKALPENVKYGIIVLDAGSSHTSLYIYKWPAREKENDTGVVHQBECRVKGPISKFVQ 60
Db 39 STQNKALPENVKYGIIVLDAGSSHTSLYIYKWPAREKENDTGVVHQBECRVKGPISKFVQ 98
QY 61 KNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 120
Db 99 KNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 158
QY 121 SNYPDFQGARITIQEERAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 180
Db 159 SNYPDFQGARITIQEERAGYGTITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGG 218
QY 181 ASTQVTFVPQNTIESPDNALQFLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIOVASNE 240
Db 219 ASTQVTFVPQNTIESPDNALQFLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIOVASNE 278
QY 241 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 300
Db 279 ILRDCPCHPGYKVVVNSDLYKTPCTKRFEMTLPPQOEIOGIGNYQOCHOSILELNTS 338
QY 301 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 360
Db 339 YCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKFCAQPWEE 398
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QY 361 IKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYML 420
Db 399 IKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYML 458
QY 421 NLTNMIPAEQPLSTPLSHST 440
Db 459 NLTNMIPAEQPLSTPLSHST 478

RESULT 8
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Plisky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 99.8%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 1e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TONKALPENVKYIGIVLDAGSSHTSLIYKPAEKENDTGVVHQBECRVKGGISKFVQK 61
Db 1 TONKALPENVKYIGIVLDAGSSHTSLIYKPAEKENDTGVVHQBECRVKGGISKFVQK 60

QY 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 121
Db 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 120

QY 122 NYPDFQAGRIITGOEAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 181
Db 121 NYPDFQAGRIITGOEAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 180

QY 182 STQTVFVQNTIESPDNALQRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 241
Db 181 STQTVFVQNTIESPDNALQRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 240

QY 242 LRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTSY 301
Db 241 LRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTSY 300

QY 302 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 361
Db 301 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 360

QY 362 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYMLN 421
Db 361 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYMLN 420

QY 422 LTNMIPAEQPLSTPLSHST 440
Db 421 LTNMIPAEQPLSTPLSHST 439

RESULT 9
US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 99.8%; Score 2348; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.2e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TONKALPENVKYIGIVLDAGSSHTSLIYKPAEKENDTGVVHQBECRVKGGISKFVQK 61
Db 49 TONKALPENVKYIGIVLDAGSSHTSLIYKPAEKENDTGVVHQBECRVKGGISKFVQK 108

QY 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 121
Db 109 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 168

QY 122 NYPDFQAGRIITGOEAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 181
Db 169 NYPDFQAGRIITGOEAGYMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 228

QY 182 STQTVFVQNTIESPDNALQRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 241
Db 229 STQTVFVQNTIESPDNALQRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 288

QY 242 LRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTSY 301
Db 289 LRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHQSILELFTSY 348

QY 302 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 361
Db 349 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 408

QY 362 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYMLN 421
Db 409 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIFIGIKIQSDAGWTGLYMLN 468

QY 422 LTNMIPAEQPLSTPLSHST 440
Db 469 LTNMIPAEQPLSTPLSHST 487

RESULT 10
US-09-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31			; PRIOR APPLICATION NUMBER: US 60/107,466		
; PRIOR FILING DATE: 1998-11-06			; PRIOR FILING DATE: 1998-11-06		
; PRIOR FILING DATE: 1999-07-16			; PRIOR FILING DATE: 1999-08-13		
; PRIOR FILING DATE: 1999-07-16			; PRIOR FILING DATE: 1999-08-13		
; PRIOR FILING DATE: 1999-07-09			; PRIOR FILING DATE: 1999-10-13		
; PRIOR FILING DATE: 1999-07-09			; NUMBER OF SEQ ID NOS: 31		
; PRIOR FILING DATE: 1999-03-19			; SOFTWARE: Patent in Ver. 2.0		
; PRIOR FILING DATE: 1999-03-19			; SEQ ID NO 2		
; PRIOR FILING DATE: 1999-02-04			; LENGTH: 510		
; PRIOR FILING DATE: 1999-02-04			; TYPE: PRT		
; PRIOR FILING DATE: 1998-07-24			; ORGANISM: Homo sapiens		
; PRIOR FILING DATE: 1998-07-24			; ORGANISM: Homo sapiens		
; PRIOR FILING DATE: 1998-07-16			; US-09-835-147-2		
; NUMBER OF SEQ ID NOS: 39			; Query Match		
; SOFTWARE: Patent in Ver. 2.0			; Best Local Similarity 100.0%; Pred. No. 1.3e-209;		
; SEQ ID NO 38			; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
; LENGTH: 502					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; US-10-092-063-38					
Query Match			99.8%; Score 2348; DB 13; Length 502;		
Best Local Similarity 100.0%; Pred. No. 1.3e-209;					
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2	TQNKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQK 61			
DB	38	TQNKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKVFQK 97			
QY	62	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSL 121			
DB	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVVERSL 157			
QY	122	NYPFDFQARIITQOEGAYGMITINYLKGFQKTRFWSIVPYETNNQETFGALDLGGA 181			
DB	158	NYPFDFQARIITQOEGAYGMITINYLKGFQKTRFWSIVPYETNNQETFGALDLGGA 217			
QY	182	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKQKQALWOKLAKDIQVASNEI 241			
DB	218	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKQKQALWOKLAKDIQVASNEI 277			
QY	242	LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFNTSY 301			
DB	278	LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFNTSY 337			
QY	302	CPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 361			
DB	338	CPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397			
QY	362	KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTLGYMLN 421			
DB	398	KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTLGYMLN 457			
QY	422	LTNMIPAEQPLSTPLSHST 440			
DB	458	LTNMIPAEQPLSTPLSHST 476			
RESULT 11			US-09-835-147-2		
; Sequence 2, Application US/09835147			; Sequence 1, Application US/09374586		
; Patent No. US2002002277A1			; Patent No. US20020138858A1		
; GENERAL INFORMATION:			; GENERAL INFORMATION:		
; APPLICANT: Maliszewski, Charles R.			; APPLICANT: Pinsky, David J.		
; APPLICANT: Price, Virginia L.			; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND		
; APPLICANT: Gimpel, Steven D.			; TITLE OF INVENTION: ISCHEMIC DISORDERS		
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			; FILE REFERENCE: 0575/59167		
; FILE REFERENCE: 2879-US			; CURRENT APPLICATION NUMBER: US/09/374,586		
; CURRENT APPLICATION NUMBER: US/09/835,147			; CURRENT FILING DATE: 1999-08-13		
; CURRENT FILING DATE: 2001-04-13			; NUMBER OF SEQ ID NOS: 2		
; PRIOR APPLICATION NUMBER: US 60/104,585			; SOFTWARE: Patent in Ver. 2.1		
; PRIOR FILING DATE: 1998-10-16			; SEQ ID NO 1		
			; LENGTH: 510		
			; TYPE: PRT		
			; ORGANISM: HOMO-SAPIEN		
			; US-09-374-586-1		
Query Match			99.8%; Score 2348; DB 9; Length 510;		
Best Local Similarity 100.0%; Pred. No. 1.3e-209;					
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

QY 2 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 61
DB 38 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 97
QY 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 121
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 157
QY 122 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 181
DB 158 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 182 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 241
DB 218 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 277
QY 242 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 301
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 337
QY 302 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 361
DB 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 362 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKIQSDAGWTLYMLN 421
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKIQSDAGWTLYMLN 457
QY 422 LTNMIPAEQPLSTPLSHST 440
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 13

US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US2003040094A1
; GENERAL INFORMATION:
; APPLICANT: BRAUDIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 99.8%; Score 2348; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-209; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 0;
QY 2 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 61
DB 38 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 97
QY 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 121

DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 157
QY 122 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 181
DB 158 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 182 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 241
DB 218 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 277
QY 242 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 301
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 337
QY 302 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 361
DB 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 362 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKIQSDAGWTLYMLN 421
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFIGIKIQSDAGWTLYMLN 457
QY 422 LTNMIPAEQPLSTPLSHST 440
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 14

US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 99.8%; Score 2348; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-209; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 0;
QY 2 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 61
DB 38 TONKALPENVKYGVLDAGSSHTSLYIYKPAEKENDTGTVHQVEECRVKGFISKFVOK 97
QY 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 121
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLDVVERSUS 157
QY 122 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 181
DB 158 NYPDFQOARITGOEGAYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 182 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 241
DB 218 STQTVFVQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDQALWKLAKDIQVASNEI 277
QY 242 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 301
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKREMTLPFOQFEIOGIGNYQOCHQSILELFTSY 337

QY

302

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361

Db

338

CFYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI

397

QY

362

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421

Db

398

KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTILGYMLN

457

QY

422

LTNMIPAEQPLSTPLSHST

440

Db

458

LTNMIPAEQPLSTPLSHST

476

Search completed: March 7, 2005, 14:12:46

Job time : 54.6189 secs

QY

304

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Db

340

YSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI

399

QY

364

SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTILGYMLN

423

Db

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QY

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440

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460

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476

RESULT 15

US-09-835-147-4

; Sequence 4, Application US/09835147

; Patent No. US2002002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39

; NAME/KEY: VARIANT

; LOCATION: (39)

; OTHER INFORMATION: Any amino acid, preferably Cys or Ser

US-09-835-147-4

Query Match

97.5%

Score 2294;

DB 9;

Length 476;

Best Local Similarity

98.6%

Pred. No. 1.3e-204;

Matches 431;

Conservative 0;

Mismatches 2;

Indels 4;

Gaps 1;

QY

8

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63

Db

40

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99

QY

64

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123

Db

100

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QY

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183

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219

QY

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243

Db

220

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QY

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303

Db

280

DPCHPGYKVVNVDLYKTKTCTKREMTLPFQOFEIQGIGNYQOCHOSILELFTSYCP

339

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 18.7509 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-27_COPY_25_464

Perfect score: 2352
Sequence: 1 ATQNKALPENVKYIGVLDAG.....NLTNMIPAEQPLSTPLSHST 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	99.8	502	4	US-09-557-800C-55
2	2348	99.8	502	4	US-09-370-625A-38
3	2348	99.8	510	3	US-08-930-921-1
4	2348	99.8	510	4	US-09-781-796C-1
5	910.5	38.7	529	3	US-09-240-639-4
6	910.5	38.7	529	4	US-09-908-510A-4
7	910.5	38.7	529	4	US-09-905-744B-4
8	910.5	38.7	529	4	US-10-107-660-4
9	910.5	38.7	529	4	US-10-107-576-4
10	910.5	38.7	529	4	US-09-905-732B-4
11	910.5	38.7	529	4	US-09-923-304-4
12	910.5	38.7	529	4	US-09-949-016-6049
13	910.5	38.7	529	4	US-09-905-743B-4
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15	865	36.8	479	4	US-09-949-016-11559
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17	803	34.1	153	3	US-09-240-639-13
18	803	34.1	153	4	US-09-908-510A-13
19	803	34.1	153	4	US-09-905-744B-13
20	803	34.1	153	4	US-10-107-660-13
21	803	34.1	153	4	US-10-107-576-13
22	803	34.1	153	4	US-09-905-732B-13
23	803	34.1	153	4	US-09-905-743B-13
24	604	25.7	154	3	US-09-240-639-14
25	604	25.7	154	4	US-09-908-510A-14
26	604	25.7	154	4	US-09-905-744B-14
27	604	25.7	154	4	US-10-107-660-14

28	604	25.7	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	25.7	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	25.7	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	18.8	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	18.8	153	4	US-09-908-510A-15	Sequence 15, Appl
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36	442.5	18.8	153	4	US-09-905-732B-15	Sequence 15, Appl
37	442.5	18.8	153	4	US-09-905-743B-15	Sequence 15, Appl
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39	421.5	17.9	462	4	US-09-129-112-15	Sequence 15, Appl
40	417.5	17.8	150	3	US-09-240-639-16	Sequence 16, Appl
41	417.5	17.8	150	4	US-09-908-510A-16	Sequence 16, Appl
42	417.5	17.8	150	4	US-09-905-744B-16	Sequence 16, Appl
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44	417.5	17.8	150	4	US-10-107-576-16	Sequence 16, Appl
45	417.5	17.8	150	4	US-09-905-732B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 99.8%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	98	VNEIGVILTCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
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Db	158	NYPDFQAGARIITGOEBGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	217
Qy	182	STQVTFVPOQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQVASNEI	241
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Qy	242	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	301
Db	278	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	337
Qy	302	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	361
Db	338	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	397
Qy	362	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	421
Db	398	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	457
Qy	422	LTNMIPABQPLSTPLSHST	440
Db	458	LTNMIPABQPLSTPLSHST	476
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US-09-370-625A-38			
; Sequence 38, Application US/09370625A			
; Patent No. 6600032			
; GENERAL INFORMATION:			
; APPLICANT: Ford, John			
; APPLICANT: Mulero, Julio			
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES			
; FILE REFERENCE: 28110/35908			
; CURRENT APPLICATION NUMBER: US/09/370,625A			
; PRIOR FILING DATE: 1999-08-09			
; PRIOR APPLICATION NUMBER: PCT/US99/16180			
; PRIOR FILING DATE: 1999-07-16			
; PRIOR APPLICATION NUMBER: 09/350,836			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR APPLICATION NUMBER: 09/273,447			
; PRIOR FILING DATE: 1999-03-19			
; NUMBER OF SEQ ID NOS: 39			
; SOFTWARE: PatehtIn Ver. 2.0			
; SEQ ID NO 38			
; LENGTH: 502			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-370-625A-38			
Query Match 99.8%; Score 2348; DB 4; Length 502;			
Best Local Similarity 100.0%; Pred. No. 4,1e-244;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKPGISKFVOK	61
Db	38	TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKPGISKFVOK	97
Qy	62	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEBELADRVLDVVERSL	121
Db	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEBELADRVLDVVERSL	157
Qy	122	NYPDFQAGARIITGOEBGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	181
Db	158	NYPDFQAGARIITGOEBGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	217
Qy	182	STQVTFVPOQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQVASNEI	241
Db	218	STQVTFVPOQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQVASNEI	277
Qy	242	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	301
Db	278	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	337
Qy	302	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	361
Db	338	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	397
Qy	362	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	421
Db	398	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	457
Qy	422	LTNMIPABQPLSTPLSHST	440
Db	458	LTNMIPABQPLSTPLSHST	476
RESULT 3			
US-08-930-921-1			
; Sequence 1, Application US/08930921B			
; Patent No. 6287837			
; GENERAL INFORMATION:			
; APPLICANT: BEAUDOIN, Adrien R.			
; APPLICANT: SEVIGNY, Jean			
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION			
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT			
; TITLE OF INVENTION: TECHNOLOGY			
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEADODIN			
; CURRENT APPLICATION NUMBER: US/08/930,921B			
; EARLIER FILING DATE: 1998-01-02			
; EARLIER APPLICATION NUMBER: PCT/CA96/00223			
; EARLIER FILING DATE: 1996-04-10			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 510			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: Description of Unknown Organism: unknown			
US-08-930-921-1			
Query Match 99.8%; Score 2348; DB 3; Length 510;			
Best Local Similarity 100.0%; Pred. No. 4.2e-244;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	TOKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKPGISKFVOK	61
Db	38	TOKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKPGISKFVOK	97
Qy	62	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEBELADRVLDVVERSL	121
Db	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEBELADRVLDVVERSL	157
Qy	122	NYPDFQAGARIITGOEBGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	181
Db	158	NYPDFQAGARIITGOEBGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	217
Qy	182	STQVTFVPOQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKLAKDIQVASNEI	241
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Qy	242	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	301
Db	278	LRDPCFHPGYKKVNVNVDLYKTPCTKRFEMTLPPQOFEIQQIGNYQOCHOSIILELFTSY	337
Qy	302	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	361
Db	338	CPYSQCAFNGIFLPPLOQDGFAGFAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI	397
Qy	362	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	421
Db	398	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN	457
Qy	422	LTNMIPABQPLSTPLSHST	440
Db	458	LTNMIPABQPLSTPLSHST	476

RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6300284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEROF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 99.8%; Score 2348; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.2e-244;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGTVVHVQVECRVKPGISKFVQK 61
Db 38 TQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGTVVHVQVECRVKPGISKFVQK 97

Qy 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 121
Db 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 157

Qy 122 NYPDFQAGARIITGOEAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 181
Db 158 NYPDFQAGARIITGOEAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 217

Qy 182 STQTVFVQNOTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAKDIQVASNEI 241
Db 218 STQTVFVQNOTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAKDIQVASNEI 277

Qy 242 LRDPCHFPGYKKNVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 301
Db 278 LRDPCHFPGYKKNVNSDLYKTPCTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFTSY 337

Qy 302 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 361
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397

Qy 362 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 421
Db 398 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457

Qy 422 LTNMIPAEQPLTSLHST 440
Db 458 LTNMIPAEQPLTSLHST 476

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 38.7%; Score 910.5; DB 3; Length 529;
Best Local Similarity 41.5%; Pred. No. 5.5e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 3 QNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGTVVHVQVECRVKPGISKFVQK 62
Db 47 KOEVLPPGLKXIGVLDAGSSRTTVYVQWPAEKENNTGVWSQTFKCSVKSGSISYGNP 106

Qy 63 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSLN 122
Db 107 QDVPRAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166

Qy 123 YPDFQAGARIITGOEAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 182
Db 167 QPDFRGAQIISGQEGYGMITANLYMGNFLEKNLWHMVV--HPHGVETTGALDLGGA 224

Qy 183 TQTVFVQNOTIESPDNALQFRLYGKDYNYVTHSFLCYGKQDQALWQKLAKDIQVA-SNEI 241
Db 225 TQISFVAGEXKMDLNTSDIMQVSLYGVYVTLYTHSFQCYGRNEAEKFLAMLLQNSPTKNH 284

Qy 242 LRDPCHFPGYKKNVNSDLYKTPCT--KRFEMTLPFQOFEIQGIGNYQOCHQSILELFT 299
Db 285 LTNPCYPRDYSISFTMGHVFDSLCTVDPQRPESYNPNVDITFEGTGDPSLCKEKVASIFDF 344

Qy 300 SYC-PYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPW 358
Db 345 KACHDQETCSGDPGVYQKIKGPFVAFAGFYVYASALNL--SGSFLDFTNSSTWPCSNW 403

Qy 359 BEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYG 418
Db 404 SOLPLLLPKPDEVYARSVCFSANYIYHLFVNGYKFTETWPIIHFEKVGNSIAWSLGY 463

Qy 419 MLNLTNMPAEQPL 432
Db 464 MSLTNQIPAESPL 477

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-510A-4

Db	167	QPTDFRGAQLISQ	BEGVGYMITANLYMGNFLEKNLWHMWV--HPHGVETTTGALDLGGAS	224
Qy	183	TQVTFVFPQNTIES	PDNALQFRLYGKDYNYVTHSFLCYGKQOALWQKLAKDIQVA-SNEI	241
Db	225	TQISFVAGERKMDL	NTSDIMQVSLYGYVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
Qy	242	LRDPCFHPGYKKV	NVNSDLYKTPCT--KRFEMTLPFQOFEIQIGNYQQCHOSILELNT	299
Db	285	LTNPCYPRDYSIS	FTMGHVDFSLCTVDQRPESYNPNNDVITPEGTGDPSLCKEKVASIFDF	344
Qy	300	SYC-PYSOCAPNGI	FLPPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMMKKFCAQPW	358
Db	345	KACHDOETCSF	DGVQPKIGPFAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403
Qy	359	BEIKTSYAGVKE	KYLYSEYCFSGTYILSLLOQVHFTADSWEHIFIGIKQSDAGWTIGY	418
Db	404	SQPLPALLPKF	DEVYARSYCFSANIYIHLFVNGYKTEETWPIHPEKEVGNSSIAWSLGY	463
Qy	419	MLNLTMIPAEQPL	432	
Db	464	MLSLTNQIPAESPL	477	
RESULT 8				
US-10-107-660-4				
; Sequence 4, Application US/10107660				
; Patent No. 6780977				
; GENERAL INFORMATION:				
; APPLICANT: Chadwick, Brian Paul				
; APPLICANT: Frischauf, Anna-Maria				
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE				
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS				
; FILE REFERENCE: 9598-066				
; CURRENT APPLICATION NUMBER: US/10/107,660				
; CURRENT FILING DATE: 2002-03-27				
; PRIOR APPLICATION NUMBER: US/09/240,639				
; PRIOR FILING DATE: 1998-01-29				
; NUMBER OF SEQ ID NOS: 29				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 4				
; LENGTH: 529				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-10-107-660-4				
Query Match 38.7%; Score 910.5; DB 4; Length 529;				
Best Local Similarity 41.5%; Pred. No. 5.5e-89;				
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;				
Qy	3	QNKALPENVKYGI	VLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	62
Db	47	KQEVLPGLKYGI	VLVDAGSSRTTYYVQWPAEKENNTGVVSQTFKCSVKGSGISSYGNP	106
Qy	63	NEIGYILTCMERAREV	IPRSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN	122
Db	107	QDVPRAFECQVKV	QVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS	166
Qy	123	YPDFQAGRIITQGE	BAGYGMITINYLKFSQKTRWFSIVPYETNNQETFGALDLGGAS	182
Db	167	QPFDFRGAQLISQ	EEGVGYITANLYLMGNFLEKNLWHMWV--HPHGVETTTGALDLGGAS	224
Qy	183	TQVTFVFPQNTIES	PDNALQFRLYGKDYNYVTHSFLCYGKQOALWQKLAKDIQVA-SNEI	241
Db	225	TQISFVAGERKMDL	NTSDIMQVSLYGYVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
Qy	242	LRDPCFHPGYKKV	NVNSDLYKTPCT--KRFEMTLPFQOFEIQIGNYQQCHOSILELNT	299
Db	285	LTNPCYPRDYSIS	FTMGHVDFSLCTVDQRPESYNPNNDVITPEGTGDPSLCKEKVASIFDF	344
Qy	300	SYC-PYSOCAPNGI	FLPPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMMKKFCAQPW	358
Db	345	KACHDOETCSF	DGVQPKIGPFAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403

Query Match	38.7%;	Score 910.5;	DB 4;	Length 529;
Best Local Similarity	41.5%;	Pred. No. 5.5e-89;		
Matches 180;	Conservative	79;	Mismatches 168;	Indels 7; Gaps 5;
QY	3	QNKALPENVKYGVILV	DAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	62
Db	47	KQEVLPGLKYGVILV	DAGSSRTTYYVQWPAEKENNTGVVSQTFKCSVKGSGISSYGNP	106
QY	63	NEIGYILTCMERAREV	IPRSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN	122
Db	107	QDVPRAFECQVKGVQ	VPVSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS	166
QY	123	YPDFQAGRIITQGE	BAGYGMITINYLKFSQKTRWFSIVPYETNNQETFGALDLGGAS	182
Db	167	QPFDFRGAQLISQ	EEGVGYITANLYLMGNFLEKNLWHMWV--HPHGVETTTGALDLGGAS	224
QY	183	TQVTFVFPQNTIES	PDNALQFRLYGKDYNYVTHSFLCYGKQOALWQKLAKDIQVA-SNEI	241
Db	225	TQISFVAGERKMDL	NTSDIMQVSLYGYVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
QY	242	LRDPCFHPGYKKV	NVNSDLYKTPCT--KRFEMTLPFQOFEIQIGNYQQCHOSILELNT	299
Db	285	LTNPCYPRDYSIS	FTMGHVDFSLCTVDQRPESYNPNNDVITFEGTGDPSLCKEKVASIFDF	344
QY	300	SYC-PYSOCAPNGI	FLPPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMMKKFCAQPW	358
Db	345	KACHDOETCSF	DGVQPKIGPFAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403
QY	359	EEIKTSYAGVKE	LYSEYCFSGTYILSLLOQVHFTADSWEHIFIGIKQSDAGWTIGY	418
Db	404	SQPLPALLPKF	DEVYARSYCFSANIYIHLFVNGYKFTBETWPQIHFEKEVGNSSIAWSLGY	463
QY	419	MLNLTMIPAEQPL	432	
Db	464	MLSLTNQIPAESPL	477	
RESULT 7				
US-09-905-744B-4				
; Sequence 4, Application US/09905744B				
; Patent No. 6780410				
; GENERAL INFORMATION:				
; APPLICANT: Chadwick, Brian Paul				
; APPLICANT: Frischauf, Anna Maria				
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND				
; TITLE OF INVENTION: ACIDS				
; FILE REFERENCE: 28110/36120A				
; CURRENT APPLICATION NUMBER: US/09/905,744B				
; CURRENT FILING DATE: 2001-07-13				
; PRIOR APPLICATION NUMBER: 09/240,639				
; PRIOR FILING DATE: 1999-01-29				
; NUMBER OF SEQ ID NOS: 32				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 4				
; LENGTH: 529				
; TYPE: PRT				
; ORGANISM: Homo Sapiens				
US-09-905-744B-4				
Query Match	38.7%;	Score 910.5;	DB 4;	Length 529;
Best Local Similarity	41.5%;	Pred. No. 5.5e-89;		
Matches 180;	Conservative	79;	Mismatches 168;	Indels 7; Gaps 5;
QY	3	QNKALPENVKYGVILV	DAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	62
Db	47	KQEVLPGLKYGVILV	DAGSSRTTYYVQWPAEKENNTGVVSQTFKCSVKGSGISSYGNP	106
QY	63	NEIGYILTCMERAREV	IPRSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN	122
Db	107	QDVPRAFECQVKGVQ	VPVSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS	166
QY	123	YPDFQAGRIITQGE	BAGYGMITINYLKFSQKTRWFSIVPYETNNQETFGALDLGGAS	182

QY 359 BEIKTSYAGVKEKYLSEYCFSGTVILSLLQGYHTADSWHIIHFQIKQSDAGWTGLY 418
Db 404 SOLPLLLPKPDEVYARSYCFGSANYIYHLFVNGYKFTETWPIHFKEVGNSSIAWSLGY 463
QY 419 MLNLTNMIAPAEQPL 432
Db 464 MSLTNQIPAESPL 477

RESULT 9

US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4

Query Match 38.7%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 5.5e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 3 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKFKVQKV 62
Db 47 KQEVLPGLKYGIIVLDAGSSRTTVYVQWPAKENNTGVVSGTFCVSKVSGISSYGNP 106
QY 63 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 122
Db 107 QDVPAFECECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166
QY 123 YPFDFOGARIITGOEGAYGWITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 182
Db 167 QPFDRCQAIIISGOEGYGVWITANYLMGNFLEKNLWMMV--HPHGVTETTGALDLGGAS 224
QY 183 TQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKDOALWQKLAKDIOVA-SNEI 241
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGYVYTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
QY 242 LRDCPFHPGKVVNVDLYKTCT--KRPEMTLPFQOFEIQIGNYQOCHQSILELPT 299
Db 285 LTNPFCYPRDYSISFTMGHVFDSLCTVQRPESYNPNVDITPEGTGDSLCCKEASIFDF 344
QY 300 SYC-PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPW 358
Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYVYASALNL-SGSFSLDTFNSSTWNFCSQNW 403
QY 359 BEIKTSYAGVKEKYLSEYCFSGTVILSLLQGYHTADSWHIIHFQIKQSDAGWTGLY 418
Db 404 SOLPLLLPKPDEVYARSYCFGSANYIYHLFVNGYKFTETWPIHFKEVGNSSIAWSLGY 463
QY 419 MLNLTNMIAPAEQPL 432
Db 464 MSLTNQIPAESPL 477

RESULT 10

US-09-905-732B-4
; Sequence 4, Application US/09905732B
; Patent No. 6787328

GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-732B-4

Query Match 38.7%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 5.5e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 3 QNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKFKVQKV 62
Db 47 KQEVLPGLKYGIIVLDAGSSRTTVYVQWPAKENNTGVVSGTFCVSKVSGISSYGNP 106
QY 63 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 122
Db 107 QDVPAFECECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166
QY 123 YPFDFOGARIITGOEGAYGWITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 182
Db 167 QPFDRCQAIIISGOEGYGVWITANYLMGNFLEKNLWMMV--HPHGVTETTGALDLGGAS 224
QY 183 TQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKDOALWQKLAKDIOVA-SNEI 241
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGYVYTLTHSFQCYGRNEAEKFLAMLQNSPTKNH 284
QY 242 LRDCPFHPGKVVNVDLYKTCT--KRPEMTLPFQOFEIQIGNYQOCHQSILELPT 299
Db 285 LTNPFCYPRDYSISFTMGHVFDSLCTVQRPESYNPNVDITPEGTGDSLCCKEASIFDF 344
QY 300 SYC-PYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKKFCAQPW 358
Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYVYASALNL-SGSFSLDTFNSSTWNFCSQNW 403
QY 359 BEIKTSYAGVKEKYLSEYCFSGTVILSLLQGYHTADSWHIIHFQIKQSDAGWTGLY 418
Db 404 SOLPLLLPKPDEVYARSYCFGSANYIYHLFVNGYKFTETWPIHFKEVGNSSIAWSLGY 463
QY 419 MLNLTNMIAPAEQPL 432
Db 464 MSLTNQIPAESPL 477

RESULT 11

US-09-923-304-4
; Sequence 4, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UTSC-658US
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-4


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Db 345 KACHDQETCSFDGVYQPKIKGPFVAFAGFYTAGALNL--SGSFSLDTFNSWTNFCQNW 403
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Db 404 SOLPLLPKPFDEVVARSYCFSANVIYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 463
Qy 419 MLNLTNMIAPQPL 432
Db 464 MSLTNOIPAESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 38.7%; Score 910.5; DB 4; Length 556;
Best Local Similarity 41.5%; Pred. No. 6e-89;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 3 ONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVVHVEECRVKPGISKFKVQK 62
Db 74 KOELPLPGLKYGIVLDAGSSRTTVYVYQWPAEKENNTGWSQTFKCSYKSGSISSYGNP 133
Qy 63 NEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLRMESEELADRLDVVERSLN 122
Db 134 QDVPRAECCMKVKGVQVPSHLHGSTPIHLGATAGMRLRLQNTAANEVLESIQSYFKS 193
Qy 123 YPDPFOGARIITGOEAGYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 182
Db 194 QPDPFRGAQIISGQEGYGVWITANYLMGNFLEKNLWHMWV--HPHGVETTTGALDLGAS 251
Qy 183 TQVTFVQNTIESPDNALQRLYKGVNVTHTSFLCYGKQDALWQKLAKDIQVA-SNEI 241
Db 252 TQISFVAGEKMDLNTSDIMQVSLGYGVYVTLTHSFQCYGRNEAKKFLAMLNPSPTKNH 311
Qy 242 LRDPCEHPGYKVVNVSDLYKTCT--KRPEMTLPFQCFEIQGIGNYQQCHQSILELFTNT 299
Db 312 LTNCEYPRDYSISTMGHVFDSLCTVQDRPESYNPNVDITTEGDSLCKEKVASIFDF 371
Qy 300 SYC-PYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMMKFKCAQPW 358
Db 372 KACHDQETCSFDGVYQPKIKGPFVAFAGFYTAGALNL--SGSFSLDTFNSWTNFCQNW 430
Qy 359 BEIKTSYAGVKEKYLSEYCFSGTIVLSLLLOGYHFTADSWEHIIHFPIGKIQSDAGWTIGY 418
Db 431 SOLPLLPKPFDEVVARSYCFSANVIYHLFVNGYKFTETWPIIHFEKEVGNSSIAWSLGY 490
Qy 419 MLNLTNMIAPQPL 432
Db 491 MSLTNOIPAESPL 504
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RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 36.8%; Score 865; DB 4; Length 479;
Best Local Similarity 41.3%; Pred. No. 3.8e-84;
Matches 183; Conservative 69; Mismatches 137; Indels 54; Gaps 9;

Qy 2 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVVHVEECRVKPGISKFKVQK 61
Db 36 TRDVREPPALKYGIIVLDAGSSHTSMFYIKWPAEKENDTGIVGQHSQCDVPGGIGSSYADN 95
Qy 62 VNEIGIYLTDCMERAREVIPSQHOETPVYLCATAGMRLRMESEELADRLDVVERSLN 121
Db 96 PSGASQSLVGLCEQALQDVPKERHAGTPLYLGATAGMRLRLNLTNPEASTSVLMVTHLT 155
Qy 122 NYPDFOGARIITGOEAGYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDL 178
Db 156 QYFPDFRGARILSQEESGVFGWVTANYLLENFIKYGVGRWF-----RPRKGTILGANDL 209
Qy 179 GGASTQVTFVQNTIESPDNA--LQRLYKGVNVTHTSFLCYGKQDALWQKLAKDIQV 236
Db 210 GGASTQITF---ETTSPEADRASEVQLHLYGQHYRVYTHSFCLCYGRDQVLRLLASALQT 266
Qy 237 ASNEILLRDPCEHPGYKVVNVSDLYKTCTKCFEMTLPFQCF-----EIOGIGNYQQCH 290
Db 267 HGFH----PCWPRGFTQVILGDVYQSPCT----MAQRPNFNSARSVSUSGSDPHLCR 318
Qy 291 QSILELEFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFL--NLTSEKVSQEKVTE 348
Db 319 DLVSGLEFSFSCPSRCSFNGVFPQPPVAGNFVAFSAFYTVDFLRTSNGLPVATLQOLEA 378
Qy 349 MMKKFCAQPEEBEIKTSYAGVKEKYLSEYCFSGTIVLSLLLOGYHFTADSWEHIIHFPIGKI 408
Db 379 AAVNVCNQTWAQ-----QLLSRGYGFDERAFGCVIFQKAA 414
Qy 409 GSDAGWTGLVMNLTNMIAPQPL 431
Db 415 DTAVGWALGYMLNLTNLIAPDPP 437

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OM protein - protein search, using sw model

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(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147A-28_COPY_25_474
Perfect score: 2398
Sequence: 1 ASTKKTQLTSTONKALPEN.....NLTNMPAEQPLSTPLSHST 450

Scoring table: dLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	97.9	510	2 I56242	lymphoid cell acti
2	505	21.1	483	2 D86276	hypothetical prote
3	469.5	19.6	405	2 E86276	hypothetical prote
4	453	18.9	630	2 S50463	hypothetical prote
5	416	17.3	572	2 T40856	probable nucleotid
6	406.5	17.0	516	2 G84442	probable nucleosid
7	402.5	16.8	485	2 T34147	hypothetical prote
8	394.5	16.5	508	2 C86276	7A19.33 protein -
9	381.5	15.9	557	2 T16696	hypothetical prote
10	374	15.6	455	2 S48859	probable guanosine
11	374	15.1	556	2 T39109	nucleoside triphos
12	338	14.1	454	2 J04616	aprase (EC 3.6.1.
13	332	13.8	1052	2 T04439	hypothetical prote
14	328.5	13.7	479	2 T23508	hypothetical prote
15	323	13.5	518	2 A40732	guanosine-diphosph
16	167	7.0	628	2 A55421	nucleoside-triphos
17	103	4.3	369	2 S77299	C4-dicarboxylase-b
18	102	4.3	466	2 J06525	processing peptida
19	101.5	4.2	716	2 T21516	hypothetical prote
20	100	4.2	307	2 T27332	hypothetical prote
21	99.5	4.1	3848	2 T17414	Tipc protein - ali
22	99	4.1	883	2 B85725	probable fibrillar
23	99	4.1	1951	2 B43963	RNA viral polymera
24	98.5	4.1	590	2 A81411	autolysin, N-acety
25	98.5	4.1	797	2 D86247	hypothetical prote
26	98.5	4.1	989	2 B84532	hypothetical prote
27	98.5	4.1	1509	2 B89885	hypothetical prote
28	98	4.1	371	2 T05213	hypothetical prote
29	98	4.1	665	2 T18979	hypothetical prote

ALIGNMENTS

RESULT 1

I56242
Lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56242
R:Maliszewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994
A:Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A:Reference number: I56242; MUID:95015846; PMID:7930580
A:Accession: I56242
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-510 <RES>
A:Cross-references: UNIPROT:P49961; GB:S73813; NID:g765255; PIDN:AAB32152.1; PID:g765255
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 97.9%; Score 2348; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.7e-182; Mismatches 0; Indels 0; Gaps 0;
Matches 439; Conservative 0

Qy	12	TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFVQK	71
Db	38	TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFVQK	97
Qy	72	VNEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	131
Db	98	VNEIGVILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	157
Qy	132	NYPDFOGARLITGOESGAGVITINYLKGFSGKTRWFSIVPVETNNQETFGALDLGGA	191
Db	158	NYPDFOGARLITGOESGAGVITINYLKGFSGKTRWFSIVPVETNNQETFGALDLGGA	217
Qy	192	STQVTFVQNOTIESPNALQRLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIQVASNEI	251
Db	218	STQVTFVQNOTIESPNALQRLYKGDYNYVTHSFCLCYGKDQALWQKLAKDIQVASNEI	277
Qy	252	LRDPCFHGPKYKVVNVSDLYKTPCTKGFEMTLPFQOPEIQIGINYQQCHQSILELFTSY	311
Db	278	LRDPCFHGPKYKVVNVSDLYKTPCTKGFEMTLPFQOPEIQIGINYQQCHQSILELFTSY	337
Qy	312	CPYSCAFNGIFLPLQDGFSAFYVMKFLNLTSEKVSQEKVTEMMKFCQAPWBEI	371
Db	338	CPYSCAFNGIFLPLQDGFSAFYVMKFLNLTSEKVSQEKVTEMMKFCQAPWBEI	397
Qy	372	KTSVAGVKEKYLSEYCFSGTVILSLLOQHYFTADSWEHIFIGIKIQSDAGWTLYGMLN	431
Db	398	KTSVAGVKEKYLSEYCFSGTVILSLLOQHYFTADSWEHIFIGIKIQSDAGWTLYGMLN	457
Qy	432	LTNMPAEQPLSTPLSHST	450
Db	458	LTNMPAEQPLSTPLSHST	476

RESULT 2

hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: UNIPROT:Q9X162; GB:AE005172; NID:G5080801; PIDN:AAD39311.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 21.1%; Score 505; DB 2; Length 483;
Best Local Similarity 31.3%; Pred. No. 6.8e-33;
Matches 135; Conservative 70; Mismatches 164; Indels 62; Gaps 18;
Qy 21 VKYGLVDAGSSHTSLIYKPAEKEN---DTGVVHVQVECRVK-GPGISFVKVQKVEIG 76
Db 68 LRYSLVDAGSSGTRVHVFGVWFSGKVPVDFGEKHY---ANLKLTPGLSSYADNPEGAS 124
Qy 77 IYLTDCMERAREVTPRSQHOETPVYLGATAGWRLRMESEELADRLVDVRSLSL--SNYP 134
Db 125 VSVTKLVEFAKQRPKRMFRSDIRLMATAGWRLLEVPVQE---QILEVTRVLRSSGFM 181
Qy 135 FDFQARITQOEAGYGMITINYLKFKSQKTRWFSIVPVYETNNQETFGALDILGGASTQ 194
Db 182 FRDEWANVIGSGDEGIYSWITANYALGSLG-----TDPLETTGIVELGGASAQ 229
Qy 195 VTFVPQNTIESPDNALQFLRYGK--DYNVYTHSFLCYGKQALWQKLAKDIOVASNE--- 250
Db 230 VTFVSSSEHV---PPEYSRTIAYGNISYTIYSHSFLDYGKDAAL-KKLEKLQNSANSTVD 285
Qy 251 -ILRDPCHFPGYKKVNVNSDLYKTPCTKRFEMTLFPQOFEIQG----IGNYQOCHQSILE 305
Db 286 GVVEDPCTPKGY-----IYDTN-SKNYSSGFLADESKLGSLOANGNFSKRSATFA 336
Qy 306 LF--NTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVVMKFLNLTSEKVSQKVTMMKKF 363
Db 337 LLKEGKCNLYEHCSIGSTFTPDQGSFLATASFYTTAKFPPEL-EKGWLSSELIPAGKRY 395
Qy 364 CAQPEEIKTSYAGVKEKYLEYCFSGTYIISLLLOGHFTADSWEHFHFGKIQGSDAG 423
Db 396 CGEESKILYLPPTTDEEYLRGYCFSSAAYTISMLHDSLGIALDD-ESITYASK-----AG 449
Qy 424 -----WTLG 427
Db 450 EKHPLDVALG 460

RESULT 3

hypothetical protein F14L17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:G603592; PID:G603597; GSPDB:GN000005
C:Genetics:
A:Gene: YND1; MIPS:YER005W
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.9%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1.6e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:G7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 19.6%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 3.9e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

Qy 63 PGISKFVKQVNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGWRLRMESEELADRV 122
Db 29 PGLSSYADNPEGASVSVTKLVEFAKGRIPKGLKSDIRLMATAGWRLLDVVPVQE---QI 85
Qy 123 LDVVERSLSNVPDFQGG--ARIITQOEAGYGMITINYLKFKSQKTRWFSIVPVYETNNQ 180
Db 86 LDVTRRVLRSRSGFKFQDEWATVISTGDEGIYAMVAVNHALGSLG-----GDPL 133
Qy 181 ETFGALDILGGASTQVTFVPQNTIESPDNALQFLRYGK--DYNVYTHSFLCYGKQDA---L 236
Db 134 KTTGIVELGGASAQVTFVPSEHV---PPEFSRTISYGNVSIVYSHSFLDFGQDAEDKL 190
Qy 237 WQKLAKDIOVASNE-ILRDPCHFPGYKKVNVNSDLYKTPCTK-----RPEMTLPF 285
Db 191 LESLQNSVAASGTVGVEDECTPKGY-----IYDTHSQKSSGFLSEESFKASL-- 240
Qy 286 QQRFIQQIGNVQOCHQSILELF--NTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYVVMKF 343
Db 241 ---QVQAAGFTKCRSATLMLQEGKENCAYKHCISGISTFTPNIQGSFLATENFFHTSKP 297
Qy 344 LNLTSKVSQKVTMM---KKFCAQPEEIKTSYAGVKEKYLEYCFSGTYIISLLLOQ 400
Db 298 FGL-GEK---EWLSEMLAGKFCGEEWSKLKPKYPTTKDKYLHRYCFSSAYIISMLHDS 353
Qy 401 YHFTADSWEHFHFGKI--QGSDAGWTLG-YMLN 431
Db 354 LGVALDD-ERIKYKASKAGKENIPLDVALGAFILN 386

RESULT 4

S50463
hypothetical protein YER005W - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dieterich, F.S.

submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:G603592; PID:G603597; GSPDB:GN000005
C:Genetics:
A:Gene: YND1; MIPS:YER005W
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.9%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1.6e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

```

Db      224 NEAYRRYLGLLISENGKVGNTLSDPCLSRG-----RTYDIDGIE 263
Qy      290 IQIGTNTQQCHQSILEFTSY-CPYSQCAFNGFIPLPLOGDFCAFSAFYVMKFLNLT 348
Db      264 FAGTGLDKQCLKULTYLLNKKDKPCMDPCNFDGSIIPV--DF-ANTEFVGVSFPWYTN 320
Qy      349 EKVSQ-----EKVTEMMKFKCAQPMEEI-----KTSYAGVKKYISEYCFSGTY 392
Db      321 DVFDMGSGSYHFPNPKYKQVDE---YCGTEWETMLSRLYNKELTPTSDENKLEKCFKASW 376
Qy      393 ILSLLLOG-----VHFTADSMWEIHFTGKIQGSADAGWTLGWML 430
Db      377 ALNVLHEGFDVPKNTSNDAKGLSVIPAYHSPTSL-----KIRTEVSWTLGQVL 430

RESULT 6
G84442
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: G84442
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujimura, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Fraser, L.J.; Mess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Umayam, C.M.; Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84442
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-516 <STO>

```

[illegible]

QY *i* 23 YGIVLDCAGSSHTSLIYYKWPARKEND----TCGVHQVECRVK-GPGISKFKVOKNEIGI 77
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 44 YGVICDAGSTGRFLFVNWNISTSDSELIQEIPVIYDNKPVMKKISPLGLSTFGTKPAQAAS 103
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 78 YLTDCMERAREVIPRSQHQTVPVLGATAGWELLRWESELADRVLDVVERSLSN----- 132
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 104 YLRPUMELAEHRHPIPEEKRPYPTEVFIFATAGMRLIDPEYVLIQCK--EAVLKMLRNKLPKI 161
 |||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 133 --YPPDFCARIITCOEBGAYGIWTINYLKGFSO-KTRWFSGIVPVETNNQOTFCALDLG 189
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 162 TSMQVLKEHIRILIEKWKEGIIYSWIANNVALGFKNKTATILDFTGSTSPAHARQKVGMIDMG 221
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 190 GASTQVTFF-VFQNQTIIES-----PDNALQRLYGKDYNVYTTHSFCLCYGDQDALW 237
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 222 GASAQIAFPDPDSFDSSFSSINVENINGCREDDSL-FK-----YKLFVTTFLLGYGNREGIR 275
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 238 Q---KLAIKDIQVASNEILLRDPCFHRYGKYKVNVUSDLYKTPCTKRREMTLPFOOFEIQGIG 294
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 276 KYEHMLLSKLJDKQNGTVIQDDCMPNLHKHTVLEN-----GENFVRRTGTG 320
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 295 NYOOCHQSILEFN---TSVC-PYSOCAENGIFLP--PLOG-DEGAFAFYFMVKFLPN 345
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 321 NWNTCSNREVKKLNPPESSEVCBAKAACYFGAPOPAPSIPLSNIEWYGFEYWYSTHDVTL 380
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 346 LTSEKVSQEVKETMMMKCAQPWEBI-----KTSYAGVKEKLVSEVCSGTVILSILLOQ 400
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 381 GLGGDYDAENTAKTQQYCSCRKWSTIOAESKQLYPRADEERLTRQCFSAWITSVLHDG 440
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 401 YHFTAADSWEHIHF--IGKIQGSACGACTLGTYLMNLTNMIP---AEOPLSPTLSHSHT 450
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 441 --PSVDK--THNKFSQSVSTIAGEOVQMALGAMIYHMFRFFPLDRDSSRNLIUVKETHSS 492
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 10

T39109
probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-556 <BAR>
A;Cross-references: UNIPROT:Q9UT35; EMBL:M121741; PIDN:CAB57338.1; GSPDB:GN000000000
A;Experimental source: strain 972h; cosmid c824
C;Genetics:
A;Gene: SPDB:SPAC824.08
A;Map position: 1

Query Match	15.9%	Score 381.5;	DB 2;	Length 556;
Best Local Similarity	27.1%	Pred. No. 8.3e-23;		
Matches 121;	Conservative 71;	Mismatches 181;	Indels 73;	Gaps 17
Qy	22	KYGIVLDAAGSHTSLYIYKVPAAEKENDTGWVHOVEE--CRVKGPGIGSFVKQKWEIGIYL 79		
Db	133	QYVLMIDAGSTGRVHVYQF-----NNCNPSPKLEEFEFFKMEIPLGSFAGDPGEAAASL 187		
Qy	80	TDCMERAREVTPRSQHQETPPVLTGATAGWRLRMSESELADRLVDVVERSLN-YPPFPF- 137		
Db	188	DPLLDYAMENVPYEEYRRCSPYAVKATAG---LRLTGESEAKAILKSVRQHLNDYPPFPV 244		
Qy	138	-QGARIITGQEGAGYGITINVLCLKFKFSQKTRWFSIVPYETNNQGTFCGALDGGASTQVT 196		
Db	245	KDGVSLGSGMEGIYAWITINVLTLTGKKA-----THSTVAVMDLGGASTQLV 293		
Qy	197	FVPQ-----NOTIESPDNALQFLYKQDVNVTYTHSFLCYGKQOALMQKLAKDIQVASNEIL 252		
Db	294	FEPRFASDGESLVGDGHKYVLVDYNGEQELYQHSHLGYGLKEA---RKLIHKFVLNNAAAL 351		

```

Qy 253 RD-----PCFHPGCKVNVVSDLYKTPCTKRPK-----TLFPQOFIQQIG 294
Db 352 KESLELGDSTSIHPCLH-----LNASLTHPDSKSEAVFVGPSLAHLSLQCRGIA 405
Qy 295 NYQOCHOSIILELNTSCYPYSCAFNGIFLPLQDQFG-----AFSAFYFVNMKFLNLTSE 349
Db 406 E-----KALYKDKNCVPRPCSFNGVHQPKFTETFDSPYILISYFYDRMISLGMPS- 456
Qy 350 KVSQEKTEMMKFCAPQ--WEETKTSYAGVKE-KYLSEYCFSGTYIILSLQGHYFTAD 406
Db 457 TTTIEDMKYLANSCSGPTYQDFAFSLTDALKKEELKEPEWCLDLNMYISLISVGYEIPNN 516
Qy 407 SWEHIFGFIQSGDAGWTLYGLNML 432
Db 517 --RLHTAKKIDNKELGNCIGASLSM 540

RESULT 11
S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S65147; S48859
R:Haieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated,
A:Reference number: S65141; MUID:96197404; PMID:8616230
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <HS2>
A:Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:G563611; PIDN:CAA83655.1;
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: nucleus

```

Query Match	15.6%;	Score 374;	DB 2;	Length 455;
Best Local Similarity	25.6%;	Pred. No. 2.5e-22;		
Matches 116;	Conservative 80;	Mismatches 169;	Indels 88;	Gaps 18

Qy	23	YGIVLDAGSSHTSIYIKWPAEKENDTGVVH--QVEBCRVKPGCISFKVQKVNIGIYL 79
Db	44	YAVVFDAGSTGSRITHVHF-----NONLDLHGIGVEYYNKITPGLSSYANNPEQAASL 99
Qy	80	TDCMERAREVIPSQHOETPYVLGATAGMRLLRMESEELADRLVDLVVRSLSN-YPPDFQ 138
Db	100	IPLLEQAEDVVPDDLQPKTPVRLGATAGRLRLNGDASE--KILQSVRDLMSNRSTFNVQ 156
Qy	139	--GARIITGQEGAYGHITINYLKGKFSQKTRWFESIYPVETNNQETPGALDLGGASTQVT 196
Db	157	PDAVSIIDGTQGSYLMVTNYALNGLGKK-----YTKTVGVIDLGGSGVQWA 204
Qy	197	FVPQNQITSPDNAL-----QFRLYGKDYNVVYTHSFLCVGKXQDALWQKLAKDIOVAS 248
Db	205	YAVSKTKAKNAPKVADGGDDPYIKVVLKGIPIDYLVHSYLHFR-----EASR 252
Qy	249	NEILR-----DPCFHPGYKKVNVNSDLYKTPCTKRFEMTLFFQGFIEQIGIGNYQQCHQS 302
Db	253	AEILKLTSPSPNCLLAGFGNIYYSG-----EEPKAT-----AYTSGANFNKCKNT 299
Qy	303	ILELFTSY-CPYSQCAFNGIFLPPLOQDFG-----AFSAFVFMKFLNLTSEK----- 350
Db	300	IRKALKLNYPYPCYQNCTFGGIW----NGGGNGQKNLFASSSFPELDPDTGMVDASTPNF 355
Qy	351	-VSQEKYTEMKKFCAQPWREIKTSGYAGVKEKYLSEY-CPSGTYLTLGLLQGYHFTADSW 408
Db	356	ILRPVDTETKAKEACALNFDAKSTYFPLDKKNVASVYVCMDLIIYQVLLVDG--FGLDPL 413
Qy	409	EHTHFIGKIQGSD-----AGWTLGYMLNLTNMP 437
Db	414	QKITSKEIEYQDAIVEAANPLGNVAEISALP 446

RESULT 12
JC4616

aprase (BC 3.6.1.5) precursor - potato
N:Alternate names: adenylylphosphatase; ATP-diphosphohydrolase
C:Species: Solanum tuberosum (potato)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: J04616; PC4147
R:Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A:Reference number: J04616; MUID:96158985; PMID:8579614
A:Accession: J04616
A:Molecule type: mRNA
A:Residues: 1-454 <HAN>
A:Cross-references: UNIPROT:P80595; GB:U58597; NID:G1381632; PIDN:AAB02720.1; PID:G1381632
A:Accession: PC4147
A:Molecule type: protein
A:Residues: 59-95; 96-131; 132-160; 236-253; 332-345 <HA2>
A:Experimental source: tubers
A:Note: The authors translated the codon GCA for residue 215 as Gly
C:Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. It has a high substrate specificity, and insensitive to a variety of inhibitors. It is involved in starch synthesis.
C:Genetics:
A:Gene: rcrop1
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; hydrolase; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:8-25/Domain: transmembrane #status predicted <TM>
F:31-45/Product: ATP-diphosphohydrolase #status predicted <MAT>
F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F:44-65/Region: nucleotide binding #status predicted
F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F:192-212/Region: nucleotide binding #status predicted
F:330-410, 427-446/Region: hydrophobic carboxyl end
F:131, 362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 338; DB 2; Length 454;
Best Local Similarity 24.8%; Pred. No. 2e-19;
Matches 116; Conservative 81; Mismatches 191; Indels 80; Gaps 18;

QY 8 LTSSTQKALP-----ENVKIGIVLDAGSSHTSIYKWPAAKENDTGVVHQVEECR 59
DB 23 LLSKNVNAIPLRRHLLSHSEHYAVIFDAGSTGSRVHFRFD-EKLGALLPIGNIEYFM 81
QY 60 VKPGIISKFKVQVNEIGIYITDCMERAREVTPRSHOETPVYLCATAGMRLIRSEELA 119
DB 82 ATEPGLSSYAEDPKAAANSLEPLDAGGVVQBELQSETPLELGATAGRLMKGDA--A 138
QY 120 DRVLDDVVE--RSLSNYPDFQGARITQGEAGYGMITINYLKGFQSKTRWFSIVPYE 176
DB 139 EKILQAVENLVKNGQSTFHSKDQVITLDGTQEGSYMAAIIYLLGNLKG----- 187
QY 177 TNNQETFGALDLAGASTQVTFVQN-QTIESPDN-----ALQFLYCKDNNVYTHSFLC 229
DB 188 -DYKSTATTIDLGSGSVQMAIYASNEQFAKAPQNEDEGFPYVQOQKHLMSKNNLVHSHYN 246
QY 230 YGKDQALQKLAQDIOVASNEILRDPCHPGYKVVNVSDLYKTPCTKRFEMILPFOQFE 289
DB 247 YQQLAGRAEIPKASRNESNPCALEGC--DGYSYGGVD--YKVKAPKG----- 291
QY 290 IQIGNYQOCHQSISLELEN-TSYCPYSQAFNGIFLPLQGDG-----AFSAFYFVM 341
DB 292 ----SSWKRCLRLTRHALKNAKCNIEECTFNQVW----NGGGDQKXNHASSFFYDIG 343
QY 342 KFLNLTSEKVSQE----KVTEMMKFKCAQPMEEIKTSYAGVKYKSLSEYCFSGTYILSL 396
DB 344 AQGVGVDTKFPALAKAPQYLYNAAKVACQTNVADIKSIFPKTQDRNIPVLCMDLIYEVL 403
QY 397 LLQGYHTFADSWEHITFIKIQSD-----AGWTLYGMNL-----TNMI 436
DB 404 LVQD--FGLNPHKEITVIHDVQYKQYLVGAAMPFGCALDLVSSSTNKI 449

RESULT 13

[illegible]

Query Match 13.7%; Score 328.5; DB 2; Length 479;

Best Local Similarity 27.0%; Pred. No. 1.3e-18;
Matches 121; Conservative

Qy 23 YGIVLDAGSSHTSLYIKW---PAEKENDTGVVHQVEE---CRVKGGIGKPFQKVNEIG 76
:
Db 43 FTVIDAGSTCTRLHLXFIHDPAAISH--GMFPKVEKEIFQEVK-PGLSSPAKSPSAA 99
:
Qy 77 IYLTDCHMERAREVIPRSQHQTVPVLGATAGMRLLRMESELADRVLDVVVERLSNYPF- 135
:
Db 100 DSEPLLLQARAKEVPHFMWEKTPTTLKATAGLRL---PGDMADDILLESVEERIFNSGFF 156
:
Qy 136 -DFOGA-RITIQSEGAGWITTNYLGK-FSQTRWFSIIVPYETNNQETFGALDIGGAS 192
:
Db 157 AAPDVAVNVPGSDEGYISWFTLNILLTETFD E-----PTVGHKPAAHRSAAPFDLGGGS 212
:
Qy 193 TQTVFVQNQOTIESP-----DNALQFRLYGKDYNVTHVSFLCYGKKDOALMQ--KLAKDIQV 246
:
Db 213 TQLTYWNENAVSEHVGYERIDTF--FGHHIRLFTHSFLNGLIARLNILQLETDNEI 270
:
Qy 247 ASNEILRDPCHFPGYKKVNVSDLYTPCKRFEMTLPPQQFEIQIGIGNYQQCHQSILE 306
:
Db 271 ESTHQLITSQWPEGYQ-----LTWEYALKFWNINGSSSHSPESCVTGTKNF 317
:
Qy 307 FNTSYCPYSQCAFNGIPLPDQDGAFSAFYPMKFELNL-----TSEKVSQEKTEWM 360
:
Db 318 VESSEI-----MHLRELKGS-PVYLFSPYFDRAINSGLVKGNEGGRKIELRQKEA 367
:
Qy 361 KKFCACQPWERIKTSYAGVKEKISEYCFSGTYILSLLOQVHYFTADSWEHIHFIGKIQS 420
:
Db 368 EIACRRKETIIDG-----SHWPQWCLDITYISLLRDGYQF--EDNQPLVLAKKIKGM 420
:
Qy 421 DAGWTLLGYMLNLTMNP-ABQPLSTPLS 447
:
Db 421 EVSWGQGLAFATANEFOLTEGAIKTALS 448
:

RESULT 15
A40732
guanosine-diphosphatase (EC 3.6.1.42) - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein YEL042w
C;Species: *Saccharomyces cerevisiae*
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C;Accession: A40732; S30837; S50502
R;Abelton, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.; J. Cell Biol. 122, 307-323, 1993
A;Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A;Reference number: A40732; PMID:93308137; PMID:8391537
A;Accession: A40732
A;Molecule type: DNA
A;Residues: 1-518 <AB>
A;Cross-references: UNIPROT:P32621; EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g34932
A;Note: sequence extracted from NCBI backbone (NCBIN:I34708, NCCHIP:I34711)
A;Accession: A40732
A;Molecule type: protein
A;Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
A;Accession: S30837
A;Molecule type: DNA
A;Residues: 1-518 <MUL>
A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of *S. cerevisiae* cosmids 8199, 8334, and 9871.
A;Reference number: S50491
A;Accession: S50502
A;Molecule type: DNA
A;Residues: 1-518 <DIE>
A;Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042w
C;Genetics:
A;Gene: SGD:GDAL
A;Cross-references: SGD:S0000768; MIPS:YEL042w

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 63.0419 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-28_COPY_25_474

Perfect score: 2398

Sequence: 1 ASTKKTQTSSTONKALPEN.....NLTNMPAEQLSTPLSHST 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	97.9	510	1 ENP1_HUMAN	P49961 homo sapien
2	1835	76.5	510	1 ENP1_MOUSE	P55772 mus musculus
3	1835	76.5	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1830	76.3	510	2 Q921Q6	Q921q6 mus musculus
5	1818	75.8	372	2 Q86WV3	Q86wv3 homo sapien
6	1794.5	74.8	511	1 ENP1_RAT	P97687 rattus norv
7	1715	71.5	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1690.5	70.5	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	65.6	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1450	60.5	508	2 Q6DFS1	Q6dfs1 xenopus tro
11	1418	59.1	508	2 Q6GP74	Q6gp74 xenopus lae
12	1308.5	54.6	492	2 Q6DC46	Q6dc46 brachydanio
13	1046	43.6	497	2 Q6UQ22	Q6uq22 mus musculus
14	1004	41.9	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	41.6	493	2 Q90X66	Q90x66 gallus gall
16	977	40.7	454	2 Q6ZM69	Q6zm69 brachydanio
17	971.5	40.5	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	40.2	495	1 ENP2_MOUSE	O55026 mus musculus
19	964.5	40.2	495	2 Q921R1	Q921r1 mus musculus
20	961	40.1	455	2 Q7T014	Q7t014 brachydanio
21	953	39.7	494	1 ENP2_CHICK	P79784 gallus gall
22	937.5	39.1	502	2 Q66L64	Q66l64 brachydanio
23	936	38.0	526	2 Q6GNA4	Q6gna4 xenopus lae
24	933	38.9	500	2 Q6NV19	Q6nv19 xenopus tro
25	913.5	38.1	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	38.0	529	1 ENP3_HUMAN	O75355 homo sapien
27	907.5	37.8	495	1 ENP2_HUMAN	Q9Y513 homo sapien
28	906.5	37.8	458	2 Q6UVZ0	Q6uvz0 homo sapien
29	902.5	37.6	529	2 Q8BFW6	Q8bfw6 m mus muscu
30	854	35.6	452	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	34.4	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	27.4	544	2	Q7YTA4	Q7yta4 schistosoma
33	620.5	25.9	300	2	Q8K0L2	Q8k0l2 mus musculus
34	596.5	24.9	209	2	Q8UVX9	Q8uvx9 torpedo mar
35	505	21.1	483	2	Q9X162	Q9x162 arabidopsis
36	504	21.0	488	2	Q6NQA8	Q6nqa8 arabidopsis
37	491	20.5	503	2	Q94AF8	Q94af8 arabidopsis
38	485	20.5	503	2	Q8H1D8	Q8h1d8 arabidopsis
39	485	20.2	537	2	Q6Z543	Q6z543 oryza sativ
40	483	20.1	634	2	Q6FRC2	Q6frc2 candida gla
41	482.5	20.1	336	2	Q8CCV2	Q8ccv2 mus musculus
42	471.5	19.7	555	2	Q94E22	Q94ez2 arabidopsis
43	469.5	19.6	405	2	Q9M977	Q9m9t7 arabidopsis
44	466	19.4	611	2	Q6DH30	Q6dh30 brachydanio
45	465.5	19.4	555	2	O80612	O80612 arabidopsis

ALIGNMENTS

RESULT 1
ENP1_HUMAN STANDARD; PRT; 510 AA.
AC P49961, OSUQO9; Q9Y3Q9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=ENTPD1; Synonyms=CD39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM VASCULAR).
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Deleseppe G.J.T., Schoenborn M.A., Armitage R.J.,
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
RA Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization.";
RL J. Immunol. 153:3574-3583(1994).
RN [2]
SEQUENCE=Umbilical vein;
RX TISSUE=Umbilical vein;
RA MEDLINE=97149443; PubMed=8996251;
RA Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Koziak K.,
RA Millan M., Hancock W.W., Bach F.H.;
RT "Loss of ATP diphosphohydrolase activity with endothelial cell
RT activation.";
RL J. Exp. Med. 185:153-163(1997).
RN [3]
SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).
RX TISSUE=Placenta;
RA MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;
RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
RA Titani K., Fujimura Y., Narita N.;
RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
RT and II.";
RL FEBS Lett. 453:335-340(1999).
RN [4]
SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
RX TISSUE=Placenta;
RA MEDLINE=96096722; PubMed=8529670;
RA Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;
RT "Purification and properties of human placental ATP
RT diphosphohydrolase.";
RL Eur. J. Biochem. 234:66-74(1995).
RN [5]
SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND
RP 399-405 (ISOFORM PLACENTAL I).
RX TISSUE=Placenta;

RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.,
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature
 RT distinct from CD39, localization and inhibition on shear-induced
 RT platelet aggregation.";
 RL Int. J. Hematol. 68:297-310 (1998).
 [6]
 RN FUNCTION.
 RP MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122 (1996).
 [7]
 RN CHARACTERIZATION.
 RP MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;
 RA Wang T.F., Guidotti G.;
 RT "CD39 is an ecto-(Ca²⁺,Mg²⁺)-ATPase.";
 RL J. Biol. Chem. 271:9898-9901 (1996).
 [8]
 RN PALMITOYLATION.
 RP MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
 RA Kozlak K., Kaczmarek E., Kittel A., Sevigny J., Blustein J.K.,
 RA Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,
 RA Robson S.C.;
 RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
 RT caveolae.";
 RL J. Biol. Chem. 275:2057-2062 (2000).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC
 CC -!- CATALYZES ATP and ADP equally well.
 CC -!- COFACTOR: Requires calcium and magnesium.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Vascular;
 CC IsoId=P49961-1; Sequence=Displayed;
 CC Name=Placental I;
 CC IsoId=P49961-2; Sequence=VSP_003607;
 CC Name=Placental II;
 CC IsoId=P49961-3; Sequence=VSP_003608, VSP_003609;
 CC -!- TISSUE SPECIFICITY: Expressed primarily on activated lymphoid
 CC cells. Also expressed in endothelial tissues. The vascular isoform
 CC and the placental isoform II are present in both placenta and
 CC umbilical vein, whereas placental isoform I is present in placenta
 CC only.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and
 CC 7.5-8.0 with ADP.
 CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd39.htm".

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 CC or send an email to license@isb-sib.ch).

 CC EMBL; S73813; AAB32152.1; --
 CC EMBL; U87967; AAB47572.1; --
 CC EMBL; AJ133133; CAB41886.1; --
 CC EMBL; AJ133134; CAB41887.1; --
 CC PIR; I56242; I56242.
 CC Genew; HGNC:3363; ENTPD1.
 CC MIM; 601752; --

DR GO: 0005887; C: integral to plasma membrane; TAS.
 DR GO: 0007596; P: blood coagulation; TAS.
 DR InterPro: IPR000407; GDAL_CD39_NTPase.
 DR Pfam: PF01150; GDAL_CD39_1.
 DR PROSITE: PS01238; GDAL_CD39_NTPase; 1.
 KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
 KW Transmembrane.
 FT DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 510 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 457 457 MEDT -> MKGTRDLTSQ (in isoform Placental
 FT VARSPLIC 1 4 I and isoform Placental II).
 FT VARSPLIC 272 299 /FTId=VSP_003607.
 FT VARSPLIC 272 299 VASNEILRDCEPHGKVKVNVSDLYKT -> ASITOSRPA
 FT PFTSAPPATSCCFLEPQIQ (in isoform Placental
 FT II).
 FT VARSPLIC 300 510 /FTId=VSP_003608.
 FT Missing (in isoform Placental II).
 FT SS -> G (in Ref. 5).
 FT D -> K (in Ref. 4).
 FT T -> TGET (in Ref. 5).
 FT V -> Y (in Ref. 5).
 FT SEQUENCE 510 AA; 57964 MW; BAD87D249649159 CRC64;
 Query Match 97.9%; Score 2348; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2,9e-173;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPISFVKQ 71
 DB 38 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVECRVKGPISFVKQ 97
 QY 72 VNEIGVILTCMERAREVIPSQHOETPVYLGATAGRLRLMESEELADRLVDVERSL 131
 DB 98 VNEIGVILTCMERAREVIPSQHOETPVYLGATAGRLRLMESEELADRLVDVERSL 157
 QY 132 NYPDFQGARIIITQOEGAYGWITINYLKFSQKTRWFSIVPYETNNQTFGALDLGGA 191
 DB 158 NYPDFQGARIIITQOEGAYGWITINYLKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
 QY 192 STQVTFVFPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQDALWOKLADIQVASNEI 251
 DB 218 STQVTFVFPQNTIESPDNALQFRLYGKDYNNYTHSFLCYGKQDALWOKLADIQVASNEI 277
 QY 252 LRDFCFHPGYKVVNSDLYKTPCTKPFEMTLPPQOFEIOGIGNYQOCHOSILEFNTSY 311
 DB 278 LRDFCFHPGYKVVNSDLYKTPCTKPFEMTLPPQOFEIOGIGNYQOCHOSILEFNTSY 337
 QY 312 CPYSQCAFNGIFLPPQLQDGFAGSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 371
 DB 338 CPYSQCAFNGIFLPPQLQDGFAGSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 397
 QY 372 KTSVAGVKEKLSYCFSGTIVLSILLOGHYHTADSWEHFTICKIQSGDAGWTGLGYMLN 431
 DB 398 KTSVAGVKEKLSYCFSGTIVLSILLOGHYHTADSWEHFTICKIQSGDAGWTGLGYMLN 457
 QY 432 LTNMIPAEQPLSTPLSHST 450
 DB 458 LTNMIPAEQPLSTPLSHST 476
 RESULT 2
 ENPL_MOUSE

ENPL_MOUSE STANDARD; PRT; 510 AA.
P55772;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-ATPase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Delepesse G.J.T., Schoenborn M.A., Armitage R.J.,
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization.";
RL J. Immunol. 153:3574-3583 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
RA Gayle R.B. III, Maliszewski C.R.;
RT "Gene structure and chromosome location of mouse Cd39 coding for an
RT ecto-ATPase.";
RL Cytogenet. Cell Genet. 81:287-289 (1998).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF037366; AAC82259.1; -;
CC EMBL; AF041818; AAC83203.1; -;
CC EMBL; AF041812; AAC83203.1; JOINED.
CC EMBL; AF041813; AAC83203.1; JOINED.
CC EMBL; AF041814; AAC83203.1; JOINED.
CC EMBL; AF041815; AAC83203.1; JOINED.
CC EMBL; AF041816; AAC83203.1; JOINED.
CC EMBL; AF041817; AAC83203.1; JOINED.
CC MGD; MGI-102805; Entpd1.
CC GO; GO:0005605; C:basal lamina; IDA.
CC GO; GO:0004050; P:ATPase activity; IDA.
CC GO; GO:0006200; P:ATP catabolism; IDA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
CC GO; GO:0030168; P:platelet activation; IDA.
CC GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
CC InterPro; IPR000407; GDA1_CD39_NTPase.
CC Pfam; PF01150; GDA1_CD39; 1.
CC PROSITE; PS01238; GDA1_CD39_NTPase; 1.
CC Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
CC DOMAIN 1 16 Cytoplasmic (Potential).
CC TRANSMEM 17 37 Potential.
CC DOMAIN 38 478 Extracellular (Potential).
CC TRANSMEM 479 499 Potential.
CC DOMAIN 500 510 Cytoplasmic (Potential).
CC FT

FT CARBOHYD 73 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 226 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 291 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 333 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 428 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 457 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 510 AA; 57205 MW; 856A6113D2E13930 CRC64;
Query Match
Best Local Similarity 76.5%; Score 1835; DB 1; Length 510;
Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;
Qy 12 TONKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGVVHQQVEEVRKVGFGSKFVKQ 71
Db 38 TONKPLPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGVVHQQVEEVRKVGFGSKFVKQ 97
Qy 72 VNEIGIVLTOMERARVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 131
Db 98 TDEIGAYLAECMELESTELIPTSRKHQTPVYLGATAGMRLLRMESEELADRLVDVVERSL 157
Qy 132 NYPDFQCARIIITGOEEGAYGWTINVLGKFSOKTRWFSIVPYETNNQETFGALDLGA 191
Db 158 SYPDFQGAIIITGOEEGAYGWTINVLGKFSOKTRWFSIVPYETNNQETFGALDLGA 216
Qy 192 STQVTFVQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQALMOKLAKDIQVASNEI 251
Db 217 STQITFVQNSTIESPNSLQFRLYGKDYNNVYTHSFLCYGKQALMOKLAKDIQVASNEI 276
Qy 252 LRDPFHPGKVVVSDLYKTPCTKRFEMTLPPQOFEIIGIGNVQOCHQSIIELEFNTSY 311
Db 277 LKDFCFNPGYKVVVSDLYKTPCTKRFEMTLPPQOFEIIGIGNVQOCHQSIIELEFNTSY 336
Qy 312 CPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLITSEK--VSQEKVTEMMKKFCAQPWE 369
Db 337 CPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLITSEK--VSQEKVTEMMKKFCAQPWE 396
Qy 370 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQGSDAGWTLYGM 429
Db 397 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQGSDAGWTLYGM 455
Qy 430 LNLTNMIPASQPLSTPLSHST 450
Db 456 LNLTNMIPASQPLSTPLSHST 476
RESULT 3
Q8CDV7 ID Q8CDV7 PRELIMINARY; PRT; 539 AA.
AC Q8CDV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4921511C05 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence.
GN Name=Entpd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium;
 RA the Riken Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saichoh K., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK029512; BAC26486.1; --
 DR MGD; MGI:102805; Entpd1.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004050; F:apoptosis; IDA.
 DR GO; GO:0006200; P:ATP catabolism; IDA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IDA.
 DR GO; GO:0030158; P:platelet activation; IDA.
 DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39; 1.
 DR PROSITE; PS01238; GDAI_CD39_NTPase; 1.
 KW Hydrolase.
 SQ SEQUENCE 539 AA; 60590 MW; 49565788313321F4 CRC64;
 Query Match 76.5%; Score 1835; DB 2; Length 539;
 Best Local Similarity 76.4%; Pred. No. 1.7e-133;
 Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;
 QY 12 TONKALPENYKIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKVQK 71
 DB 67 TONKALPENYKIGVLDAGSSHTSLYIKWPAEKENDTGVVQQLERCVQKPGISKVQK 126
 QY 72 VNEIGIYLTOMERAEVIRPSQHOETPVYLGATAGVLLRMESEELADRLVDVVERSL 131
 DB 127 TDEIGAYLAECMBELSTELIPTSKHQHPVYLGATAGVLLRMESEELADRLVDVVERSL 186

QY 132 NYPDFQCARITGOEGAYGWTITNYLLGKFSOKTRWFSIVPYETNNQETFGALDLGA 191
 DB 187 SYPDFQCARITGOEGAYGWTITNYLLGKFSOKTRWFSIVPYETNNQETFGALDLGA 245
 QY 192 STQVTFVQNTQSPDNALQFRLYGKDYNYVTHSFLCYGKQALWQKLAKDIQVASEI 251
 DB 246 STQVTFVQNTQSPDNALQFRLYGKDYNYVTHSFLCYGKQALWQKLAKDIQVSSGV 305
 QY 252 LRDPCHPGYKVVNVSDLYKTPCTKREMTLPQOFEIQTGNYQOCHQSQLELFTSY 311
 DB 306 LRDPCHPGYKVVNVSDLYKTPCTKREMTLPQOFEIQTGNYQOCHQSQLELFTSY 365
 QY 312 CYSQCAFNGIFLPLQDGFAGSAFYFMKFLNLTSEK--VSQEKVTMMKKFCAQWPE 369
 DB 366 CYSQCAFNGIFLPLQDGFAGSAFYFMKFLNLTSEK--VSQEKVTMMKKFCAQWPE 425
 QY 370 EIKTSYAGYKYLSEYCFSGTYILSLQLQGHVHTADSWEHIFGKIQGSDAGHTLGYM 429
 DB 426 EIKTSYAGYKYLSEYCFSGTYILSLQLQGHVHTADSWEHIFGKIQGSDAGHTLGYM 484
 QY 430 LNLTNMIPAEQPLSTPLSHST 450
 DB 485 LNLTNMIPAEQPLSTPLSHST 505
 RESULT 4
 Q921Q6 PRELIMINARY; PRT; 510 AA.
 ID Q921Q6 PRELIMINARY; PRT; 510 AA.
 AC Q921Q6 PRELIMINARY; PRT; 510 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Entpd1 protein.
 GN Name=Entpd1; (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyar S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011278; AAH11278.1; --
 DR MGD; MGI:102805; Entpd1.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004050; F:apoptosis; IDA.

DR GO: 0006200; P: ATP catabolism; IDA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. .; IDA.
DR GO: 0009168; P: platelet activation; IDA.
DR GO: 0009181; P: purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
DR SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 76.3%; Score 1830; DB 2; Length 510;
Best Local Similarity 76.2%; Pred. No. 3.8e-133;
Matches 336; Conservative 45; Mismatches 56; Indels 4; Gaps 3;

QY 12 TONKALPENVKYGVLDAGSSHTSLIYKPAEKENDTGVVHVVECHVKPGISKFVQK 71
DB 38 TONKPLPENVKYGVLDAGSSHTSLIYKPAEKENDTGVVQVQLEECQVKPGISKVAQK 97
QY 72 VNEIGVLTDCWREAREVIPSQHOETPVYLGATAGMELLRMESEELADRLVDVVERSL 131
DB 98 TDEIGVLAECWELSTELIPTSKHQTVPYLGATAGMELLRMESEQSADEVLAAVSTSLK 157
QY 132 NYPDFQAGRIITQGEAGYGMITINYLKFKSQKTRWFSIVPYETNNQETFGALDLGA 191
DB 158 GYPDFQAGRIITQGEAGYGMITINYLKFKSQKTRWFSIVPYETNNQETFGALDLGA 216
QY 192 STQTFVPQNTIESPDNALQRLYKDYNYVTHSFLCYGKQALWQKLAKDIQVASNEI 251
DB 217 STQTFVPQNTIESPDNALQRLYKDYNYVTHSFLCYGKQALWQKLAKDIQVASNEI 276
QY 252 LRDCPEHGVKVVNSDLYTCTKREMTLPQOEIIGVYQOCHOSILEFNTSY 311
DB 277 LKDCFPNGYKVVNSDLYTCTKREMTLPQOEIIGVYQOCHOSILEFNTSY 336
QY 312 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEK--VSQEKVTEMKKFCAQWPE 369
DB 337 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEK--VSQEKVTEMKKFCAQWPE 396
QY 370 EIKTSYAGVKEKYLEYCFSGTYILSLLOQYHFTADSWEHIFGKIQGSDAGWTLYGM 429
DB 397 EIKTSYAGVKEKYLEYCFSGTYILSLLOQYHFTADSWEHIFGKIQGSDAGWTLYGM 455
QY 430 LNLNTMIPAEQPLSTPLSHST 450
DB 456 LNLNTMIPAEQPLSTPLSHST 476

RESULT 5
Q86VW3 PRELIMINARY; PRT; 372 AA.
ID Q86VW3
AC Q86VW3
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE HTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shen D., Schuler G.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RA Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
RL EMBL; BC047664; AAH47664.1; -
DR GO: 0016787; F: hydrolase activity; IEA.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
DR PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
DR SEQUENCE 372 AA; 42731 MW; A8BDE1366356EE3 CRC64;

Query Match 75.8%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.2e-132;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 MESEELADRLVDVVERSLSNYPDFQAGRIITQGEAGYGMITINYLKFKSQKTRWFSI 172
DB 1 MESEELADRLVDVVERSLSNYPDFQAGRIITQGEAGYGMITINYLKFKSQKTRWFSI 60
QY 173 VPYETNNQETFGALDLGGASTQNTVFQNTQIESPDNALQRLYKDYNYVTHSFLCYGK 232
DB 61 VPYETNNQETFGALDLGGASTQNTVFQNTQIESPDNALQRLYKDYNYVTHSFLCYGK 120
QY 233 DQALWQKLAKDIQVASNEILRDCPFHGYKVVNSDLYTCTKREMTLPQOEIIGVYQO 292
DB 121 DQALWQKLAKDIQVASNEILRDCPFHGYKVVNSDLYTCTKREMTLPQOEIIGVYQO 180
QY 293 IGNYQOCHOSILEFNTSYCFYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVS 352
DB 181 IGNYQOCHOSILEFNTSYCFYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVS 240
QY 353 QEKVTEMKKFCAQWPEEIKTSYAGVKEKYLEYCFSGTYILSLLOQYHFTADSWEHIF 412
DB 241 QEKVTEMKKFCAQWPEEIKTSYAGVKEKYLEYCFSGTYILSLLOQYHFTADSWEHIF 300
QY 413 FIGKIQGSDAGWTLYGMILNLTNMTIPAEQPLSTPLSHST 450
DB 301 FIGKIQGSDAGWTLYGMILNLTNMTIPAEQPLSTPLSHST 338

RESULT 6
ENPL RAT
ID ENPL RAT STANDARD; PRT; 511 AA.
AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=9221928;
RA Wang T.-F., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
RT apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Cochlea; DOI=10.1016/S0169-328X(99)00244-2;
 RX MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
 RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 termination of purinergic transmission.";
 RL Brain Res. Mol. Brain Res. 73:85-92(1999).
 RN [3]
 RP SEQUENCE OF 432-511 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=39031057; PubMed=9364474; DOI=10.1016/S0028-2908(97)00115-9;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
 RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 rat brain.";
 RL Neuropharmacology 36:1189-1200(1997).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
 CC kidney, liver, muscle, thymus, lung and spleen.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U81295; AAC53195.1; -;
 CC EMBL; Y15685; CAA75730.1; -;
 CC RCD; 69265; Entrez.
 CC InterPro; IPR000407; GDA1_CD39_NTPase.
 CC Pfam; PF01150; GDA1_CD39_1.
 CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 CC Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 CC DOMAIN 1 16 Cytoplasmic (Potential).
 CC TRANSMEM 17 37 Potential.
 CC DOMAIN 38 478 Extracellular (Potential).
 CC TRANSMEM 479 499 Potential.
 CC DOMAIN 500 511 Cytoplasmic (Potential).
 CC CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 226 226 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 CC CONFLICT 332 332 F -> L (in Ref. 2).
 CC SEQUENCE 511 AA; 57408 MW; 4CC123D3B644C193 CRC64;
 Query Match 74.8%; Score 1794.5; DB 1; Length 511;
 Best Local Similarity 74.4%; Pred. No. 2.1e-130;
 Matches 328; Conservative 51; Mismatches 59; Indels 3; Gaps 3;
 QY 12 TQNKALPNVKGIVLDAGSSHTSLIYIKVPAEKENDTGVVHVQVECRVKGPGLSKFVKQ 71
 DB 38 THNKLPLPNVKGIVLDAGSSHTSLIYIKVPAEKENDTGVVHVQVECRVKGPGLSKFVKQ 97
 QY 72 VNEIGYILDCMERAREVIPSQHQETPVYLGTAGMRLRMSEELADRLVDLVVERSL 131
 DB 98 TDEIAAYLAECWKWSTERIPASKQHQETPVYLGTAGMRLRMSEELADRLVDLVVERSL 157
 QY 132 NYPDFQCARITGQEGAYGWTINYLKGFQSKTRWFSIVPTNQQETFGALDGG 191
 DB 158 SYPDFQGAIIITGQEGAYGWTINYLKGFQSKTRWFSIVPTNQQETFGALDGG 216

192 STQVTFVPMQNTIESPDNALQFLRYGKDYNNVYTHSFLCYGKDQALWQKLAKIQVASNEI 251
 217 STQVTFVPLNQTLQLEARETSLOFLRYGTDYVYTHSFLCYGKDQALWQKLAKIQVSSGI 276
 252 LRDPCHPGYKKVNVSDLYKTCTKRFEMTLPPQPFQFIQIGNYQOCHOSILELFTSY 311
 277 LKDPFCFPGYKKVNVSELYGTCTKRFEXKLPFNOFQVQGTGDEYEQHOSILKFFNNSH 336
 312 CPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKEL-NLTSEKV-SQEKVTEMMKKFCAQPWE 369
 337 CPYSQCAFNGVFLPPLOGDFGAFSAFYVNMDFPKKMANDSVSSQEKMTETIKMFCSPWE 396
 370 EIKTSVAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFHFGIKQISDAGWTILGYM 429
 397 EVKASPTVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFHFGIKQISDAGWTILGYM 456
 430 LNLTNMIPAEQPLSTPLSHST 450
 457 LNLTNMIPAEQPLSPPLPHST 477

RESULT 7
 ENPI_PIG
 ID ENPI_PIG STANDARD; PRT; 510 AA.
 AC Q9MYU4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 03-JUL-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (lymphoid cell
 DE activation antigen) (ecto-apyrase) (CD39 antigen).
 GN Name=ENTPD1; Synonyms=CD39;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buthera; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic endothelium;
 RX MEDLINE=20325090; PubMed=1086813;
 RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezak O.,
 RA Sevigny J.;
 RT "Distribution, cloning, and characterization of porcine nucleoside
 RT triphosphate diphosphohydrolase-1.";
 RL Eur. J. Biochem. 267:4106-4114(2000).
 RN [2]
 RP SEQUENCE OF 202-220.
 RC TISSUE=Pancras;
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Highest expression found in vascular
 CC endothelium, smooth muscle, spleen and lung.
 CC -1- PTM: Cleaved into two polypeptides that seem to stay together by
 CC noncovalent interactions.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL; AJ133746; CAB95871.1; -
CC InterPro; IPR000407; GDA1_CD39_NTPase.
CC Pfam; PF01150; GDA1_CD39; 1.
CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT CHAIN 1 510
FT FT
FT FT Ectonucleoside triphosphate
FT FT diposphohydrolase 1.
FT CHAIN 1 201
FT FT Ectonucleoside triphosphate
FT FT diposphohydrolase 1 27 kDa subunit.
FT CHAIN 202 510
FT FT Ectonucleoside triphosphate
FT FT diposphohydrolase 1 54 kDa subunit.
FT FT
FT FT Cytoplasmic (Potential).
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 477
FT TRANSMEM 38 477
FT DOMAIN 478 498
FT TRANSMEM 478 498
FT DOMAIN 499 510
FT TRANSMEM 499 510
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 274 274 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).
FT CONFLICT 203 203 G -> S (in Ref. 2).
SQ SEQUENCE 510 AA; 57757 MW; 82F8686940D7735 CRC64;
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Query Match 71.5%; Score 1715; DB 1; Length 510;
Best Local Similarity 70.7%; Pred. No. 3.1e-124;
Matches 311; Conservative 63; Mismatches 64; Indels 2; Gaps 2;

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Qy 12 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECKVPGISKVQK 71
Db 38 TQNKPLPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVSVQVECKLKGPGISEFAKK 97
Qy 72 VNEIGYIVLCWREAREVIPSQHOETPVYLGATAGMELLRMESEELADRLVDVVERSL 131
Db 98 LGEIDIVLEACMERARTVVPKSHQAEVYVYLGATAGMELLRKKNENLASKILSTVASIT 157
Qy 132 NYEFDQGIARIITGOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 191
Db 158 RYPFDQGIARIITGOEGAYGMITINYLKGFQSKTRWFLKPRKGDQTQTYGALDLGA 217
Qy 192 STQTVFQONQIESPDNALQFRLYGKDYNYVTHSFLCYGKQDALWQKLAKDIQVASNEI 251
Db 218 STQITFVPQNVLESPEPTLHFRLYGKNYSVYTHSFLCYGKQDALWQKLAKDIQVASNEI 276
Qy 252 LRDPGFHFGYKVVNVSDLYKTPCTKPEMTLPFOPEIQGIGNVQOCHQSILELNTSY 311
Db 277 IHEPCFHSYGQRNMVSHLYEAPCTRLTSLPPELIEQTGDFQKQCOQIRPLENTSY 336
Qy 312 CPYSQAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVS-QEKVTEMMKKFCAQPMEE 370
Db 337 CPYSRCSFDGVFLPLPQGDFAAFSAFYVMGMFLNLTSEGSFQSKVTSTLEAFCSRPAE 396
Qy 371 IKTSYAGVKEKLYSEYCPGSGYIISLLQGHFTADSWEHIFHTKIGSDAGWTGLGYML 430
Db 397 LQMYFGDVKEKLYSEYCPGSGYIISLLQGHFTADSWEHIFHTKIGSDAGWTGLGYML 456
Qy 431 NLTNWIPAEQPLSTPLSHST 450
Db 457 NLTNWIPSEEPSRLSHST 476
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RESULT 8
ENP1_BOVIN
ID_ENP1_BOVIN STANDARD; PRT; 513 AA.
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diposphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diposphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPDL; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Seigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diposphohydrolase.";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

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CC EMBL; AF005940; AAB62382.1; -
CC InterPro; IPR000407; GDA1_CD39_NTPase.
CC Pfam; PF01150; GDA1_CD39; 1.
CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 481
FT TRANSMEM 38 481
FT TRANSMEM 482 502
FT DOMAIN 503 513
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 336 336 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 373 373 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 460 460 N-linked (GlcNAc...) (Potential).
FT CONFLICT 97 97 K -> N (in Ref. 2).
FT CONFLICT 101 103 INV -> CGF (in Ref. 2).
FT CONFLICT 464 464 K -> V (in Ref. 2).
SQ SEQUENCE 513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;
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Query Match 70.5%; Score 1690.5; DB 1; Length 513;
Best Local Similarity 69.8%; Pred. No. 2.4e-122;
Matches 309; Conservative 64; Mismatches 65; Indels 5; Gaps 3;

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Qy 12 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECKVPGISKVQK 71
Db 38 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVTVQVECKVPGISGFARK 97
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Db 300 FCSKSWETKTSYPSVKKYLSYCFSGAYILS-LLQYNGFTGSWEQHFMGKIKDSNA 358
Qy 423 GWTLCYMLNLTNMPAEQPLSPHST 450
Db 359 GWTLCYMLNLTNMPAEQPLSPHST 386

RESULT 10
Q6DFS1 PRELIMINARY; PRT; 508 AA.
AC Q6DFS1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Entpdl-prov prov.
GN Name=entpdl-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076662; AAH76662.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39 NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39 NTPASE; 1.
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 60.5%; Score 1450; DB 2; Length 508;
Best Local Similarity 60.2%; Pred. No. 1e-103;
Matches 263; Conservative 75; Mismatches 97; Indels 2; Gaps 2;

Qy 13 QNKALPENYKGVILVDAGSSHTSLYIKWPAEKENDTGVHVECRKVGPGISKVFQKV 72
Db 39 QNKPLPNKIKGVILVDAGSSHTSVIYEWPAEKENDTGVVQINECKVEGNGISYGH 98
Qy 73 NEIGYILYTCMERAREVIPSQHQBTVPYLGATAGMRLLRMESEBELADRLVDVRSLSN 132
Db 99 LKAGLSLQCKMNAKQVPEKQRETPVYLGATAGMRLRLTNATMAEVLSSVENTLRS 158
Qy 133 YPFDQGARITQBEAGYGHITINYLKGPSQKTRWFSIVPYTNNOETFGALDGLGAS 192
Db 159 YPFDQGARITQBEAGYGHITINYLKGNFTQDSGNFKYIP-NPKPTETSGALDGLGAS 217
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RESULT 11

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Q6GP74 PRELIMINARY; PRT; 508 AA.
ID Q6GP74;
AC Q6GP74;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80631 protein.
GN Name=MGC80631;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
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Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

EMBL: BC073267.1; AAH73267.1; -.
GO: CO:0016787; F:hydrolase activity; IEA.
InterPro: IPR004047; GDAI_CD39_NTPase.
Pfam: PF01158; GDAI_CD39; 1.
PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
SEQUENCE 508 AA; 57049 MW; BD205818A06C523B CRC64;

Query Match 59.1%; Score 1418; DB 2; Length 508;
Best Local Similarity 59.1%; Pred. No. 3.1e-101;
Matches 259; Conservative 72; Mismatches 105; Indels 2; Gaps 2;

13 QNKALPENVKYGI VLDAGSSHTSYIYKWAPEKNDGTGVHVQSECRVKGPGISKFQVKV 72
39 QNKPLPKNIKYGI VLDAGSSHTSVYIYEWPESEKNDGTGVQVQINDCKVEGNGISSYGHEP 98
73 NEIGIYLTDCHERAREVTPRSHQETPVYLGATAGMRLLRMESELADRLVDLVVERSLN 132
99 TKAGLSLQCKMKNKARQVPEWQOKETPVYLGATAGMRLRLNNATMAEVLSSVENMLRS 158
133 YPFDQGARITGQEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDGLGAS 192
159 FFPDFQGARITGQEGAYGMITINYLGNFIQDSGWFKYMP-NFKPTGTSGALDGLGAS 217
193 TQVTVFQNQITTESPDNALQPLRYKDNVYTHSFLCYGKQDAWLQKAKDIQVASNEL 252
218 TQITTESKKE-IESQENSLHPELYKSDVYVTHSFLCYGKQDAURLANSVPATDSIL 276
253 RDPCHPGKVKVNVSDLYKTPCTKRFEMLTPFQOFEIQGIGNYQQCHQSILEFNTSYC 312
277 MDPCHNSGRRNTSISDLYSSFCISNLRISTAPSLDVKGTGNYQLCKRNEAIPDRTRC 336
313 PYSQAFNGIPLPLOGDFGAFSAFYVNMKFLNLTSEKVSQBKVETMMKKFCAQPWESIK 372
337 TYSHCSFNGIFQPTLDGTGFAFSAYFYVMDFLKLTGGEISLSDKVKETVERHCKSPWDEVK 396
373 TSYAGVKEKYLSYECFSGFYIISLLQLGYHFTADSWEHIFHTGKIQGS DAGWTLGLYMLNL 432
397 KEFPFKIKELYLSYECFSGFYIITLLEFGYGFNSWNNDIRFLGKIKSDAGWTLGLYMLNL 456
433 TNMIPAEQLSTPLSHST 450
457 TNMIPAEFLVSPPLSHAT 474

RESULT 12
6DC46 PRELIMINARY; PRT; 492 AA.

D O6DC46
C O6DC46; 28, Created)
T 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
T 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
E Zgc:100819 protein.
E Names=zgc:100819;
S Brachydanio rerio (Zebrafish) (Danio rerio).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
C Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A.
STRAIN=Singapore local strain; TISSUE=Embryo;
PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Zeeberg B., Moore T., Max S.I., Wang J., Heien F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
[1] Hulsk S.W.

diphosphohydrolase.";
J. Biol. Chem. 273:16043-16049(1998).
[2]
SEQUENCE OF 1-17.
TISSUE=Stomach;
MEDLINE#97442428; PubMed#9295305; DOI=10.1074/jbc.272.38.23645;
Lewis-Carl S., Kirley T.L.;
RA "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-apyrase."
RL J. Biol. Chem. 272:23645-23652(1997).
CC -I- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -I- COFACTOR: Requires calcium and magnesium (By similarity).
CC -I- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- PTM: N-glycosylated.
CC -I- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF041355; AAC26491.1; -;
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39_1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 7 Cytoplasmic (Potential).
FT TRANSMEM 8 28 Potential.
FT DOMAIN 29 463 Extracellular (Potential).
FT TRANSMEM 464 496 Potential.
FT DOMAIN 487 493 Cytoplasmic (Potential).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 16 16 C -> W (in Ref. 2).
FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
SQ SEQUENCE 493 AA; 54034 MW; F14FF4C3AA2F3603 CRC64;

Query Match 41.9%; Score 1004; DB 1; Length 493;
Best Local Similarity 45.7%; Pred. No. 3,4e-69;
Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

QY 17 LPENVKYGVLVDAGSHTSLYYIKWPAEKENDTGVVHVVEECRVKPGISKFPQKVNEIG 76
DB ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
35 LPPGTGYGLVDFDAGSTHLYVTQNFDKENGITGVQSVCCTVNGSGISYADDPPAG 94
:
QY 77 IYLTCMERAREVIPRSQHETPVYLGATAGMELLRMSEBELADRYLDVVYSLSNYPFD 136
DB ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
95 ASLKPCLDKAWAVIPVEQWQTPTYLGAAGMELLRQNSKTAEQVFAEVSKAIRFEPPVD 154
:
QY 137 FQARIITCGEGAYCIITINILLG---KFQSKTRWFISVPYTNQETFGALDLGGAST 193
DB ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
155 FRQAQILTGNESGSFWITVNYLETLLKPSFAGRW-----EHPQNTVEVLGALLDGAST 209

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 73.5121 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147A-28_COPY_25_474
Perfect score: 2398
Sequence: 1 ASTKKTQTSSTONKALPEN.....NLTNMPAEQLSTPLSHST 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : J_A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2398	100.0	474	3 AAY70923	Aay70923 Human sol
2	2398	100.0	474	3 AAY70900	Aay70900 Protein e
3	2395	99.9	454	3 AAY70913	Aay70913 Human sol
4	2395	99.9	454	3 AAY70890	Aay70890 Protein e
5	2395	99.9	473	3 AAY70924	Aay70924 Human sol
6	2395	99.9	473	3 AAY70901	Aay70901 Protein e
7	2395	99.9	478	3 AAY70914	Aay70914 Human sol
8	2395	99.9	478	3 AAY70891	Aay70891 Protein e
9	2380.5	99.3	487	3 AAY70921	Aay70921 Human sol
10	2380.5	99.3	487	3 AAY70898	Aay70898 Protein e
11	2356	98.2	476	3 AAY70911	Aay70911 Human CD3
12	2356	98.2	476	3 AAY70888	Aay70888 Protein e
13	2354	98.2	463	3 AAY70925	Aay70925 Human sol
14	2354	98.2	463	3 AAY70902	Aay70902 Protein e
15	2353	98.1	464	3 AAY70922	Aay70922 Human sol
16	2353	98.1	464	3 AAY70899	Aay70899 Protein e
17	2348	97.9	439	4 AAB71918	Aab71918 Soluble h
18	2348	97.9	510	2 AAW04334	Aaw04334 Human lym
19	2348	97.9	510	3 AAW04264	Aaw04264 Human CD3
20	2348	97.9	510	3 AAY70910	Aay70910 Human sol
21	2348	97.9	510	3 AAY70887	Aay70887 Human sol
22	2348	97.9	510	4 AAB71917	Aab71917 Human CD3
23	2348	97.9	510	7 ADJ57262	Adj57262 Human CD3
24	2348	97.9	510	8 ADL24295	Adl24295 Human CD3
25	2348	97.9	510	8 ADQ99453	Adq99453 Human CD3

26	2348	97.9	510	8 ADR69210	Adr69210 Human CD3
27	2348	97.9	510	8 ADR69042	Adr69042 Human CD3
28	2348	97.9	510	8 ADS17924	Ads17924 Human CD3
29	2348	97.9	510	8 ABO84674	Abo84674 Human can
30	2348	97.9	510	8 ADR87821	Adr87821 Human CD3
31	2348	97.9	511	8 ADK60421	Adk60421 Angiogene
32	2348	97.9	511	8 ADK60722	Adk60722 Angiogene
33	2348	97.9	511	8 ADP73345	Adp73345 CD39 lym
34	2348	97.9	517	7 ADN95839	Adn95839 Human BEC
35	2348	97.9	517	8 ADK60221	Adk60221 Angiogene
36	2348	97.9	517	8 ADK60522	Adk60522 Angiogene
37	2348	97.9	517	8 ADP73145	Adp73145 Angiogene
38	2348	97.9	522	8 ABO84672	Abo84672 Human can
39	2295	95.7	529	3 AEM83376	Aem83376 Human dia
40	2294	95.7	476	3 AAY70912	Aay70912 Human CD3
41	2294	95.7	476	3 AAY70889	Aay70889 Protein e
42	2137	89.1	503	8 ABM83377	Abm83377 Human dia
43	1969	82.1	402	8 ABO84671	Abo84671 Human can
44	1841	76.8	377	7 ADI62735	Adi62735 Human apo
45	1118	46.6	311	8 ABO84673	Abo84673 Human can

ALIGNMENTS

RESULT 1

AAY70923
ID AAY70923 standard; protein; 474 AA.

AC AAY70923;

XX
DT 17-AUG-2000 (first entry)

XX Human soluble CD39 fusion protein construct, pIL2LTrim3.

XX Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; anitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..24

FT /label= Leader peptide

FT /note= "Derived from human interleukin 2 (hIL2)"

FT Cleavage-site 24..25

FT /note= "Cleavage site of leader sequence"

FT Protein 36..474

FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMMV) IMMUNEX CORP.

XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

XX New soluble CD39 polypeptides having apyrase activity, useful for

PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX Claim 6; Page 113-114; 122pp; English.
XX The present sequence is the fusion protein construct, pIL2Trim3. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity.
CC Soluble CD39 is constructed by removing the N- and C-terminal
CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
CC at relevant concentrations and the ability to block and reverse ADP-
CC induced platelet activation and recruitment, including platelet
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
CC myocardial infarction, coronary artery disease or injury, embolism,
CC atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
CC associated ischaemic disorders including lung, coronary and cerebral
CC ischaemia, thrombotic disorders including coronary, peripheral and
CC cerebral artery thrombosis, intracardiac and venous thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
SQ Sequence 474 AA;
Query Match 100.0%; Score 2398; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.6e-237;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKTKLTSSQNKALPENVKYGLVDAGSSHTSLIYKWPAPKENDTGVVHVEECRV 60
DB 25 ASTKTKLTSSQNKALPENVKYGLVDAGSSHTSLIYKWPAPKENDTGVVHVEECRV 84
QY 61 KPGISKFQVKVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELAD 120
DB 85 KPGISKFQVKVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELAD 144
QY 121 RVLDDVVERSLNYPDFQARITGOEGAYGWTINVLGKFSQKRWFSIVPVTNNQ 180
DB 145 RVLDDVVERSLNYPDFQARITGOEGAYGWTINVLGKFSQKRWFSIVPVTNNQ 204
QY 181 ETGALDLGASTQVTFVQNOTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKL 240
DB 205 ETGALDLGASTQVTFVQNOTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKL 264
QY 241 AKDIQVASNEILRDPCHFPGYKVVNVSDLYKTPCTKRPEMTLPQQFPIQIGNYQOCH 300
DB 265 AKDIQVASNEILRDPCHFPGYKVVNVSDLYKTPCTKRPEMTLPQQFPIQIGNYQOCH 324
QY 301 QSTLELFNTSYCPYSQCAFNGIELPLQDGFAGSAFYFMKFLNLTSEKVSQEKVTENN 360
DB 325 QSTLELFNTSYCPYSQCAFNGIELPLQDGFAGSAFYFMKFLNLTSEKVSQEKVTENN 384
QY 361 KFTCAQPEWBEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGKIQGS 420
DB 385 KFTCAQPEWBEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFADSWEHIFIGKIQGS 444
QY 421 DAGWTLYMLNLNMPAEQPLSTPLSHST 450
DB 445 DAGWTLYMLNLNMPAEQPLSTPLSHST 474
RESULT 2
ID AAY70900 standard; protein; 474 AA.
XX
AC AAY70900;
XX
DT 17-AUG-2000 (first entry)
XX
DE Protein encoded by Trim 3 construct.
XX

KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pIL2Trim3 variant.
XX Homo sapiens.
OS Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Cleavage-site 24..25
FT Protein 36..474
FT /note="Soluble portion of CD39"
FT
FT
PN W0200023094-A2.
XX
PD 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US023641.
XX
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339518/29.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
XX
XX Example 11; Page 113-114; 118pp; English.
PS
XX
XX The present sequence is the protein encoded by Trim3 construct. pIL2Trim3
XX variant was constructed by removing the human IL2 residues from solCD39
XX fusion construct. Fusion of 12 amino acids from the N-terminus of mature
XX human IL2 to the solCD39 coding region results in high levels of both
XX expression and activity in the supernatants of transfected cells. SolCD39
XX is used in the treatment of unstable angina, myocardial infarction,
XX stroke, coronary artery disease or injury, atherosclerosis, peripheral
XX vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
XX disorder including lung ischaemia, coronary ischaemia and cerebral
XX ischaemia, a thrombotic disorder including coronary artery thrombosis,
XX cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
XX thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
XX thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
XX Soluble CD39 is also useful for preventing thrombus formation or
XX reformation, occlusion, reocclusion, stenosis or restenosis of blood
XX vessels or stroke
XX
SQ Sequence 474 AA;

Query Match 100.0%; Score 2398; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.6e-237;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKTKLTSSQNKALPENVKYGLVDAGSSHTSLIYKWPAPKENDTGVVHVEECRV 60
DB 25 ASTKTKLTSSQNKALPENVKYGLVDAGSSHTSLIYKWPAPKENDTGVVHVEECRV 84
QY 61 KPGISKFQVKVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELAD 120

Db 85 KPGISKFVQKNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELAD 144
Qy 121 RVLDDVRSLSNYPDFQAGARIITQOERGAYGWIITVYLLGKFSQKTRWFSIVPYETNNQ 180
Db 145 RVLDDVRSLSNYPDFQAGARIITQOERGAYGWIITVYLLGKFSQKTRWFSIVPYETNNQ 204
Qy 181 ETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFICYGKDQALWOKL 240
Db 205 ETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFICYGKDQALWOKL 264
Qy 241 AKDIOVASNEILRDCPFHPGKVVVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 300
Db 265 AKDIOVASNEILRDCPFHPGKVVVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 324
Qy 301 QSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMM 360
Db 325 QSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMM 384
Qy 361 KKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGS 420
Db 385 KKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGS 444
Qy 421 DAGWTGLGYMLNLTNMPAEQPLSTPLSHST 450
Db 445 DAGWTGLGYMLNLTNMPAEQPLSTPLSHST 474

RESULT 3

AAV70913
ID AAV70913 standard; protein; 454 AA.

AC AAV70913;

DT 17-AUG-2000 (first entry)

DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.

Kw Soluble CD39; human; apyrase activity; platelet activation;
Kw unstable angina; myocardial infarction; stroke; coronary artery disease;
Kw atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
Kw platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
Kw coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
Kw thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
Kw antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
Kw cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Protein 1..15

FT /label= Mature human interleukin_2

FT /note= "N-terminal region"

FT Protein 16..454

FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX PN

XX 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US022955.

XX PR 16-OCT-1998; 98US-0104585P.

XX PR 06-NOV-1998; 98US-0107466P.

XX PR 13-AUG-1999; 99US-0149010P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX XX WPI; 2000-339644/29.

XX DR N-PSDB; AAD00206.

XX XX

PT New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.

PS Claim 6a; Page 95-97; 122pp; English.

XX The present sequence is a fusion construct, comprising the N-terminal
CC amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
CC region, that has apyrase activity. This results in high levels of solCD39
CC expression and activity in the transfected cells. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations
CC and the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
CC embolism, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke

XX Sequence 454 AA;

Query Match 99.9%; Score 2395; DB 3; Length 454;

Best Local Similarity 99.8%; Pred. No. 4.9e-237;

Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKTKTQTSSTQNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVVHVQVECRV 60

Db :|||||

5 SSTKTKTQTSSTQNKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGTVVHVQVECRV 64

Qy 61 KGPGISKFVQKNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELAD 120

Db :|||||

65 KGPGISKFVQKNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELAD 124

Qy 121 RVLDDVRSLSNYPDFQAGARIITQOERGAYGWIITVYLLGKFSQKTRWFSIVPYETNNQ 180

Db :|||||

125 RVLDDVRSLSNYPDFQAGARIITQOERGAYGWIITVYLLGKFSQKTRWFSIVPYETNNQ 184

Qy 181 ETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFICYGKDQALWOKL 240

Db :|||||

185 ETFGALDLGGASTQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFICYGKDQALWOKL 244

Qy 241 AKDIOVASNEILRDCPFHPGKVVVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 300

Db :|||||

245 AKDIOVASNEILRDCPFHPGKVVVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 304

Qy 301 QSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMM 360

Db :|||||

305 QSILELNTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYVFMKFLNLTSEKVSQEKVTMM 364

Qy 361 KKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGS 420

Db :|||||

365 KKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGKIQGS 424

Qy 421 DAGWTGLGYMLNLTNMPAEQPLSTPLSHST 450

Db :|||||

425 DAGWTGLGYMLNLTNMPAEQPLSTPLSHST 454

RESULT 4

AAV70890

ID AAV70890 standard; protein; 454 AA.

XX AC AAV70890;

XX XX

XX DT 17-AUG-2000 (first entry)

XX DE Protein encoded by fusion construct of human soluble CD39 cDNA-1.

61	QY	KGPGISKFVQKVNNEIGYILTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD	120
65	Db	KGPGISKFVQKVNNEIGYILTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD	124
121	QY	RVLVDVERSLSNTPPFDQGARIIITGQEGAGYGMTINILLGKFSOKTRWFESIVPVETNNQ	180
125	Db	RVLVDVERSLSNTPPFDQGARIIITGQEGAGYGMTINILLGKFSOKTRWFESIVPVETNNQ	184
181	QY	ETFGALDGGASTQVTFVPQNIETSPDNALQFRLYGKDYNVYTHSFLCYGKQDQALWQKL	240
185	Db	ETFGALDGGASTQVTFVPQNIETSPDNALQFRLYGKDYNVYTHSFLCYGKQDQALWQKL	244
241	QY	AKDIQVASNEILRDCPFHPGCKKVVNVSDLYKTPCTKRFEMTLPQQOFEIQIGNYQOCH	300
245	Db	AKDIQVASNEILRDCPFHPGCKKVVNVSDLYKTPCTKRFEMTLPQQOFEIQIGNYQOCH	304
301	QY	QSIILELNTSCYPYSQCAFNGIELPLQGDGFAFSAFYVMKFLNLTSEKYSQEKVTEWM	360
305	Db	QSIILELNTSCYPYSQCAFNGIELPLQGDGFAFSAFYVMKFLNLTSEKYSQEKVTEWM	364
361	QY	KKFCAQPWEEIKTSYAGVKEKYLSEYCFSGSTYILSLLLQYHFTADSWEHIFIKIQGS	420
365	Db	KKFCAQPWEEIKTSYAGVKEKYLSEYCFSGSTYILSLLLQYHFTADSWEHIFIKIQGS	424
421	QY	DAGWTLGYMLNLTMNIPAEQPLTPLSHST	450
425	Db	DAGWTLGYMLNLTMNIPAEQPLTPLSHST	454
RESULT 5			
AAAY70924			
AC	AAAY70924	ID	AAAY70924 standard; protein; 473 AA.
AC	AAAY70924;		
DT	17-AUG-2000	(first entry)	
XX	XX	Human soluble CD39 fusion protein construct, pIL2LTrim4.	
DE	XX		
XX	XX	Soluble CD39; sCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; intraluminal; cerebroprotective; antihypertensive; anticoagulant; cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.	
OS	XX	Homo sapiens.	
OS	XX	Synthetic.	
XX	XX		
XX	XX	Location/Qualifiers	
FT	FT	1..24	/label= Leader peptide
FT	FT	/note= "Derived from human interleukin 2 (hIL2)"	
FT	FT	26..27	/note= "Cleavage site of leader sequence"
FT	FT	35..473	/note= "Human soluble CD39 protein"
FT	FT		
XX	XX	WO200023459-A1.	
PN	XX		
XX	XX	27-APR-2000.	
PD	XX		
XX	XX	13-OCT-1999;	99WO-US022955.
XX	XX		
XX	XX	16-OCT-1998;	98US-0104585P.
PR	XX	06-NOV-1998;	98US-0107466P.
PR	XX	13-AUG-1999;	99US-0149010P.
XX	XX	(IMMV) IMMUNEX CORP.	
FA	XX		

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 114-116; 122pp; English.
XX
XX The present sequence is the fusion protein construct, pIL2LTrim4. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity.
CC Soluble CD39 is constructed by removing the N- and C-terminal
CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
CC at relevant concentrations and the ability to block and reverse ADP-
CC induced platelet activation and recruitment, including platelet
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
CC myocardial infarction, coronary artery disease or injury, embolism,
CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, platelet-
CC associated ischaemic disorders including lung, coronary and cerebral
CC ischaemia, thrombotic disorders including coronary, peripheral and
CC cerebral artery thrombosis, intracardiac and venous thrombosis, PE)
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
XX Sequence 473 AA;
XX
XX Query Match 99.9%; Score 2395; DB 3; Length 473;
XX Best Local Similarity 99.8%; Pred. No. 5.2e-237;
XX Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ASTKTKTQTSSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRV 60
Db :|||||
QY 24 SSTKTKTQTSSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRV 83
Db :|||||
QY 61 KPGISKFQVKQNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMSEELAD 120
Db :|||||
QY 84 KPGISKFQVKQNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMSEELAD 143
Db :|||||
QY 121 RVLVDVRSLSNYPDFQARIITQOEGAYGWITINYLKGFQSKTRFWSIVPYETNNQ 180
Db :|||||
QY 144 RVLVDVRSLSNYPDFQARIITQOEGAYGWITINYLKGFQSKTRFWSIVPYETNNQ 203
Db :|||||
QY 181 ETFGALDLGGASTQVTFPQNTIESPDNALQFRLYGKDYNYTHSFYCYGKQDALWQKL 240
Db :|||||
QY 204 ETFGALDLGGASTQVTFPQNTIESPDNALQFRLYGKDYNYTHSFYCYGKQDALWQKL 263
Db :|||||
QY 241 AKDIQVANSNEILRDCFPHPGKVVNSDLYKTPCTKPFEMTLPPQQPEIOGIGNYQOCH 300
Db :|||||
QY 264 AKDIQVANSNEILRDCFPHPGKVVNSDLYKTPCTKPFEMTLPPQQPEIOGIGNYQOCH 323
Db :|||||
QY 301 OSILELFTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVKFNLMTSEKVSQEKVTEMM 360
Db :|||||
QY 324 OSILELFTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVKFNLMTSEKVSQEKVTEMM 383
Db :|||||
QY 361 KFKCAQPWEEIKTSVAGVKEKYLSCYSGTYVILSLILLOGHFTFADSWEHIFIGKIQGS 420
Db :|||||
QY 384 KFKCAQPWEEIKTSVAGVKEKYLSCYSGTYVILSLILLOGHFTFADSWEHIFIGKIQGS 443
Db :|||||
QY 421 DAGWTGLGMLNLTNNMIPAEQPLSTPLSHST 450
Db :|||||
QY 444 DAGWTGLGMLNLTNNMIPAEQPLSTPLSHST 473
Db :|||||
XX
XX RESULT 6
XX ID AAY70901
XX AAY70901 standard; proteain; 473 AA.
XX
XX AC AAY70901;
XX
XX DT 17-AUG-2000 (first entry)
XX
XX Protein encoded by Trim 4 construct.
XX
XX Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;
KW unstable angina; myocardial infarction; pre-eclampsia; embolism;
KW atherosclerosis; peripheral vascular occlusion; thrombolytic;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; anti-angiogenic; cardiant;
KW cerebroprotective; anti-arteriosclerotic; vasotrophic; anticoagulant;
KW coronary ischaemia; vascular occlusion; pIL2Trim4 variant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Cleavage-site 26..27
XX Protein 35..473
XX /note= "Soluble portion of CD39"
XX
XX WO200023094-A2.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US023641.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.
XX
XX Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339518/29.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39
PT polypeptides.
XX
XX Example 11; Page 114-116; 118pp; English.
XX
XX The present sequence is the protein encoded by Trim4 construct. pIL2Trim4
CC variant was constructed by removing the human IL2 residues from solCD39
CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
CC human IL2 to the solCD39 coding region results in high levels of both
CC expression and activity in the supernatants of transfected cells. SolCD39
CC is used in the treatment of unstable angina, myocardial infarction,
CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
CC vascular occlusion, pre-eclampsia, embolism, platelet-associated ischaemic
CC disorder including lung ischaemia, coronary ischaemia and cerebral
CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
CC Soluble CD39 is also useful for preventing thrombus formation or
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke
XX
XX Sequence 473 AA;
XX
XX Query Match 99.9%; Score 2395; DB 3; Length 473;
XX Best Local Similarity 99.8%; Pred. No. 5.2e-237;
XX Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ASTKTKTQTSSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRV 60
Db :|||||
QY 24 SSTKTKTQTSSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRV 83
Db :|||||
QY 61 KPGISKFQVKQNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMSEELAD 120
Db :|||||
QY 84 KPGISKFQVKQNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMSEELAD 143
Db :|||||
QY 121 RVLVDVRSLSNYPDFQARIITQOEGAYGWITINYLKGFQSKTRFWSIVPYETNNQ 180
Db :|||||
QY 144 RVLVDVRSLSNYPDFQARIITQOEGAYGWITINYLKGFQSKTRFWSIVPYETNNQ 203
Db :|||||
QY 181 ETFGALDLGGASTQVTFPQNTIESPDNALQFRLYGKDYNYTHSFYCYGKQDALWQKL 240
Db :|||||
QY 204 ETFGALDLGGASTQVTFPQNTIESPDNALQFRLYGKDYNYTHSFYCYGKQDALWQKL 263
Db :|||||
QY 241 AKDIQVANSNEILRDCFPHPGKVVNSDLYKTPCTKPFEMTLPPQQPEIOGIGNYQOCH 300
Db :|||||
QY 264 AKDIQVANSNEILRDCFPHPGKVVNSDLYKTPCTKPFEMTLPPQQPEIOGIGNYQOCH 323
Db :|||||
QY 301 OSILELFTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVKFNLMTSEKVSQEKVTEMM 360
Db :|||||
QY 324 OSILELFTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVKFNLMTSEKVSQEKVTEMM 383
Db :|||||
QY 361 KFKCAQPWEEIKTSVAGVKEKYLSCYSGTYVILSLILLOGHFTFADSWEHIFIGKIQGS 420
Db :|||||
QY 384 KFKCAQPWEEIKTSVAGVKEKYLSCYSGTYVILSLILLOGHFTFADSWEHIFIGKIQGS 443
Db :|||||
QY 421 DAGWTGLGMLNLTNNMIPAEQPLSTPLSHST 450
Db :|||||
QY 444 DAGWTGLGMLNLTNNMIPAEQPLSTPLSHST 473
Db :|||||
XX
XX RESULT 6
XX ID AAY70901
XX AAY70901 standard; proteain; 473 AA.
XX
XX AC AAY70901;
XX

Db 24 SSTRKKTQLTSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGTVHGVVECRV 83
Qy 61 KPGGSKFVKQVKEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD 120
Db 84 KPGGSKFVKQVKEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD 143
Qy 121 RVLVDVERSLSNYPDFQAGRIITGQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQ 180
Db 144 RVLVDVERSLSNYPDFQAGRIITGQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQ 203
Qy 191 ETFGALDLGGASTQVTFVPOQNTIESPDNALQFLYKGDYNNVTHSLCYGKQDALWQKL 240
Db 204 ETFGALDLGGASTQVTFVPOQNTIESPDNALQFLYKGDYNNVTHSLCYGKQDALWQKL 263
Qy 241 AKDIOVASNEILRDPFCFHPGKVKVNVSDLYKTKRFEMLTLPFOQFEIQQIGNYQOCH 300
Db 264 AKDIOVASNEILRDPFCFHPGKVKVNVSDLYKTKRFEMLTLPFOQFEIQQIGNYQOCH 323
Qy 301 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMM 360
Db 324 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMM 383
Qy 361 KKFCQAPWEEIKTSVAGVKEKYLSEYCFSGTYIILSLLLQGHFTADSWEHIFGKIQGS 420
Db 384 KKFCQAPWEEIKTSVAGVKEKYLSEYCFSGTYIILSLLLQGHFTADSWEHIFGKIQGS 443
Qy 421 DAGWTGLGYMLNLTNMIPEAQPLSTPLSHST 450
Db 444 DAGWTGLGYMLNLTNMIPEAQPLSTPLSHST 473
RESULT 7
AAV70914
ID AAY70914 standard; protein; 478 AA.
XX AC AAY70914;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 fusion protein construct, pIL2LsolCD39.
XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Peptide
XX FT 1..24 Location/Qualifiers
XX FT /label= Leader peptide
XX FT /note= Derived from human interleukin 2 (hIL2) "
XX FT 25..36
XX FT /label= Mature human interleukin_2
XX FT /note= Derived from N-terminal end of human IL2 "
XX FT 37..39
XX FT /note= "Linker"
XX FT 40..478
XX FT /note= "Human soluble CD39 protein"
XX WO200023459-A1.
XX 27-APR-2000.
XX 13-OCT-1999; 99WO-US022955.
XX 16-OCT-1998; 98US-0104585P.
PR

PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX (IMMV) IMMUNEX CORP.
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI: 2000-339644/29.
XX N-PSDB; AAD00207.
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX Disclosure; Page 99-101; 122pp; English.
XX The present sequence is a fusion construct pIL2LsolCD39, comprising the
XX leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
XX mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,
XX having apyrase activity. This produces high levels of solCD39 expression
XX and activity in the transfected cells. Soluble CD39 is constructed by
XX removing the N- and C-terminal transmembrane domains. It retains the
XX capacity to metabolise ATP and ADP at relevant concentrations and the
XX ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular disorders including lung,
XX embolism, platelet-associated ischaemic disorders including coronary,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis (DVT), pulmonary
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX SQ Sequence 478 AA;
Query Match 99.9%; Score 2395; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 5.3e-237;
Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTKKTQLTSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGTVHGVVECRV 60
Db 29 SSTRKKTQLTSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGTVHGVVECRV 88
Qy 61 KPGGSKFVKQVKEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD 120
Db 89 KPGGSKFVKQVKEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELAD 148
Qy 121 RVLVDVERSLSNYPDFQAGRIITGQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQ 180
Db 149 RVLVDVERSLSNYPDFQAGRIITGQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQ 208
Qy 181 ETFGALDLGGASTQVTFVPOQNTIESPDNALQFLYKGDYNNVTHSLCYGKQDALWQKL 240
Db 209 ETFGALDLGGASTQVTFVPOQNTIESPDNALQFLYKGDYNNVTHSLCYGKQDALWQKL 268
Qy 241 AKDIOVASNEILRDPFCFHPGKVKVNVSDLYKTKRFEMLTLPFOQFEIQQIGNYQOCH 300
Db 269 AKDIOVASNEILRDPFCFHPGKVKVNVSDLYKTKRFEMLTLPFOQFEIQQIGNYQOCH 328
Qy 301 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMM 360
Db 329 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVNMKFLNLTSEKVSQEKVTMM 388
Qy 361 KKFCQAPWEEIKTSVAGVKEKYLSEYCFSGTYIILSLLLQGHFTADSWEHIFGKIQGS 420
Db 389 KKFCQAPWEEIKTSVAGVKEKYLSEYCFSGTYIILSLLLQGHFTADSWEHIFGKIQGS 448
Qy 421 DAGWTGLGYMLNLTNMIPEAQPLSTPLSHST 450
Db 449 DAGWTGLGYMLNLTNMIPEAQPLSTPLSHST 478

```

CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
CC useful for preventing thrombus formation or reformation, occlusion,
CC reocclusion, stenosis or restenosis of blood vessels or stroke
XX
SQ Sequence 478 AA;

Query Match          99.9%; Score 2395; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 5.3e-237;
Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTTKTOLTSTQNKALPENVKYIGVLDAGSSHTSLIYKWPARKENDTGVVHVEECRV 60
Db 29 SSTTKTOLTSTQNKALPENVKYIGVLDAGSSHTSLIYKWPARKENDTGVVHVEECRV 88
Qy 61 KPGIGSKFVKVQKVEIGIYVLTDCMERAREVTPRSQHQETPVYLGATAGNRLRMESEELAD 120
Db 89 KPGIGSKFVKVQKVEIGIYVLTDCMERAREVTPRSQHQETPVYLGATAGNRLRMESEELAD 148
Qy 121 RVLDDVERSLSNYPDFQGARIIITQSEGA YGMITINYLKGFQSKTRWFSIVPYETNNQ 180
Db 149 RVLDDVERSLSNYPDFQGARIIITQSEGA YGMITINYLKGFQSKTRWFSIVPYETNNQ 208
Qy 181 ETFGALDLGGASTQVTFVPQNTTIESPDNALQFLYCKDYNVYTHSFLCYCKDQALWOKL 240
Db 209 ETFGALDLGGASTQVTFVPQNTTIESPDNALQFLYCKDYNVYTHSFLCYCKDQALWOKL 268
Qy 241 AKDIQVASNEILTRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 300
Db 269 AKDIQVASNEILTRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCH 328
Qy 301 QSILELENTSYCPYSQCAFNGIFLPLQGDGFGAFSAFYVMKFLNLITSEKVSQSKVTEMM 360
Db 329 QSILELENTSYCPYSQCAFNGIFLPLQGDGFGAFSAFYVMKFLNLITSEKVSQSKVTEMM 388
Qy 361 KKFCAPWEEIKTSYAGVKERYLSEYCFSGTYILSLLIQGYHFTADSWEHIFIGKIQGS 420
Db 389 KKFCAPWEEIKTSYAGVKERYLSEYCFSGTYILSLLIQGYHFTADSWEHIFIGKIQGS 448
Qy 421 DAGWTLGYMLNLTNMIPAEQPLSTPLSHST 450
Db 449 DAGWTLGYMLNLTNMIPAEQPLSTPLSHST 478

RESULT 9
AAY70921
ID AAY70921 standard; protein; 487 AA.
XX AC AAY70921;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 fusion protein construct, pIL2LFlagSolCD39.
XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
XX KW unstable angina; myocardial infarction; stroke; coronary artery disease;
XX KW atherosclerosis; peripheral vascular occlusion; preecclampsia; embolism;
XX KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
XX KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
XX KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
XX KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
XX KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Peptide
XX FT /label= Leader peptide
XX FT /note= "Derived from human interleukin 2 (hIL2)"
XX FT Peptide
XX FT /note= "Mature human interleukin 2 (hIL2) N-terminal end"
XX FT Region
XX FT /note= "37..40"

RESULTS
AAY70921
ID AAY70921 standard; protein; 478 AA.
XX AC AAY70921;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by pIL2Lsol CD39.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
XX KW unstable angina; myocardial infarction; stroke; coronary artery disease;
XX KW atherosclerosis; peripheral vascular occlusion; preecclampsia; embolism;
XX KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
XX KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
XX KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
XX KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
XX KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
XX KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
XX KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
XX KW coronary ischaemia; vascular occlusion.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Peptide
XX FT /note= "huIL2 leader sequence"
XX FT Protein
XX FT /note= "Mature human IL2"
XX FT Region
XX FT /note= "Linker"
XX FT Protein
XX FT /note= "SolCD39 protein"
XX PN WO200023094JA2.
XX PD 27-APR-2000;
XX PF 13-OCT-1999; 98NO-US023641.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 98US-0145010P.
XX PA (IMMV ) IMMUNEX CORP.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
XX DR N-PSDB; AAD00202.
XX KW Inhibiting platelet activation and recruitment, useful for treating a
XX KW mammal suffering from unstable angina, myocardial infarction, stroke,
XX KW coronary artery disease or injury, comprises administering soluble CD39
XX KW polypeptides.
XX PS Disclosure; Page 99-101; 118pp; English.
XX CC The present sequence is protein encoded by the coding region of
XX CC pIL2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase
XX CC activity. Fusion of 12 amino acids from the N-terminus of mature human
XX CC IL2 to the solCD39 coding region results in high levels of both
XX CC expression and activity in the supernatants of transfected cells. This is
XX CC used in the treatment of unstable angina, myocardial infarction, stroke,
XX CC coronary artery disease or injury, atherosclerosis, peripheral vascular
XX CC occlusion, preecclampsia, embolism, platelet-associated ischaemic disorder
XX CC including lung ischaemia, coronary ischaemia and cerebral ischaemia, a
XX CC thrombotic disorder including coronary artery thrombosis, cerebral artery
XX CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
```

FT	Region	/note= "Linker sequence"	
FT	41. .48		
FT	Protein	/note= "FLAG Tag sequence"	
FT	49. .487		
FT		/note= "Human soluble CD39 protein"	
XX			
PN	WO200023459-A1.		
XX			
PD	27-APR-2000.		
XX			
PF	13-OCT-1999; 99WO-US022955.		
XX			
PR	16-OCT-1998; 98US-0104585P.		
PR	06-NOV-1998; 98US-0107466P.		
PR	13-AUG-1999; 99US-0149010P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;		
XX			
DR	WPI; 2000-339644/29.		
DR	N-PSDB; AAD00209.		
XX			
XX	New soluble CD39 polypeptides having apyrase activity, useful for		
PT	inhibiting angiogenesis and treating unstable angina, myocardial		
PT	infarction, stroke, coronary artery disease or injury.		
XX			
PS	Disclosure; Page 109-111; 122pp; English.		
XX			
CC	The present sequence is the fusion protein construct pIL2FlagSolCD39,		
CC	comprising the leader peptide of human interleukin 2 (hIL2), 12 amino		
CC	acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and		
CC	soluble CD39; (solCD39) protein region, that has apyrase activity. This		
CC	produces high levels of solCD39 expression and activity in the		
CC	transfected cells. Soluble CD39 is constructed by removing the N- and C-		
CC	terminal transmembrane domains. It retains the capacity to metabolise ATP		
CC	and ADP at relevant concentrations and the ability to block and reverse		
CC	ADP-induced platelet activation and recruitment, including platelet		
CC	aggregation. Soluble CD39 polypeptides are useful for inhibiting		
CC	angiogenesis. It is useful for the treatment of unstable angina,		
CC	myocardial infarction, stroke, coronary artery disease or injury,		
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,		
CC	platelet-associated ischaemic disorders including lung, coronary and		
CC	cerebral ischaemia, thrombotic disorders including coronary, peripheral		
CC	and cerebral artery thrombosis, intracardiac and venous thrombosis,		
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), and		
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing		
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or		
CC	restenosis of blood vessels or stroke		
XX			
SQ	Sequence 487 AA;		
	Query Match 99.3%; Score 2380.5; DB 3; Length 487;		
	Best Local Similarity 97.8%; Pred. No. 1.7e-235;		
	Matches 449; Conservative 1; Mismatches 0; Indels 9; Gaps 1;		
QY	1 ASTKTKQLTSS-----TQKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGV 51		
Db	29 SSTKTKQLTSSGDYKDDDKTKQKALPENVKYGVLDAGSSHTSLIYKWPAREKNDTGV 88		
QY	52 VHOVEECRVKPGISKFVQKVEIGIYLTDCMERAREVIPRSHOHTPVYLGATAGMRLL 111		
Db	89 VHOVEECRVKPGISKFVQKVEIGIYLTDCMERAREVIPRSHOHTPVYLGATAGMRLL 148		
QY	112 RMESEELADRLVDVRSLSNYPDFQAGARIITGQEGAYGMITINYLKGFSSQKTRWFS 171		
Db	149 RMESEELADRLVDVRSLSNYPDFQAGARIITGQEGAYGMITINYLKGFSSQKTRWFS 208		
QY	172 IVPYETNNQTFQALDLCGASTQVTPVQNTIESPDNALQRLYKGDYNNVYTHSFLCYG 231		
Db	209 IVPYETNNQTFQALDLCGASTQVTPVQNTIESPDNALQRLYKGDYNNVYTHSFLCYG 268		
QY	232 KQALWQKLAKDIQVANSNEILRDCPHGKGVVNSDLYKTPCTKRFEWTLFPOQFEIQ 291		

PT coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
PS Example 9; Page 109-111; 118pp; English.
XX
CC The present sequence is encoded by soluble CD39(solCD39) expression
CC plasmid. This was used for the transient expression of solCD39 protein in
CC mammalian expression systems. SolCD39 is used in the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,
CC embolism, platelet-associated ischaemic disorder including lung
CC ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder
CC including coronary artery thrombosis, cerebral artery thrombosis,
CC intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis,
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE), transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX Sequence 487 AA;
Query Match 99.3%; Score 2380.5; DB 3; Length 487;
Best Local Similarity 97.8%; Pred. No. 1.7e-235;
Matches 449; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 1 ASTKTKTQTSS-----TONKALPENVKYGVLDAGSSHTSLYIYKWPAAEKENDTGV 51
DB :|||||
29 SSTKTKTQTSSGDYDDDKTONKALPENVKYGVLDAGSSHTSLYIYKWPAAEKENDTGV 88
QY 52 VHOVEECRVKGGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRL 111
DB 89 VHOVEECRVKGGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRL 148
QY 112 RMESEELADRLDVVERSLSNYPFQGARITGQEGAYGWITINLLGKFSQKTRWFS 171
DB 149 RMESEELADRLDVVERSLSNYPFQGARITGQEGAYGWITINLLGKFSQKTRWFS 208
QY 172 IVPYETNNQETFGALDLGGASTQVTFVFNQNTIESPDNALQFRLYGKDYNVYTHSFLCYG 231
DB 209 IVPYETNNQETFGALDLGGASTQVTFVFNQNTIESPDNALQFRLYGKDYNVYTHSFLCYG 268
QY 232 KQALWQKLADIQVANSNEILLRDCPHGKYKKNVNSLYKTPCTKREMTLPQQPFIQ 291
DB 269 KQALWQKLADIQVANSNEILLRDCPHGKYKKNVNSLYKTPCTKREMTLPQQPFIQ 328
QY 292 GIGNYQQCHQSILELFTNSYCPYSOCANFGIFLPLQGDGFAFSFYFWMKFLNLTSEKV 351
DB 329 GIGNYQQCHQSILELFTNSYCPYSOCANFGIFLPLQGDGFAFSFYFWMKFLNLTSEKV 388
QY 352 SOEKVTEMMKXFCAPWEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEH 411
DB 389 SOEKVTEMMKXFCAPWEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEH 448
QY 412 HFIGKIQSDAGWTGLYMLNLTNMTIPAEQPLSTPLSHST 450
DB 449 HFIGKIQSDAGWTGLYMLNLTNMTIPAEQPLSTPLSHST 487
RESULT 11
ID AAY70911 standard; protein; 476 AA.
XX
AC AAY70911;
XX
DT 17-AUG-2000 (first entry)
XX Human CD39-L4-1 protein construct.
XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..37
XX FT /note= "Human CD39-L4 protein N-terminal end"
XX FT Cleavage-site 20..21
XX FT /note= "Cleavage site of leader sequence"
XX FT Region 38..476
XX FT /note= "Human soluble CD39 protein"
XX WO200023459-A1.
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US022955.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX DR New soluble CD39 polypeptides having apyrase activity, useful for
XX PT inhibiting angiogenesis and treating unstable angina, myocardial
XX PT infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 89-91; 122pp; English.
XX
CC The present sequence is a fusion protein construct CD39-L4-1, comprising
CC the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is
CC a secreted apyrase, belonging to the CD39 family. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations
CC and the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, myocardial infarction, stroke, coronary artery disease
CC or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,
CC embolism, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 476 AA;
Query Match 98.2%; Score 2356; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.5e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 SSTQNKALPENVKYGVLDAGSSHTSLYIYKWPAAEKENDTGVVHQVEECRVKGGISKFV 69
DB :|||||
36 SSTQNKALPENVKYGVLDAGSSHTSLYIYKWPAAEKENDTGVVHQVEECRVKGGISKFV 95
QY 70 QKVNIEGILYTDCHMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVER 129
DB 96 QKVNIEGILYTDCHMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVER 155
QY 130 LSNYPFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 189
DB 156 LSNYPFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLG 215


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QY 190 GASTQVTFVFPQNTIESPDNALQRLYKGYKYNVYTHSFLCYGKQDALWQKLAKDIQVASN 249
DB 216 GASTQVTFVFPQNTIESPDNALQRLYKGYKYNVYTHSFLCYGKQDALWQKLAKDIQVASN 275
QY 250 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFIEIQIGNYQQCHQSILELFNT 309
DB 276 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFIEIQIGNYQQCHQSILELFNT 335
QY 310 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 369
DB 336 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
QY 370 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 429
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 455
QY 430 LNLTNMIPAEQPLSTPLSHST 450
DB 456 LNLTNMIPAEQPLSTPLSHST 476

RESULT 12
ID AAY70888 standard; protein; 476 AA.
AC AAY70888;
XX
DT 17-AUG-2000 (first entry)
XX
DE Protein encoded by CD39-L4-1 construct.
XX
KW Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;
unstable angina; myocardial infarction; stroke; coronary artery disease;
atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
occlusion; reocclusion; stenosis; restenosis; anti-anginal; cardiac;
cerebroprotective; anti-arteriosclerotic; vasotropic; anticoagulant;
coronary ischaemia; vascular occlusion.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT Region 1..37 Location/Qualifiers
FT /note= "Derived from CD39-L4"
FT Cleavage-site 20..21
FT Region 38..476
FT /note= "Soluble portion of CD39"

WO200023094-A2.
XX
PN 27-APR-2000.
XX
PF 13-OCT-1999; 99WO-US023641.
XX
PR 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
PA (IMMUNEX CORP.
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339518/29.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke
PT coronary artery disease or injury, comprises administering soluble CD39
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PT polypeptides.
XX Claim 6; Page 89-91; 118pp; English.
XX
CC The present sequence is a fusion construct of human soluble CD39 encoded
by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the
CD39 family. The fusion construct is used for the expression and activity
of soluble CD39 in CHO (Chinese hamster ovary) cells. Soluble CD39
retains the capacity of wildtype CD39 to metabolise ATP and ADP at
physiologically relevant concentrations as well as the ability to block
and reverse ADP-induced platelet activation and recruitment including
platelet aggregation. This is used in the treatment of unstable angina,
myocardial infarction, stroke, coronary artery disease or injury,
atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,
platelet-associated ischaemic disorder including lung ischaemia, coronary
ischaemia and cerebral ischaemia, thrombotic disorder including coronary
artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
peripheral artery thrombosis, venous thrombosis, thrombosis,
coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
transient ischaemic attack. Soluble CD39 is also useful for preventing
thrombus formation or reformation, occlusion, reocclusion, stenosis or
restenosis of blood vessels or stroke
XX
SQ Sequence 476 AA;
Query Match 98.2%; Score 2356; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 5.5e-233;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 SSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDGVVHVVEECRVKPGISKFV 69
DB 36 SSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDGVVHVVEECRVKPGISKFV 95
QY 70 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 129
DB 96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERS 155
QY 130 LSNYPDFQGARITGOEGAGYCWITINYLKGFQSKTRWFSIVPIYETNNQETFGALDLG 189
DB 156 LSNYPDFQGARITGOEGAGYCWITINYLKGFQSKTRWFSIVPIYETNNQETFGALDLG 215
QY 190 GASTQVTFVFPQNTIESPDNALQRLYKGYKYNVYTHSFLCYGKQDALWQKLAKDIQVASN 249
DB 216 GASTQVTFVFPQNTIESPDNALQRLYKGYKYNVYTHSFLCYGKQDALWQKLAKDIQVASN 275
QY 250 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFIEIQIGNYQQCHQSILELFNT 309
DB 276 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPFQOFIEIQIGNYQQCHQSILELFNT 335
QY 310 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 369
DB 336 SYCPYSQCAFNGIFLPLPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
QY 370 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 429
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 455
QY 430 LNLTNMIPAEQPLSTPLSHST 450
DB 456 LNLTNMIPAEQPLSTPLSHST 476

RESULT 13
ID AAY70925 standard; protein; 463 AA.
XX
XX AAY70925;
AC AAY70925;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, Igkappa/solCD39.
XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
```

unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiatic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig; immunoglobulin kappa.

Homo sapiens.
Synthetic.
Key
Peptide
Location/Qualifiers
1..20
/label= Leader peptide
/note= "Derived from human immunoglobulin Ig kappa"
Cleavage-site
20..21
/note= "Cleavage site of leader sequence"
Region
21..24
/note= "Residues derived from human interleukin 2 (IL2)"
Protein
25..463
/note= "Human soluble CD39 protein"

WO200023459-A1.
27-APR-2000.
13-OCT-1999; 99WO-US022955.
16-OCT-1998; 98US-0104585P.
06-NOV-1998; 98US-0107466P.
13-AUG-1999; 99US-0149010P.
(IMV) IMMUNEX CORP.

Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
WPI; 2000-339644/29.
New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
Claim 6; Page 116-118; 122pp; English.

The present sequence is the fusion protein construct, IgkappaSolCD39. This construct comprises of the leader peptide from human immunoglobulin Ig kappa, linked to the soluble CD39 (solCD39) protein region by few residues derived from human interleukin 2 (IL2). SolCD39 has apyrase activity and is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 463 AA;
Query Match 98.2%; Score 2354; DB 3; Length 463;
Best Local Similarity 99.1%; Pred. No. 8.4e-233;
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

6 TQLTSSTQNKALPENVKYGVLDAGSSHTSYLYYKWPAAEKNDTGTVHQBECRVKGPFI 65
:|||||

Db 19 TGAPTSTQNKALPENVKYGVLDAGSSHTSYLYYKWPAAEKNDTGTVHQBECRVKGPFI 78
Qy 66 SKFQVKYNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMILLRMESELADRVLDV 125
Db 79 SKFQVKYNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMILLRMESELADRVLDV 138
Qy 126 VERSLSNYPDFQGARITGQEGAGYMITTNYLLGKFSQKTRWFSIVPYETNNQETFGA 185
Db 139 VERSLSNYPDFQGARITGQEGAGYMITTNYLLGKFSQKTRWFSIVPYETNNQETFGA 198
Qy 186 LDLGASTQVTFVPQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKQDALWOKLADIQ 245
Db 199 LDLGASTQVTFVPQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKQDALWOKLADIQ 258
Qy 246 VASNEILLRDCPFHGYKVVNVSDLYKTPCTKREMTLPFOQFETIQGIGNYQQCHQSILE 305
Db 259 VASNEILLRDCPFHGYKVVNVSDLYKTPCTKREMTLPFOQFETIQGIGNYQQCHQSILE 318
Qy 306 LFNTSYCPYSCAFNGIFLPLQDGFAGFAFYFVMKPLNLTSEKVSQEKVTEMMKFCFA 365
Db 319 LFNTSYCPYSCAFNGIFLPLQDGFAGFAFYFVMKPLNLTSEKVSQEKVTEMMKFCFA 378
Qy 366 QPWEIKTSYAGVKEKYLSEYCFSGTYLTLGLLQGYHFTADSWEHIFIGIKQSDAGMT 425
Db 379 QPWEIKTSYAGVKEKYLSEYCFSGTYLTLGLLQGYHFTADSWEHIFIGIKQSDAGMT 438
Qy 426 LGYMLNLTNMIAPQPLSTPLSHST 450
Db 439 LGYMLNLTNMIAPQPLSTPLSHST 463

RESULT 14

AA70902
ID AAY70902 standard; protein; 463 AA.
XX AC AAY70902;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by IgkappaSolCD39 construct.

Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antiangiinal; cardiatic; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; IgkappaSolCD39 construct.

Homo sapiens.
Synthetic.
Key
Peptide
Location/Qualifiers
1..20
/note= "Igkappa leader sequence"
Cleavage-site
20..21
Region
21..24
/note= "Derived from IL-2"
Region
25..463
/note= "Soluble portion of CD39"
Region
25..32
/note= "Derived from solCD39"

WO200023094-A2.
27-APR-2000.
13-OCT-1999; 99WO-US023641.

PR 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
PA (CORR) CORNELL RES FOUND INC.
XX
XX
PI Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339644/29.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39
PT polypeptides.
XX
XX Claim 6; Page 116-118; 118pp; English.
XX
XX The present sequence is the protein encoded by IgkappaLsolCD39 construct.
CC This is used for transient expression of soluble(sol)CD39 in recombinant
CC cells for determining enzymatic activity and platelet inhibitory activity
CC for each protein product. SolCD39 is used in the treatment of unstable
CC angina, myocardial infarction, stroke, coronary artery disease or injury,
CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
CC platelet-associated ischaemic disorder including lung ischaemia, coronary
CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary
CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
XX Sequence 463 AA;

Query Match 98.2%; Score 2354; DB 3; Length 463;
Best Local Similarity 99.1%; Pred. NO. 8.4e-233;
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 TQLTSTONKALPENVKYGVILVDSHTSYLYKPAEKENDTGCVHVEECRVKPGI 65
Db 19 TGAPTSTONKALPENVKYGVILVDSHTSYLYKPAEKENDTGCVHVEECRVKPGI 78
QY 66 SKFVKVNEIGYLTDCMERAREVTPRSOQHTPVYLGATGMRLRMESEBELADRLDV 125
Db 79 SKFVKVNEIGYLTDCMERAREVTPRSOQHTPVYLGATGMRLRMESEBELADRLDV 138
QY 126 VERLSNYPFPDQGARIITGOEAGYGMTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 185
Db 139 VERSLSNYPFPDQGARIITGOEAGYGMTITNYLLGKFSQKTRWFSIVPYETNNQETFGA 198
QY 186 LDLGASTQVTFVPONQITIEPNDALQRLYKDYNNVTHSFLCYGKDQALWOKLADIQ 245
Db 199 LDLGASTQVTFVPONQITIEPNDALQRLYKDYNNVTHSFLCYGKDQALWOKLADIQ 258
QY 246 VASNEILRDCPFHGYKVVNSDLYKTPCKRPEMTLPFOQFRTQGTGNYQCHQSILE 305
Db 259 VASNEILRDCPFHGYKVVNSDLYKTPCKRPEMTLPFOQFRTQGTGNYQCHQSILE 318
QY 306 LFNTSYCFYSCAFNGIFLPLQDGFAGSFYFVWKFNLNLTSEKVSQEKVTMMKKFCA 365
Db 319 LFNTSYCFYSCAFNGIFLPLQDGFAGSFYFVWKFNLNLTSEKVSQEKVTMMKKFCA 378
QY 366 QPWBEIKTSYAGVKEKYLSEYCFSGTSTYLSLLQGHYHTADSWEHIFIGIKQSDAGWT 425
Db 379 QPWBEIKTSYAGVKEKYLSEYCFSGTSTYLSLLQGHYHTADSWEHIFIGIKQSDAGWT 438
QY 426 LGYMLNLTNMPAEOPLTPLSHST 450
Db 439 LGYMLNLTNMPAEOPLTPLSHST 463

AAAY70922
ID AAY70922 standard; protein; 464 AA.
XX
AC AAY70922;
XX
XX 17-AUG-2000 (first entry)
XX
XX Human soluble CD39 fusion protein construct, pIL2LTrim1.
XX
XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX Location/Qualifiers
Key 1. .24
Peptide /label= Leader_peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT
FT Cleavage-site 24. .25
FT /note= "Cleavage site of leader sequence"
FT
FT Protein 26. .464
FT /note= "Human soluble CD39 protein"
XX
XX WO200023459-A1.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-USO22955.
XX
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
FT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 111-112; 122pp; English.
XX
XX The present sequence is the fusion protein construct, pIL2LTrim1. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity. The
CC two regions are joined by an intervening Ala residue. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations and
CC the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, stroke, myocardial infarction, coronary artery disease,
CC or injury, embolism, atherosclerosis, peripheral vascular occlusion,
CC preclampsia, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 464 AA;

Query Match : 98.1%; Score 2353; DB 3; Length 464;
Best Local Similarity 99.8%; Pred. No. 1.le-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB :|||||
QY 324 SYCPYSQCAFNGIFLPPLODGFAPSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 383
DB :|||||
QY 370 EIKTSYAGVKEKYJSEYCFSGTYILSLLOGVHFTADSWEHIFTKIQGSDAGWTILGYM 429
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QY 384 EIKTSYAGVKEKYJSEYCFSGTYILSLLOGVHFTADSWEHIFTKIQGSDAGWTILGYM 443
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QY 430 LNLTNMIPAEQPLSTPLSHST 450
DB :|||||
QY 444 LNLTNMIPAEQPLSTPLSHST 464
DB :|||||

Search completed: March 7, 2005, 13:13:10
Job time : 75.6232 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
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Run on: March 7, 2005, 13:23:03 ; Search time 52.7921 Seconds
(without alignments)
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Perfect score: 2398
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1391452 seqs, 329044822 residues
Total number of hits satisfying chosen parameters: 1391452
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA: *
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep: *
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep: *
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2395	99.9	454	9	US-09-835-147-6
3	2395	99.9	473	9	US-09-835-147-29
4	2395	99.9	478	9	US-09-835-147-8
5	2380.5	99.3	487	9	US-09-835-147-26
6	2356	98.2	476	9	US-09-835-147-3
7	2354	98.2	463	9	US-09-835-147-30
8	2353	98.1	464	9	US-09-835-147-27
9	2348	97.9	439	9	US-09-374-586-2
10	2348	97.9	502	13	US-10-092-083-38
11	2348	97.9	510	9	US-09-835-147-2
12	2348	97.9	510	9	US-09-374-586-1
13	2348	97.9	510	10	US-09-781-796B-1

14	2348	97.9	510	16	US-10-646-308-30	Sequence 30, Appl
15	2294	95.7	476	9	US-09-835-147-4	Sequence 4, Appl
16	1009	42.1	495	9	US-09-823-356-4	Sequence 4, Appl
17	910.5	38.0	529	9	US-09-923-304-4	Sequence 4, Appl
18	906.5	37.8	458	13	US-10-052-586-496	Sequence 496, App
19	906.5	37.8	458	14	US-10-174-590-496	Sequence 496, App
20	906.5	37.8	458	14	US-10-176-758-496	Sequence 496, App
21	906.5	37.8	458	14	US-10-175-737-496	Sequence 496, App
22	906.5	37.8	458	14	US-10-174-581-496	Sequence 496, App
23	906.5	37.8	458	14	US-10-176-483-496	Sequence 496, App
24	906.5	37.8	458	14	US-10-176-749-496	Sequence 496, App
25	906.5	37.8	458	14	US-10-176-914-496	Sequence 496, App
26	906.5	37.8	458	14	US-10-176-915-496	Sequence 496, App
27	906.5	37.8	458	14	US-10-173-706-496	Sequence 496, App
28	906.5	37.8	458	14	US-10-175-738-496	Sequence 496, App
29	906.5	37.8	458	14	US-10-175-752-496	Sequence 496, App
30	906.5	37.8	458	14	US-10-176-482-496	Sequence 496, App
31	906.5	37.8	458	14	US-10-176-757-496	Sequence 496, App
32	906.5	37.8	458	14	US-10-176-913-496	Sequence 496, App
33	906.5	37.8	458	14	US-10-180-552-496	Sequence 496, App
34	906.5	37.8	458	14	US-10-180-557-496	Sequence 496, App
35	906.5	37.8	458	14	US-10-173-700-496	Sequence 496, App
36	906.5	37.8	458	14	US-10-174-572-496	Sequence 496, App
37	906.5	37.8	458	14	US-10-174-579-496	Sequence 496, App
38	906.5	37.8	458	14	US-10-174-582-496	Sequence 496, App
39	906.5	37.8	458	14	US-10-174-588-496	Sequence 496, App
40	906.5	37.8	458	14	US-10-175-739-496	Sequence 496, App
41	906.5	37.8	458	14	US-10-175-740-496	Sequence 496, App
42	906.5	37.8	458	14	US-10-175-743-496	Sequence 496, App
43	906.5	37.8	458	14	US-10-176-488-496	Sequence 496, App
44	906.5	37.8	458	14	US-10-176-492-496	Sequence 496, App
45	906.5	37.8	458	14	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US202002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835.147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match 100.0%; Score 2398; DB 9; Length 474;
Best Local Similarity 100.0%; Fred. No. 2.9e-207; Indels 0; Gaps 0;
Matches 450; Conservative 0; Mismatches 0;

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DB 25 ASTKTKTQLTSSSTONKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTG VVHVQVEECRV 84
QY 61 KPGGISKFKVQKNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELAD 120
DB 85 KPGGISKFKVQKNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELAD 144
QY 121 RVLVDVVERSLSNYPDFQAGARIITQGBEGAYGWIITINLLGKFSOKTRWFSIVPYETNNQ 180
DB 145 RVLVDVVERSLSNYPDFQAGARIITQGBEGAYGWIITINLLGKFSOKTRWFSIVPYETNNQ 204
QY 181 ETFGALDLGGASTQVTFVQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKL 240
DB 205 ETFGALDLGGASTQVTFVQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWOKL 264
QY 241 AKDIQVASNEILRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLFPQOFEIQGIGNYQOCH 300
DB 265 AKDIQVASNEILRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLFPQOFEIQGIGNYQOCH 324
QY 301 QSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMM 360
DB 325 QSIILELFNTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMM 384
QY 361 KKFCAPQWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFKIGQGS 420
DB 385 KKFCAPQWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFKIGQGS 444
QY 421 DAGWTLYMLNLTNMIPAEQPLSTPLSHST 450
DB 445 DAGWTLYMLNLTNMIPAEQPLSTPLSHST 474

RESULT 2

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; TYPE: PRT
; LENGTH: 454
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 99.9%; Score 2395; DB 9; Length 454;
Best Local Similarity 99.8%; Pred. No. 5e-207;
Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 361 KKFCAPQWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFKIGQGS 420
DB 365 KKFCAPQWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFKIGQGS 424
QY 421 DAGWTLYMLNLTNMIPAEQPLSTPLSHST 450
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RESULT 3

US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 99.9%; Score 2395; DB 9; Length 473;
Best Local Similarity 99.8%; Pred. No. 5.3e-207;
Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 24 SSKTKTQLTSSSTONKALPENVKYGI VLDAGSSHTSLYIKWPAEKENDTG VVHVQVEECRV 83
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DB 444 DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHST 473

RESULT 4

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match 99.9%; Score 2395; DB 9; Length 478;
Best Local Similarity 99.8%; Pred. No. 5.4e-207;
Matches 449; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTKTKTQLTSS-----TONKALPENVKYGVILDAGSSHTSLYIKVPAEKENDTGTVHVEECRV 60
DB 29 SSTKTKTQLTSS-----TONKALPENVKYGVILDAGSSHTSLYIKVPAEKENDTGTVHVEECRV 88
QY 61 KGPFGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLEMESEELAD 120
DB 89 KGPFGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLEMESEELAD 148
QY 121 RVLDDVVERSLSNYPDFQAGARIITGOEAGYAGWITINVLGKFSQKTRWFSIVPVETNNQ 180
DB 149 RVLDDVVERSLSNYPDFQAGARIITGOEAGYAGWITINVLGKFSQKTRWFSIVPVETNNQ 208

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DB 209 ETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQDALWOKL 268
QY 241 AKDIQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPPQFQFEIOGIGNYQOCH 300
DB 269 AKDIQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPPQFQFEIOGIGNYQOCH 328
QY 301 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEM 360
DB 329 QSILELFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEM 388
QY 361 KKFCAPQWEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKOQS 420
DB 389 KKFCAPQWEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIGIKOQS 448
QY 421 DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHST 450
DB 449 DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHST 478

RESULT 5

US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 99.3%; Score 2380.5; DB 9; Length 487;
Best Local Similarity 97.8%; Pred. No. 1.1e-205;
Matches 449; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 1 ASTKTKTQLTSS-----TONKALPENVKYGVILDAGSSHTSLYIKVPAEKENDTGTV 51
DB 29 SSTKTKTQLTSS-----TONKALPENVKYGVILDAGSSHTSLYIKVPAEKENDTGTV 88
QY 52 VHOVEECRVKFGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLE 111
DB 89 VHOVEECRVKFGISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLE 148
QY 112 RMESEELADRVLDVVERSLSNYPDFQAGARIITGOEAGYAGWITINVLGKFSQKTRWFS 171
DB 149 RMESEELADRVLDVVERSLSNYPDFQAGARIITGOEAGYAGWITINVLGKFSQKTRWFS 208
QY 172 IPVYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYG 231
DB 209 IPVYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYG 268

QY 232 KDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIQ 291
Db 269 KDQALWQKLAKDIOVASNEILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIQ 328
QY 292 GIGNYQOCHQSILELFPNTSYCYSCAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKV 351
Db 329 GIGNYQOCHQSILELFPNTSYCYSCAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKV 388
QY 352 SOEKYTEMMKFCAPWBEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHI 411
Db 389 SOEKYTEMMKFCAPWBEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHI 448
QY 412 HFIGKIQSDAGWTGLGYMLNLTNMIPEOPLSTPLSHST 450
Db 449 HFIGKIQSDAGWTGLGYMLNLTNMIPEOPLSTPLSHST 487

RESULT 6

US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-3

Query Match 98.2%; Score 2356; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.8e-203;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 SSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVF 69
Db 36 SSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGISKVF 95
QY 70 QKVNIGIYLTDCMERAREVIPSQOETPVYLGATAGWLLRMESEELADRLVDVVERS 129
Db 96 QKVNIGIYLTDCMERAREVIPSQOETPVYLGATAGWLLRMESEELADRLVDVVERS 155
QY 130 LSNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETFGALDLG 189
Db 156 LSNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETFGALDLG 215
QY 190 GASTQVTFVQNTTIESPDNALQFRLYKDYNNVYTHSLFCYKQDQALWQKLAKDIOVASN 249
Db 216 GASTQVTFVQNTTIESPDNALQFRLYKDYNNVYTHSLFCYKQDQALWQKLAKDIOVASN 275
QY 250 EILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIOGIGNYQOCHQSILELNT 309
Db 276 EILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIOGIGNYQOCHQSILELNT 335

QY 310 SYCPYSQACAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 369
Db 336 SYCPYSQACAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
QY 370 BIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIHFIGIKIQSDAGWTGLGYM 429
Db 396 BIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIHFIGIKIQSDAGWTGLGYM 455
QY 430 LNLNLTNMIPEOPLSTPLSHST 450
Db 456 LNLNLTNMIPEOPLSTPLSHST 476
RESULT 7
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 98.2%; Score 2354; DB 9; Length 463;
Best Local Similarity 99.1%; Pred. No. 2.6e-203;
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 TQLTSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGFI 65
Db 19 TQAPTSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKPGFI 78
QY 66 SKFQVKQNEIGIYLTDCMERAREVIPSQOETPVYLGATAGWLLRMESEELADRLVDV 125
Db 79 SKFQVKQNEIGIYLTDCMERAREVIPSQOETPVYLGATAGWLLRMESEELADRLVDV 138
QY 126 VERSLSNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETFGA 185
Db 139 VERSLSNYPDFOGARIITGOEEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETFGA 198
QY 186 LDLGAGSTQVTFVQNTTIESPDNALQFRLYKDYNNVYTHSLFCYKQDQALWQKLAKDIO 245
Db 199 LDLGAGSTQVTFVQNTTIESPDNALQFRLYKDYNNVYTHSLFCYKQDQALWQKLAKDIO 258
QY 246 VASNEILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIOGIGNYQOCHQSILE 305
Db 259 VASNEILRDPCHFGPKYKVVNVSDLYKTPCTKRREMTLPFOQFEIOGIGNYQOCHQSILE 318
QY 306 LPNTSYCPYSQACAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 365
Db 319 LPNTSYCPYSQACAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCA 378

QY 366 QWERIKTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWT 425
DB 379 QWERIKTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWT 438
QY 426 LGVMLNLTNNMIPAEQPLSTPLSHST 450
DB 439 LGVMLNLTNNMIPAEQPLSTPLSHST 463

RESULT 8
US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 98.1%; Score 2353; DB 9; Length 464;
Best Local Similarity 99.8%; Pred. No. 3.2e-203;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 10 SSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFV 69
DB 24 SATONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFV 83
QY 70 QKVNIGIYLTDCMERAREVIPSQHOETPVYLGTAGMRLLRMESEELADRLVDVVERS 129
DB 84 QKVNIGIYLTDCMERAREVIPSQHOETPVYLGTAGMRLLRMESEELADRLVDVVERS 143
QY 130 LSNYPDFOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDVG 189
DB 144 LSNYPDFOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDVG 203
QY 190 GASTQVTFPQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 249
DB 204 GASTQVTFPQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 263
QY 250 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSILELFT 309
DB 264 EILRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSILELFT 323
QY 310 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMW 369
DB 324 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMW 383
QY 370 EIKTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWTGLYM 429
DB 384 EIKTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWTGLYM 443

QY 430 LNLTNMIPAEQPLSTPLSHST 450
DB 444 LNLTNMIPAEQPLSTPLSHST 464

RESULT 9
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 97.9%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 8.3e-203;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFVOK 71
DB 1 TONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFVOK 60
QY 72 VNEIGIYLTDCMERAREVIPSQHOETPVYLGTAGMRLLRMESEELADRLVDVVERSIS 131
DB 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGTAGMRLLRMESEELADRLVDVVERSIS 120
QY 132 NYPDFOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDVG 191
DB 121 NYPDFOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDVG 180
QY 192 STQVTFPQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 251
DB 181 STQVTFPQNTIESPDNALQFRLYKDYNYVTHSFLCYGKDQALWQKLAKDIOVASNEI 240
QY 252 LRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSILELFTSY 311
DB 241 LRDPCHFPGYKVVNVDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSILELFTSY 300
QY 312 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMWEEI 371
DB 301 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPMWEEI 360
QY 372 KTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWTGLYM 431
DB 361 KTSYAGVKELSEYCFSGTYILSLLOGVHFTADSWEHIFGKIQSDAGWTGLYM 420
QY 432 LTNMIPAEQPLSTPLSHST 450
DB 421 LTNMIPAEQPLSTPLSHST 439

RESULT 10
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-38

Query Match 97.9%; Score 2348; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 1e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHGVQVEECRVKGGISKFVQK 71
DB 38 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHGVQVEECRVKGGISKFVQK 97
QY 72 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVVERSL 131
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVVERSL 157
QY 132 NYPDFQGARITGOEAGAYGWTINYLKGFSOKTRWFSIVPYETNNQETFGALDLGGA 191
DB 158 NYPDFQGARITGOEAGAYGWTINYLKGFSOKTRWFSIVPYETNNQETFGALDLGGA 217
QY 192 STQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKDQALWQKLAKDIQVASNEI 251
DB 218 STQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKDQALWQKLAKDIQVASNEI 277
QY 252 LRDPCHFPGYKXVNVSDLYKTPCTKRPMTLPFOQFEIQIGNYQQCHQSILELFNTSY 311
DB 278 LRDPCHFPGYKXVNVSDLYKTPCTKRPMTLPFOQFEIQIGNYQQCHQSILELFNTSY 337
QY 312 CPYSQAFNGIFLPLQDGFAGSAFYVFMKFLNLTSEKVSQKVTMMKKFCAQPWEEI 371
DB 338 CPYSQAFNGIFLPLQDGFAGSAFYVFMKFLNLTSEKVSQKVTMMKKFCAQPWEEI 397
QY 372 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 431
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 432 LTNMIPAEQPLSTPLSHST 450
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 11
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimbel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match 97.9%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHGVQVEECRVKGGISKFVQK 71
DB 38 TQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHGVQVEECRVKGGISKFVQK 97
QY 72 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVVERSL 131
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVVERSL 157
QY 132 NYPDFQGARITGOEAGAYGWTINYLKGFSOKTRWFSIVPYETNNQETFGALDLGGA 191
DB 158 NYPDFQGARITGOEAGAYGWTINYLKGFSOKTRWFSIVPYETNNQETFGALDLGGA 217
QY 192 STQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKDQALWQKLAKDIQVASNEI 251
DB 218 STQVTFVQNTIESPDNALQRLYKDYVYTHSFLCYGKDQALWQKLAKDIQVASNEI 277
QY 252 LRDPCHFPGYKXVNVSDLYKTPCTKRPMTLPFOQFEIQIGNYQQCHQSILELFNTSY 311
DB 278 LRDPCHFPGYKXVNVSDLYKTPCTKRPMTLPFOQFEIQIGNYQQCHQSILELFNTSY 337
QY 312 CPYSQAFNGIFLPLQDGFAGSAFYVFMKFLNLTSEKVSQKVTMMKKFCAQPWEEI 371
DB 338 CPYSQAFNGIFLPLQDGFAGSAFYVFMKFLNLTSEKVSQKVTMMKKFCAQPWEEI 397
QY 372 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 431
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 432 LTNMIPAEQPLSTPLSHST 450
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 12
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match 97.9%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 71
DB 38 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 97
QY 72 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 131
DB 98 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 157
QY 132 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 191
DB 158 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 192 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 251
DB 218 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 252 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 311
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 337
QY 312 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 371
DB 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 397
QY 372 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 431
DB 398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 432 LTNMIPAEQPLSTPLSHST 450
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 13

US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 97.9%; Score 2348; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 71
DB 38 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 97
QY 72 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 131

DB 98 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 157
QY 132 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 191
DB 158 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 192 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 251
DB 218 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 252 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 311
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 337
QY 312 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 371
DB 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWBEI 397
QY 372 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 431
DB 398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKQSDAGWTLYGMLN 457
QY 432 LTNMIPAEQPLSTPLSHST 450
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 14

US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 97.9%; Score 2348; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 1e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 71
DB 38 TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDTG VHVQVBECEKRVKPGISKFKVQK 97
QY 72 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 131
DB 98 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVERSUS 157
QY 132 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 191
DB 158 NYPFDFQAGARIITGOEAGYGWITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 192 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 251
DB 218 STQVTFVPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 252 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 311
DB 278 LRDPCHFPGYKVVNVSDLYKTPCTKRPMTLPPOQFEIQGIGNYQOCHQSILELFNTSY 337

QY	312	CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	371
Db	338	CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	397
QY	372	KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGKIQGSDAGWTLGYMLN	431
Db	398	KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGKIQGSDAGWTLGYMLN	457
QY	432	LTNMIPAEQPLSTPLSHST	450
Db	458	LTNMIPAEQPLSTPLSHST	476

RESULT 15
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

Query Match 95.7%; Score 2294; DB 9; Length 476;
Best Local Similarity 98.6%; Pred. No. 6.9e-198;
Matches 431; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY	18	PENVK-----YGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKGGISKFKVQKN	73
Db	40	PINVSASTLXGIVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKGGISKFKVQKN	99
QY	74	EIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLDVVVERLSNY	133
Db	100	EIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLRMESEELADRLDVVVERLSNY	159
QY	134	PFDFQGARIIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGGAST	193
Db	160	PFDFQGARIIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGGAST	219
QY	194	QVTFVPQNQTIESPDNALQRLYKQDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILR	253
Db	220	QVTFVPQNQTIESPDNALQRLYKQDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILR	279
QY	254	DPCFHPGKVKVNVSDLYKTPCTKRPEMTLPFQOFELQIGNYQOCHOSILELFTNTSYCP	313
Db	280	DPCFHPGKVKVNVSDLYKTPCTKRPEMTLPFQOFELQIGNYQOCHOSILELFTNTSYCP	339

Search completed: March 7, 2005, 14:12:48
Job time : 54.7921 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 19.1771 Seconds
(without alignments)
1751.679 Million cell updates/sec

Title: US-09-835-147A-28_COPY_25_474

Perfect score: 2398

Sequence: 1 ASTKKTLTSTQNKALPEN.....NLTNMPAEQPLSTPLSHST 450

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	97.9	502	4	US-09-557-800C-55
2	2348	97.9	502	4	US-09-370-625A-38
3	2348	97.9	510	3	US-08-930-921-1
4	2348	97.9	510	4	US-09-781-796C-1
5	910.5	38.0	529	3	US-09-240-639-4
6	910.5	38.0	529	4	US-09-908-510A-4
7	910.5	38.0	529	4	US-09-905-744B-4
8	910.5	38.0	529	4	US-10-107-660-4
9	910.5	38.0	529	4	US-10-107-576-4
10	910.5	38.0	529	4	US-09-905-732B-4
11	910.5	38.0	529	4	US-09-923-304-4
12	910.5	38.0	529	4	US-09-949-016-6049
13	910.5	38.0	529	4	US-09-905-743B-4
14	910.5	38.0	556	4	US-09-943-016-11328
15	865	36.1	479	4	US-09-949-016-11328
16	847.5	35.3	282	4	US-09-949-016-11559
17	803	33.5	153	4	US-09-240-639-13
18	803	33.5	153	4	US-09-908-510A-13
19	803	33.5	153	4	US-09-905-744B-13
20	803	33.5	153	4	US-10-107-660-13
21	803	33.5	153	4	US-10-107-576-13
22	803	33.5	153	4	US-09-905-732B-13
23	803	33.5	153	4	US-09-905-743B-13
24	604	25.2	154	3	US-09-240-639-14
25	604	25.2	154	4	US-09-908-510A-14
26	604	25.2	154	4	US-09-905-744B-14
27	604	25.2	154	4	US-10-107-660-14

28	604	25.2	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	25.2	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	25.2	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	18.5	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	18.5	153	4	US-09-908-510A-15	Sequence 15, Appl
33	442.5	18.5	153	4	US-09-905-744B-15	Sequence 15, Appl
34	442.5	18.5	153	4	US-10-107-660-15	Sequence 15, Appl
35	442.5	18.5	153	4	US-10-107-576-15	Sequence 15, Appl
36	442.5	18.5	153	4	US-09-905-732B-15	Sequence 15, Appl
37	442.5	18.5	153	4	US-09-905-743B-15	Sequence 15, Appl
38	423	17.6	462	4	US-09-129-112-2	Sequence 2, Appl
39	421.5	17.6	462	4	US-09-129-112-15	Sequence 15, Appl
40	417.5	17.4	150	3	US-09-240-639-16	Sequence 16, Appl
41	417.5	17.4	150	4	US-09-908-510A-16	Sequence 16, Appl
42	417.5	17.4	150	4	US-09-905-744B-16	Sequence 16, Appl
43	417.5	17.4	150	4	US-10-107-660-16	Sequence 16, Appl
44	417.5	17.4	150	4	US-10-107-576-16	Sequence 16, Appl
45	417.5	17.4	150	4	US-09-905-732B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 97.9%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	12	TQNKALPENVKYGVLDAGSSHTSLYYIKYKPAEKENDTGVVHVQVECEKVGPGISKFKYOK	71
Db	38	TQNKALPENVKYGVLDAGSSHTSLYYIKYKPAEKENDTGVVHVQVECEKVGPGISKFKYOK	97
Qy	72	VNEIGVILYTDCEMAREVIPSQHQETPVYLGATAGMRLRMESEELADRLDVLVVERSL	131
Db	98	VNEIGVILYTDCEMAREVIPSQHQETPVYLGATAGMRLRMESEELADRLDVLVVERSL	157
Qy	132	NYPDFQARIITGQEEGAYGWITINYLKFKSQTRWFSIVPYETNNQTFGALDLGGA	191

158 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
192 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 251
218 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 277
252 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 311
278 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 337
312 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 371
338 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 397
372 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 431
398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 457
432 LTNMIPAEQPLSTPLSHST 450
458 LTNMIPAEQPLSTPLSHST 476

RESULT 3
US-08-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 6287837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; EARLIER FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CA96/00223
; EARLIER FILING DATE: 1996-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
; US-08-930-921-1

Query Match 97.9%; Score 2348; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.4e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHQBECRVKGPISKFVQK 71
38 TONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHQBECRVKGPISKFVQK 97
72 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 131
98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
132 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 191
158 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
192 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 251
218 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 277
252 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 311
278 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 337
312 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 371
338 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 397
372 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 431
398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 457
432 LTNMIPAEQPLSTPLSHST 450
458 LTNMIPAEQPLSTPLSHST 476

158 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
192 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 251
218 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 277
252 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 311
278 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 337
312 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 371
338 CPYSQCAFNGIFLPLQDGFAGFAFYFMKFLNLTSEKVSQEKVTEMKKFCAQPWEEI 397
372 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 431
398 KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTLGYMLN 457
432 LTNMIPAEQPLSTPLSHST 450
458 LTNMIPAEQPLSTPLSHST 476

RESULT 2
US-09-370-625A-38
; Sequence 38, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Forth, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110735908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-370-625A-38

Query Match 97.9%; Score 2348; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHQBECRVKGPISKFVQK 71
38 TONKALPENVKYGIIVLDAGSSHTSLYIYKWPAAKENDTGVVHQBECRVKGPISKFVQK 97
72 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 131
98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
132 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 191
158 NYPDFQAGRIITGQEGAYGWIINLLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
192 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 251
218 STQVTFVFPNQTIESPONALQFRLYKGDYNNVYTHSFLCYGKQDQALWOKLAKDIOVASNEI 277
252 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 311
278 LRDCPCFHPGKVKVNVSDLYKTPCTKGFEMTLPRQOFEIQGIGNYQOCHOSILELFNTSY 337

RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEROF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 97.9%; Score 2348; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.4e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TONKALPENKYGIVLDAGSSHTSLIYKPAEKENDTGVVHVQVECKRVKPGISKFVQK 71
Db 38 TONKALPENKYGIVLDAGSSHTSLIYKPAEKENDTGVVHVQVECKRVKPGISKFVQK 97
Qy 72 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVERSL 131
Db 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVERSL 157
Qy 132 NYPDFQAGIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 191
Db 158 NYPDFQAGIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217
Qy 192 STQVTFVQNTIESPDNALQRLYKDYNNVTHSFCLCYGKQDALWQKLADIQVASNEI 251
Db 218 STQVTFVQNTIESPDNALQRLYKDYNNVTHSFCLCYGKQDALWQKLADIQVASNEI 277
Qy 252 LRDPCHFPGYKVVNVDLYKTPCTKREMTLPFOQFEIQQIGNYQQCHQSILELFTSY 311
Db 278 LRDPCHFPGYKVVNVDLYKTPCTKREMTLPFOQFEIQQIGNYQQCHQSILELFTSY 337
Qy 312 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 371
Db 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397
Qy 372 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMLN 431
Db 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLYMLN 457
Qy 432 LTNMIPAEQPLSTPLSHST 450
Db 458 LTNMIPAEQPLSTPLSHST 476

RESULT 5
US-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 529
TYPE: PRT
ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 38.0%; Score 910.5; DB 3; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENKYGIVLDAGSSHTSLIYKPAEKENDTGVVHVQVECKRVKPGISKFVQK 72
Db 47 KQEVLPPELKYGIVLDAGSSRTTVVYQWPAEKENNTGVVSQTFKCSVKSGISSYGNP 106
Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVERSLN 132
Db 107 QDVPRAFEECKQKVGQVPSHLHGSTPIHLGATAGMRLLRMLLQNETAANEVLESIQSYPKS 166
Qy 133 YPDFQAGIITGOEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 192
Db 167 QPDFRGAQLISGQEEGVYGHITANYLMGNFLEKXNLWHMVV--HPHGVTETGALDLGGA 224
Qy 193 TQVTFVQNTIESPDNALQRLYKDYNNVTHSFCLCYGKQDALWQKLADIQVA-SNEI 251
Db 225 TQISFVAGERKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLLQNSPTKH 284
Qy 252 LRDPCHFPGYKVVNVDLYKTPCT--KRFEMTLPFOQFEIQQIGNYQQCHQSILELFT 309
Db 285 LTNPFCYPRDYSISITMGHVFDSLCTVQRPESYNPNVDITFEGTGDPSLCKEKVASIFDP 344
Qy 310 SYC-PYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 368
Db 345 KACHDQETCSDGVYQKIKGPFVAFAGFYTASALNL--SGSFSLDTFNSSTWPCSQNW 403
Qy 369 EEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLY 428
Db 404 SOLPULLPKPDEVYARSYCFSANIYHLYFVNGYKFTETWPOIHFEKEVGNSSIAWSLGY 463
Qy 429 MLNLTNMPAEQPL 442
Db 464 MSLTNTQIPAESPL 477

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

Query Match		38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity		41.5%; Pred. No. 1.3e-88;
Matches		180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;
Qy	13 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	72
Db	47 KOEVLPPGLKYIGVLDAGSSRTTVVYQWPAEKENNTGVVSTQTFKCSVKSGSISSYGNP	106
Qy	73 NEIGYILTDCHMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSLN	132
Db	107 QDVPRAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESISQSYFKS	166
Qy	133 YPFDFOGARIITGOEGAGYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDLGGAS	192
Db	167 QPFDPRGAQIISGQEGYGVWITANYLMGNFLEKNLWMMV--HPHGVETTTGALDLGGAS	224
Qy	193 TQVTFVQNTQIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVA-SNEI	251
Db	225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
Qy	252 LRDCPCFHPGYKVVNVDLYKTPTCT--KRFEMTLPFQOFEIQIGNYOQCHQSILEFNT	309
Db	285 LTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNNDVITPEGTGDPSLCKEKVASIFDF	344
Qy	310 SYC-PYSOCAFNGIFLPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMKKKCAQPW	368
Db	345 KACHDQETCSFDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403
Qy	369 BEIKTSYAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIFTKIQGSDAGWTILGY	428
Db	404 SOLPLLLLPKFDEYARSYCFYSANYIYHLFVNGYKFTETWPIHFEKEVGNSSIAWSLGY	463
Qy	429 MLNLTNMPAEQPL 442	
Db	464 MSLTNQIPAESPL 477	
RESULT 8		
US-10-107-660-4		
; Sequence 4, Application US/10107660		
; Patent No. 6780977		
; GENERAL INFORMATION:		
; APPLICANT: Chadwick, Brian Paul		
; APPLICANT: Frischauf, Anna-Maria		
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE		
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS		
; FILE REFERENCE: 9598-065		
; CURRENT APPLICATION NUMBER: US/10/107,660		
; CURRENT FILING DATE: 2002-03-27		
; PRIOR APPLICATION NUMBER: US/09/240,639		
; PRIOR FILING DATE: 1998-01-29		
; NUMBER OF SEQ ID NOS: 29		
; SOFTWARE: PatentIn Ver. 2.0		
; SEQ ID NO 4		
; LENGTH: 529		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
US-10-107-660-4		
Query Match		38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity		41.5%; Pred. No. 1.3e-88;
Matches		180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;
Qy	13 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	72
Db	47 KOEVLPPGLKYIGVLDAGSSRTTVVYQWPAEKENNTGVVSTQTFKCSVKSGSISSYGNP	106
Qy	73 NEIGYILTDCHMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSLN	132
Db	107 QDVPRAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESISQSYFKS	166
Qy	133 YPFDFOGARIITGOEGAGYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDLGGAS	192
Db	167 QPFDPRGAQIISGQEGYGVWITANYLMGNFLEKNLWMMV--HPHGVETTTGALDLGGAS	224
Qy	193 TQVTFVQNTQIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVA-SNEI	251
Db	225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
Qy	252 LRDCPCFHPGYKVVNVDLYKTPTCT--KRFEMTLPFQOFEIQIGNYOQCHQSILEFNT	309
Db	285 LTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNNDVITPEGTGDPSLCKEKVASIFDF	344
Qy	310 SYC-PYSOCAFNGIFLPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMKKKCAQPW	368
Db	345 KACHDQETCSFDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403
Qy	369 BEIKTSYAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIFTKIQGSDAGWTILGY	428
Db	404 SOLPLLLLPKFDEYARSYCFYSANYIYHLFVNGYKFTETWPIHFEKEVGNSSIAWSLGY	463
Qy	429 MLNLTNMPAEQPL 442	
Db	464 MSLTNQIPAESPL 477	

Query Match		38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity		41.5%; Pred. No. 1.3e-88;
Matches		180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;
Qy	13 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	72
Db	47 KOEVLPPGLKYIGVLDAGSSRTTVVYQWPAEKENNTGVVSTQTFKCSVKSGSISSYGNP	106
Qy	73 NEIGYILTDCHMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSLN	132
Db	107 QDVPRAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESISQSYFKS	166
Qy	133 YPFDFOGARIITGOEGAGYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDLGGAS	192
Db	167 QPFDPRGAQIISGQEGYGVWITANYLMGNFLEKNLWMMV--HPHGVETTTGALDLGGAS	224
Qy	193 TQVTFVQNTQIESPDNALQFRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIQVA-SNEI	251
Db	225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH	284
Qy	252 LRDCPCFHPGYKVVNVDLYKTPTCT--KRFEMTLPFQOFEIQIGNYOQCHQSILEFNT	309
Db	285 LTNPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNNDVITPEGTGDPSLCKEKVASIFDF	344
Qy	310 SYC-PYSOCAFNGIFLPLQDGFAGSAPFYFMKFLNLTSEKVSQEKVTEMKKKCAQPW	368
Db	345 KACHDQETCSFDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW	403
Qy	369 BEIKTSYAGVKEKYLSEYCFSGTYILSLQGYHFTADSWEHIFTKIQGSDAGWTILGY	428
Db	404 SOLPLLLLPKFDEYARSYCFYSANYIYHLFVNGYKFTETWPIHFEKEVGNSSIAWSLGY	463
Qy	429 MLNLTNMPAEQPL 442	
Db	464 MSLTNQIPAESPL 477	
RESULT 7		
US-09-905-744B-4		
; Sequence 4, Application US/09905744B		
; Patent No. 6780410		
; GENERAL INFORMATION:		
; APPLICANT: Chadwick, Brian Paul		
; APPLICANT: Frischauf, Anna Maria		
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND		
; TITLE OF INVENTION: ACIDS		
; FILE REFERENCE: 28110/36120A		
; CURRENT APPLICATION NUMBER: US/09/905,744B		
; CURRENT FILING DATE: 2001-07-13		
; PRIOR APPLICATION NUMBER: 09/240,639		
; PRIOR FILING DATE: 1999-01-29		
; NUMBER OF SEQ ID NOS: 32		
; SOFTWARE: PatentIn version 3.1		
; SEQ ID NO 4		
; LENGTH: 529		
; TYPE: PRT		
; ORGANISM: Homo Sapiens		
US-09-905-744B-4		
Query Match		38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity		41.5%; Pred. No. 1.3e-88;
Matches		180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;
Qy	13 QNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGPISKFQKV	72
Db	47 KOEVLPPGLKYIGVLDAGSSRTTVVYQWPAEKENNTGVVSTQTFKCSVKSGSISSYGNP	106
Qy	73 NEIGYILTDCHMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLDVVVERSLN	132
Db	107 QDVPRAFEECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESISQSYFKS	166
Qy	133 YPFDFOGARIITGOEGAGYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDLGGAS	192


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Query Match      38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPISKFQKV 72
Db 47 KQEVLPGLKXGIVLDAGSSRTTVYVQWPAKENNTGVVQTFKCSVKSGISSYGNP 106

Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDIVERLSN 132
Db 107 QDVPRAFECQKVGQVPSHLHGSTPIHLGATAGMRLLESEELADRLDIVERLSN 166

Qy 133 YPFDFOGARIITGOBEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 192
Db 167 QPFDPRGAQIISGOBEGYGVWITANYLGNFLEKMLHWMV--HPHGVETTALDLGGAS 224

Qy 193 TOVTFVPCNQTIESP DNALQRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVA-SNEI 251
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYLYTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284

Qy 252 LRDPCFHPGYKXKVNVSPLYKTPCT--KRPEMTLPFQOFEIQGIGNYQOCHQSILELPT 309
Db 285 LTNPYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPSLCKEKVASIFDF 344

Qy 310 SYC-PYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW 368
Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYITASALNL--SGSFSLDTFNSSTWFCQNW 403

Qy 369 EEIKTSYAGVKYKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 428
Db 404 SOLPILLPKFDEYARSYCFSANIYHLFVNGYKFTETWPQIHFEKEVGNSSIAWSLGY 463

Qy 429 MLNLTNMPAEQPL 442
Db 464 MSLTNQIPAESPL 477

RESULT 13
US-09-905-743B-4
; Sequence 4, Application US/0905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-743B-4

Query Match      38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPISKFQKV 72
Db 47 KQEVLPGLKXGIVLDAGSSRTTVYVQWPAKENNTGVVQTFKCSVKSGISSYGNP 106

Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDIVERLSN 132
Db 107 QDVPRAFECQKVGQVPSHLHGSTPIHLGATAGMRLLESEELADRLDIVERLSN 166

Qy 133 YPFDFOGARIITGOBEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 192
Db 167 QPFDPRGAQIISGOBEGYGVWITANYLGNFLEKMLHWMV--HPHGVETTALDLGGAS 224

Qy 193 TOVTFVPCNQTIESP DNALQRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVA-SNEI 251
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYLYTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284

Qy 252 LRDPCFHPGYKXKVNVSPLYKTPCT--KRPEMTLPFQOFEIQGIGNYQOCHQSILELPT 309
Db 285 LTNPYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPSLCKEKVASIFDF 344

Qy 310 SYC-PYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW 368
Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYITASALNL--SGSFSLDTFNSSTWFCQNW 403

Qy 369 EEIKTSYAGVKYKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 428
Db 404 SOLPILLPKFDEYARSYCFSANIYHLFVNGYKFTETWPQIHFEKEVGNSSIAWSLGY 463

Qy 429 MLNLTNMPAEQPL 442
Db 464 MSLTNQIPAESPL 477

RESULT 12
US-09-949-016-6049
; Sequence 6049, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6049
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6049

Query Match      38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPISKFQKV 72
Db 47 KQEVLPGLKXGIVLDAGSSRTTVYVQWPAKENNTGVVQTFKCSVKSGISSYGNP 106

Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDIVERLSN 132
Db 107 QDVPRAFECQKVGQVPSHLHGSTPIHLGATAGMRLLESEELADRLDIVERLSN 166
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Qy 133 YPFDFOGARIITGOBEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 192
Db 167 QPFDPRGAQIISGOBEGYGVWITANYLGNFLEKMLHWMV--HPHGVETTALDLGGAS 224

Qy 193 TOVTFVPCNQTIESP DNALQRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVA-SNEI 251
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYLYTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284

Qy 252 LRDPCFHPGYKXKVNVSPLYKTPCT--KRPEMTLPFQOFEIQGIGNYQOCHQSILELPT 309
Db 285 LTNPYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPSLCKEKVASIFDF 344

Qy 310 SYC-PYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW 368
Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYITASALNL--SGSFSLDTFNSSTWFCQNW 403

Qy 369 EEIKTSYAGVKYKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 428
Db 404 SOLPILLPKFDEYARSYCFSANIYHLFVNGYKFTETWPQIHFEKEVGNSSIAWSLGY 463

Qy 429 MLNLTNMPAEQPL 442
Db 464 MSLTNQIPAESPL 477

RESULT 13
US-09-905-743B-4
; Sequence 4, Application US/0905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-743B-4

Query Match      38.0%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPISKFQKV 72
Db 47 KQEVLPGLKXGIVLDAGSSRTTVYVQWPAKENNTGVVQTFKCSVKSGISSYGNP 106

Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDIVERLSN 132
Db 107 QDVPRAFECQKVGQVPSHLHGSTPIHLGATAGMRLLESEELADRLDIVERLSN 166

Qy 133 YPFDFOGARIITGOBEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 192
Db 167 QPFDPRGAQIISGOBEGYGVWITANYLGNFLEKMLHWMV--HPHGVETTALDLGGAS 224

Qy 193 TOVTFVPCNQTIESP DNALQRLYKDYNNVYTHSFLCYGKQDQALWQKLAKDIOVA-SNEI 251
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYLYTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284

Qy 252 LRDPCFHPGYKXKVNVSPLYKTPCT--KRPEMTLPFQOFEIQGIGNYQOCHQSILELPT 309
Db 285 LTNPYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITPEGTGDPSLCKEKVASIFDF 344

Qy 310 SYC-PYSQAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKMKFCAQPW 368
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Db 345 KACHQETCSFQVQPKIKGFVAFAGFYTTASALNL--SGSFLDTFNSSTWFCNQW 403
Qy 369 EIKTSYAGVKEKYLSEYCFSTYILSLLLQGHYFTADSWEHIFIGIKQSDAGWTGLY 428
Db 404 SOLPLLLPKFDEVIARSYCSFANYIHLFVNGYKTEETWPOIHFEKEVGNSSIAWSLGY 463
Qy 429 MLNLTMIPAEQPL 442
Db 464 MLSLTNQIPAESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 38.0%; Score 910.5; DB 4; Length 556;
Best Local Similarity 41.5%; Pred. No. 1.4e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 13 QNKALPENKYGIVLDAGSSHTSLYIKYKPAEKENDTGTVHQBECRVKGPISKFVKV 72
Db 74 KOEVLPPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVSTFKCSYKSGSISSYGNP 133
Qy 73 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLDVLDDVVERSLN 132
Db 134 QDVPRAPFECMKVKGQVPSHLGSGTPHILGATAGMRLLRQNETAANEVLESIGSYPKS 193
Qy 133 YPFDQGARITGOBEGAYGMITINYLKFKSQKTRWFSIVPYETNNQETFGALDLGGAS 192
Db 194 QPFDPRGAQIISQEGVYGMITANYLMGNFLEKMLHMMV--HPHGVETTTGALDLGGAS 251
Qy 193 TQVTFVQNOTTESPDNALQFLRYKDYNNVYTHSFLCYGKQALMOKLAKOIVA-SNEI 251
Db 252 TQISFVAGEKMDLSDIMQVSLYGVVYTYLTHSFQCYGRNEAEKKFLAMLQNSPTKNH 311
Qy 252 LRDPCHFPGYKVVNVSDLYKTPCT--KFEFTLFPQFEIOGIGNYQOCHQSILELNT 309
Db 312 LTNPCYPRDYSISFTGHGVFDSLCTVDQRPESYNPDVITFEGTGDPSLCRKBVASIFDF 371
Qy 310 SYC-PYSQCAFNGIFLPLQGGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCAPW 368
Db 372 KACHQETCSFQVQPKIKGFVAFAGFYTTASALNL--SGSFLDTFNSSTWFCNQW 430
Qy 369 EIKTSYAGVKEKYLSEYCFSTYILSLLLQGHYFTADSWEHIFIGIKQSDAGWTGLY 428
Db 431 SOLPLLLPKFDEVIARSYCSFANYIHLFVNGYKTEETWPOIHFEKEVGNSSIAWSLGY 490
Qy 429 MLNLTMIPAEQPL 442
Db 491 MLSLTNQIPAESPL 504
```

```
RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 36.1%; Score 865; DB 4; Length 479;
Best Local Similarity 41.3%; Pred. No. 8.3e-84;
Matches 183; Conservative 69; Mismatches 137; Indels 54; Gaps 9;

Qy 12 TONKALPENKYGIVLDAGSSHTSLYIKYKPAEKENDTGTVHQBECRVKGPISKFVKV 71
Db 36 TRDVREPPALKYGIVLDAGSSHTSMFIYKWPADKENDTGIVGQHSSCDVPGGGISSYADN 95
Qy 72 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLDVLDDVVERSLN 131
Db 96 PSGASQSLVGLCEALQDVPRKAGTFLYLGATAGMRLLRNLTNPEASTVLMVTHLT 155
Qy 132 NYPFDQGARITGOBEGAYGMITINYLK--XFSQKTRWFSIVPYETNNQETFGALDL 188
Db 156 QYFDFRGARILSQEGVFCWVTANYLLENFIKYGWGRF-----RPRKGTILGAMD 209
Qy 189 GGASTQVTFVQNOTIESPDNA--LQFLRYKDYNNVYTHSFLCYGKQALMOKLAKOIVA 246
Db 210 GGASTQITF---ETTSPAEDRASEVQLHLYGQHYRVYTHSFLCYGRDQVLRLLASALQT 266
Qy 247 ASNEILRDPCHFPGYKVVNVSDLYKTPCTKFEFTLFPQF-----EIOGIGNYQOCH 300
Db 267 HGTH----PCWPRGFSTQVLGLDVYQSPCT----MAQRPNFNSARVSLSGSDPHLCR 318
Qy 301 QSILELFNTSYCPYSQCAFNGIFLPLQGGDFGAFSAFYFVMKFL--NLTSEKVSQEKVTE 358
Db 319 DLVSGLSFSFSCPSRSCFNGVFPQPVAGNFVAFAFYTVDFLETSGNLPAVLQOLEA 378
Qy 359 MMKFKCAPWBEIKTSYAGVKEKYLSEYCFSTYILSLLLQGHYFTADSWEHIFIGIKQ 418
Db 379 AAVNVCNQTAQ-----QLLSRGYGFDERAFAGGVI FQKAA 414
Qy 419 GSDAGWTLYGMLNLTNMIPEQ 441
Db 415 DTAVGWALGYMLNLTNLIADPP 437

Search completed: March 7, 2005, 13:27:59
Job time : 21.1771 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 13.7943 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147A-29_COPY_27_473
Perfect score: 2385
Sequence: 1 KKTQLTSTQNKALPENVKY.....NLTNMIPAEQPLSTPLSHST 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	98.4	510	2 I56242	lymphoid cell acti
2	505	21.2	483	2 D86276	hypothetical prote
3	469.5	19.7	405	2 E86276	hypothetical prote
4	453	19.0	630	2 S50463	hypothetical prote
5	416	17.4	572	2 T40856	probable nucleotid
6	406.5	17.0	516	2 G84442	probable nucleosid
7	402.5	16.9	485	2 T34147	hypothetical prote
8	394.5	16.5	508	2 C86276	7A19.33 protein -
9	383.5	16.1	557	2 T16696	hypothetical prote
10	381.5	16.0	556	2 T39109	probable guanosine
11	374	15.7	455	2 S48859	nucleoside triphos
12	338	14.2	454	2 J4616	apyrase (EC 3.6.1.
13	332	13.9	1052	2 T04439	hypothetical prote
14	328.5	13.8	479	2 T23508	hypothetical prote
15	322.5	13.5	518	2 A40732	guanosine-diphosph
16	167	7.0	628	2 A55421	C4-dicarboxylase-b
17	103	4.3	369	2 S77299	hypothetical prote
18	101.5	4.3	716	2 T21516	hypothetical prote
19	100	4.2	307	2 T27332	RNA viral polymera
20	99	4.2	1951	2 B43963	autolysin, N-acety
21	98.5	4.1	590	2 A81411	hypothetical prote
22	98.5	4.1	797	2 D86247	hypothetical prote
23	98.5	4.1	989	2 B84532	hypothetical prote
24	98.5	4.1	1509	2 B89985	hypothetical prote
25	98	4.1	371	2 T05213	hypothetical prote
26	98	4.1	665	2 T18979	hypothetical prote
27	98	4.1	3848	2 T17414	T1pc protein - eli
28	97.5	4.1	392	2 A96738	hypothetical prote
29	97	4.1	466	2 J66525	processing peptida

30	97	4.1	494	2 T03774	probable histidine
31	96	4.0	883	2 B85725	probable fibrinial
32	96	4.0	1028	2 I51173	myosin I beta - bu
33	96	4.0	1415	2 A72369	(R)-2-hydroxygluta
34	95.5	4.0	591	2 F89770	hypothetical prote
35	95.5	4.0	1900	2 AG2391	serine/threonine k
36	95	4.0	288	1 B48583	spore germination
37	95	4.0	451	2 G59859	Mg2+ transporter h
38	95	4.0	461	2 G91228	probable permease
39	95	4.0	461	2 R86075	probable permease
40	95	4.0	564	2 S15962	hypothetical prote
41	95	4.0	927	2 T43110	lactacin 481/facto
42	94	3.9	1299	2 AH2090	two-component hybr
43	93	3.9	468	2 H65192	hypothetical 51.7
44	92.5	3.9	404	2 T21251	hypothetical prote
45	92.5	3.9	556	2 A90715	probable dnaK prot

ALIGNMENTS

RESULT 1

156242
lymphoid cell activation antigen - human
C:Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56242
R;Maliszewski, C.R.; Dellespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994
A;Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A;Reference number: I56242; MUID:95015846; PMID:7930580
A;Accession: I56242
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-510 <RES>
A;Cross-references: UNIPROT:P49961; GB:S73813; NID:g765255; PIDN:AAB32152.1; PID:g765255
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 98.4%; Score 2348; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 2e-182;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	9	TQNKALPENVKY	GIVLDAGSSHTSLY	YKWP	AEKENDTGVVHVQVE	ECRVKPGGISK	FVQK	68
Db	38	TQNKALPENVKY	GIVLDAGSSHTSLY	YKWP	AEKENDTGVVHVQVE	ECRVKPGGISK	FVQK	97
Qy	69	VNEIGIYLTDCMER	AREVIPRSQHOETPV	ILGATAGHRL	LMSESELADRLD	VVERSL	128	
Db	98	VNEIGIYLTDCMER	AREVIPRSQHOETPV	ILGATAGHRL	LMSESELADRLD	VVERSL	157	
Qy	129	NYPDFQGARIT	IQBEGAGVWITINYL	LKFSOKTRWFS	IVPYETNNQET	FGALD	188	
Db	158	NYPDFQGARIT	IQBEGAGVWITINYL	LKFSOKTRWFS	IVPYETNNQET	FGALD	217	
Qy	189	STQVTFVPQNT	IESPNALQFRLYG	KDYNVYTHSFL	CYCKDQALWK	AKDIQV	248	
Db	218	STQVTFVPQNT	IESPNALQFRLYG	KDYNVYTHSFL	CYCKDQALWK	AKDIQV	277	
Qy	249	LRDPCFHPGK	VKVNVS	DLKTPCTKRF	EMTLPPQOFE	IQGIGNYQ	308	
Db	278	LRDPCFHPGK	VKVNVS	DLKTPCTKRF	EMTLPPQOFE	IQGIGNYQ	337	
Qy	309	CPYSQCAFNG	IPLPLOGDFG	AFYFVWKFL	NLTSEKVSQ	EKVTEMMK	368	
Db	338	CPYSQCAFNG	IPLPLOGDFG	AFYFVWKFL	NLTSEKVSQ	EKVTEMMK	397	
Qy	369	KTSYAGVKE	KYLSEYCFSG	YVILSL	LQGYHFTAD	SWEHIFIG	428	
Db	398	KTSYAGVKE	KYLSEYCFSG	YVILSL	LQGYHFTAD	SWEHIFIG	457	
Qy	429	LTNNMIPAE	QPLSTPLSHST	447				
Db	458	LTNNMIPAE	QPLSTPLSHST	476				

anssen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 19.7%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 3.3e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

QY 60 PGISKFQVKVNEIGVLTDCMERAREVPRSQHOETPVVYLGATAGMRLRMESEELADRV 119
DB 29 PGLSSYADNPEGASVSVTKLVFAKGRIPKGLKXSDIRLMATAGMRLDVPQVE--QI 85
QY 120 LDVVERSLSNYPDFQO--ARIITGOEGAYGMITNYLLGKPSOKTRWFSIVPYETNNQ 177
DB 86 LDVTRVLRSSGFKFQDEWATVIGTDEGIYAVWVANHALGSLG-----GDPL 133
QY 178 ETFGALDLGASTQVTFVQNTQIESPDNALQRLYK--DYNVYTHSFLCYGKDOA---L 233
DB 134 KTTGIVELGASAQVTFVSEHV---PPFSRTISYGNVSYTYIYSHSLDFDQDAEDKL 190
QY 234 WQKLAKDIQVANS--ILRDPCHPHGKVKVNVSDLYKTPCTK-----RFEMTLPP 282
DB 191 LESLQNSVAASGQGVDEPCTPKGY-----IYDTHSQDSSGFLSESKFKASL-- 240
QY 283 QQFEIGIGNYQOCHOSILELF--NTSYCPYSOCAPNGIFLPPLOGDFGAFSAFYVMKF 340
DB 241 --QVQAAGDFTKCRSATLAMLQEGKENCAYKHCISGISTFTPNIQGSFLATENFFHTSKF 297
QY 341 LNLTSKVSQEKVTEWM---KKFCAPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQ 397
DB 298 FGL-GEK---EWLEMLAGKRCFGEWSKLKKKYPITTKDKLHRYCFSSAYIISMLHDS 353
QY 398 YHFTADSWEIHFIKGI--QGS DAGWTG-YMLN 428
DB 354 LGVALDD-ERIKYASKAGKENIPLDWALGAFILN 386

RESULT 4
S50463
hypothetical protein YER005w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dieterich, F.S.
A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:G603592; PID:G603597; GSPDB:GN00005
C:Genetics:
A:Gene: SGD:YND1; MIPS:YER005w
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.0%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1.4e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

anssen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 19.7%; Score 469.5; DB 2; Length 405;
Best Local Similarity 31.2%; Pred. No. 3.3e-30;
Matches 123; Conservative 65; Mismatches 145; Indels 61; Gaps 17;

QY 60 PGISKFQVKVNEIGVLTDCMERAREVPRSQHOETPVVYLGATAGMRLRMESEELADRV 119
DB 29 PGLSSYADNPEGASVSVTKLVFAKGRIPKGLKXSDIRLMATAGMRLDVPQVE--QI 85
QY 120 LDVVERSLSNYPDFQO--ARIITGOEGAYGMITNYLLGKPSOKTRWFSIVPYETNNQ 177
DB 86 LDVTRVLRSSGFKFQDEWATVIGTDEGIYAVWVANHALGSLG-----GDPL 133
QY 178 ETFGALDLGASTQVTFVQNTQIESPDNALQRLYK--DYNVYTHSFLCYGKDOA---L 233
DB 134 KTTGIVELGASAQVTFVSEHV---PPFSRTISYGNVSYTYIYSHSLDFDQDAEDKL 190
QY 234 WQKLAKDIQVANS--ILRDPCHPHGKVKVNVSDLYKTPCTK-----RFEMTLPP 282
DB 191 LESLQNSVAASGQGVDEPCTPKGY-----IYDTHSQDSSGFLSESKFKASL-- 240
QY 283 QQFEIGIGNYQOCHOSILELF--NTSYCPYSOCAPNGIFLPPLOGDFGAFSAFYVMKF 340
DB 241 --QVQAAGDFTKCRSATLAMLQEGKENCAYKHCISGISTFTPNIQGSFLATENFFHTSKF 297
QY 341 LNLTSKVSQEKVTEWM---KKFCAPWEIKTSYAGVKEKYLSEYCFSGTYILSLLOQ 397
DB 298 FGL-GEK---EWLEMLAGKRCFGEWSKLKKKYPITTKDKLHRYCFSSAYIISMLHDS 353
QY 398 YHFTADSWEIHFIKGI--QGS DAGWTG-YMLN 428
DB 354 LGVALDD-ERIKYASKAGKENIPLDWALGAFILN 386

RESULT 4
S50463
hypothetical protein YER005w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50463
R:Dieterich, F.S.
A:Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50463
A:Molecule type: DNA
A:Residues: 1-630 <DIE>
A:Cross-references: UNIPROT:P40009; EMBL:U18778; NID:G603592; PID:G603597; GSPDB:GN00005
C:Genetics:
A:Gene: SGD:YND1; MIPS:YER005w
A:Cross-references: SGD:S0000807
A:Map position: 5R

Query Match 19.0%; Score 453; DB 2; Length 630;
Best Local Similarity 27.2%; Pred. No. 1.4e-28;
Matches 130; Conservative 91; Mismatches 153; Indels 104; Gaps 22;

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.; Venter, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A; Reference number: A86141; MUID:21016719; PMID:11130712

RESULT 7
T34147
hypothetical protein C33H5.14 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34147
R:Bradshaw, H.; Stelliyes, L.
A:Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of *C. elegans* cosmid C33H5.
A:Reference number: Z21482
A:Accession: T34147
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-485 <RA>
A:Cross-references: UNIPROT:Q18411; EMBL:U41007; PIDN:AAA82272.1; CBSP:C33H5.14
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CBSP:C33H5.14
A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	16.9%;	Score 402.5;	DB 2;	Length 485;	
Best Local Similarity	26.7%;	Pred. No. 1.2e-247;			
Matches 116;	Conservative	69;	Mismatches 187;	Indels 63;	Gaps 15;
QY	17	NVKYGVILDAQSSHTSLYIKWPAEKENDTGV---VHVQEECRVK-GPGISKVFOKVNEI	72		
DB	22	NIKYGVICDAGSSGIRLFPVYTLKPLSGGLTNIDTLIHESPPVKVTPGLSGFGDKPQV	81		
QY	73	GYILTDCMRAREVTPRSQHGETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPF	132		
DB	82	VEYLTPLLRFAEBHPIYEQLGETDLLIFATAGMRLLPEAQKDAILIKNLONGUKSVIALRV	141		
QY	133	DFQGARIITGQEGAYGMITNYLIGKFSQKTRWFISIVPYETNNQETFGALDGLGCASTQV	192		
DB	142	SDSNIRIIDGAEIGYSIAVNYILGRFDKE-----NDSKVGMIDMGASVQI	189		
QY	193	TFVPQNOTTESPD--NALQFRLYKGD-----YNVYTHSELCYCKDOALQWKLANDIOVA	244		
DB	190	AFEIANEK-ESYNGGNVYEINLGSITETNEDYKVIYSTTFLGAGANEGL-KYTESNLVKS	247		
QY	245	SNEILLDPCHFPGYKXKVVNSDLYKTPCTKRFEMTLFPQOFEQIGIGNYQQOCHQSILELF	304		
DB	248	GNS--NDSCSPRGLNRLIG-----EFTVNGTGMVDVCLAAQVSSLI	285		
QY	305	NTS---YCPYSOCAFNGLFPLPQ---GDGAFSAFVFWKFLNLITSEKVSQOEKTEMMK	358		
DB	286	GDXAQPSCPNPTCFLRNVIAPSNVLSTVQLYGFSEYMYTTSTNFGSGGE-YHYOKFTFDEV	344		
QY	359	KFCAQPWEEI-----KTSYAGVKCYLSEYCFSGTYILSLLLQCYHFTADSWEHI-HFTG	412		
DB	345	KYCKQWNIIDQCFKNEPNFADIBELGTNCFKAAWTVSLHDG--FNVDKTKHLFQSVL	402		
QY	413	KIQGSDAGWTLYGML	427		
DB	403	KIAGEEMQWALGAML	417		

RESULT 8
C86276
7A19.33 protein - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86276
R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, P.; Pizzol, M.; Rooney, T.; Rowley, D.; Sakano, H.

Query Match	16.5%;	Score 394.5;	DB 2;	Length 508;	
Best Local Similarity	28.2%;	Pred. No. 5.6e-24;			
Matches 123;	Conservative	71;	Mismatches 171;	Indels 71;	Gaps 20;
QY	17	NVKGIVLDAGSGHTSLYIYKPAEKENDTGVVHVQVEECRVK-GPGISKFPVKVKNIEIGIY	75		
DB	63	SLHVSVIDGSSGSTRVHVFGYRIESGKPVDFGEEYASLKLSPGLSADNPNPEGVSES	122		
QY	76	LTDCEMAREVIPSQHOETPVYLGATAGMRLRMSEELADRLVDVVERSLSNYPDFQ	135		
DB	123	VTLEVPFAKCRVHKGKLKSDIRLMATAGMRLLELPVQE---QLDVTTRVLRSSGGDFP-	178		
QY	136	GARIITQEGEGAYWITINLLGKFSOKTRWFSGIVPYETNN-QETFGALDLG-----GA	188		
DB	179	-----RDWASVISEILENFQDLMKVYMLGLLLIMRSV	211		
QY	189	STQVTFVPQNTTSPDNALQFRLYK-KDYNVYTHSLCYKCOALWQKLAKDI-QVASN	246		
DB	212	RLEVTFV---STELVPSEFSRTLAYGNVSNLYSHSFLDFQD-AAQEKISESYLSYNSAAN	267		
QY	247	E---ILRDCPEHFGYKKVNV-SDLKTPCTK-RPEMTLPFQFEIQGIGNYQQCHSI	300		
DB	268	STGEGIVDPDCIPKGYILETNLQKDLPGFLADKGFATL-----QAAGNFSECRSAA	320		
QY	301	LELF--NTSYCPYSQCAPNGIFLPPLOGDPGAPSAFYVMVKFLNTSEKYSQEKVTEMM-	357		
DB	321	FAMLOEKGKCTYKRCISIGSIFTNLOGSFLATENFHTSKFFGL-GEK---EWLSEMIL	376		
QY	358	--KKFCQPWEEIKTSYAGVKKEKYLSEYCSGTVILSLLLQGYHFTADSWEHIFIGIKQ	415		
DB	377	AKGRFCEEWKSLKVKYPTFKDENLLRYCFSSAYIISMLHSLGLVALDD-BRIKYASKAG	435		
QY	416	GSD--AGWTLG-YMLN	428		
DB	436	FEDIPIDWAIAGAFILN	451		

RESULT 9

Tl6696
hypothetical protein R07E4.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: Tl6696

R:Miller, N.
submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid R07E4.
A:Reference number: Z18561
A:Accession: Tl6696
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-557 <MTL>
A:Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CEP8/R07E4.4
A:Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match 16.1%; Score 383.5; DB 2; Length 557;
Best Local Similarity 25.9%; Pred. No. 5e-23;
Matches 123; Conservative 85; Mismatches 194; Indels 73; Gaps 20;

Query Match	15.7%	Score	374;	DB	2;	Length	455;
Best Local Similarity	25.6%;	Pred.	No. 2.2e-22;				
Matches	116;	Conservative	80;	Mismatches	169;	Indels	88; Gaps
							18;
Qy	20	YGIVLDAGSHTSLYIKKPAEKENDTGVVH---	OYECECVKGPGISKFKVOKNEIGIYL	76			
Db		: : : : : : : :	: : : :				
Db	44	YAVVPDAGSTGSRHIYHF-----NQNLDDLHLHGKVEYYNKKITPGLSSSYANNPEQAAKSL	99				
Qy	77	TDCMERAREVIPRSQHETPPVLGATAGMRLLMSESELADRLDVVVVERLSN--YPDFDQ	135				
Db		:	:				
Db	100	IPLEQAEADVDDLPQKTPFVLGATAGLLNGDASE---KILQSVRDMLSNRSTENVQ	156				
Qy	136	--GARIIQGEAGYGWITINYLGLKPSOKTRWFSIVPYETNNQETFGALDLGGASTQVT	193				
Db		:	:				
Db	157	PDVAISIIDGTQEGSLWTVTYVALGNLGGK-----YTKTVGVIDLGGSYQMA	204				
Qy	194	FVPQNTIESPNAL-----QFRLYGKVNVYTHSFELCYCKDQALWQLAKDIQVAS	245				
Db		: :	: :				
Db	205	YAVSKTKANAPKVAOGDDPYIKKVVVLKGPYDLVHSYLHFR-----EASR	252				
Qy	246	NEILR-----DPCFHGPKVKVNVSIDLKTPCTKRPFEMTLPPQQFEIGIGNYQQCHQS	299				
Db		: :	: :				
Db	253	AELIKLTSPSPNCLLAGNGIITYSG-----EEFKAT-----AYTSGANFNKCNT	299				
Qy	300	ILELFNTSY-CPVSQCAFNGIFLUPPLQGDPG-----AFSAFYVMKFLNLITSEK----	347				
Db		: :	: :				
Db	300	IRKALKLNTPCPYONCTFGGIW----NGGGNGQKNLFASSSPFLYPEDTMVDASTPNF	355				
Qy	348	-VSQEKVTMMKFCAQPHEEIKTSYAGVKEKYLSEY-CFSGNYILLSLQLGYHFTADSW	405				
Db		: :	: :				
Db	356	ILRPVDIETKAECALNFEDAFASTYFFLDKKNVASVCMDLIIQYVLLVDG--FGLDPL	413				
Qy	406	EHTHFTGKIQGS-----AGWTGLMYMLNTNMIP	434				
Db		: :	: :				
Db	414	OKITSCKEIEYDAIVEAAMP LGNAVEIASLP	446				

RESULT 12
JC4616

apyrase (EC 3.6.1.5) precursor - potato
N;Alternate names: adenylpyrophosphatase, ATP-diphosphohydrolase
C;Species: Solanum tuberosum (potato)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: J04616; PC4147
R;Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A;Reference number: J04616; MUID:96158985; PMID:8579614
A;Accession: J04616
A;Molecule type: mRNA
A;Residues: 1-454 <HAN>
A;Cross-references: UNIPROT:P80595; GB:U58597; NID:gl1381632; PID:gl1381632
A;Accession: PC4147
A;Molecule type: protein
A;Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. It has a high substrate specificity, and is involved in starch synthesis.
C;Genetics:
A;Gene: rlopl
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TM>
F;31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F;44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F;44-65/Region: nucleotide binding #status predicted
F;192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F;192-212/Region: nucleotide binding #status predicted
F;390-410,427-446/Region: hydrophobic carboxyl end
F;151,262/Binding site: carbohydrate (Asn) #status predicted

Query Match 14.2%; Score 338; DB 2; Length 454;
Best Local Similarity 24.8%; Pred. No. 1.8e-19;
Matches 116; Conservative 81; Mismatches 191; Indels 80; Gaps 18;

QY 5 LPSSTONKALP-----ENVKIGVLDAGSSHTSLYKWPAREKNDTGTVHQVECR 56
DB 23 LLSKNVNAQIPLRRHLLSHESHYAVIFDAGSTGRVHFDFD-EKGLDPIGNNEYFM 81
QY 57 VKRGISKPVQKNEIGIYLTDCMERAREVIPSQHOETPVVLGATAGWMLLR-MESELEA 116
DB 82 ATEPGLSSYAEDPKAAANSLEPLDGAEGVVPQELQSTPLELGTAGIRMLKGA---A 138
QY 117 DRVLQVVE---RSLSNYPFDFQGARIIITQOEAGYGWITINLLKGFQSKTRWFSIVPEY 173
DB 139 EXILOAVRNLVKNQSTFFHSKQWVILDTQSGSYMAAIIYLLGNLKG----- 187
QY 174 TNNQETFGALDGGASTQVTFPQN-QTIESPDN-----ALOPFLYKGVNVTHTSELC 226
DB 188 -DYKSTTAVIDLGGSVQVMAVIAISNEQFAKAPQNEDEGPYVQOQKHLMSKDVNLYVHSLN 246
QY 227 YGKDQALWOKLAKIDQVANSNEILRDCPFPKPVKVVNVSDLYKTPCTKRFEMTLFPQOFE 286
DB 247 YGO-LAGRAEIKASRNESNPALGEC--DGYYSYGGVD--YKVPKPKG----- 291
QY 287 IQGIGNYQOCHOSILEFN-TSYPVSQCAFNGIFLPPLOQDFG-----AFSAFYFM 338
DB 292 ----SSWKKRRLTRHALKINAKNIECTFNGW----NGGGDGGQKNIHASSPFDIG 343
QY 339 KFLNLTSEKVSQE-----KVTEMMKFKCAQWPEIKTSYAGVKEKYLSEYCFSGYVILSL 393
DB 344 AQGVGVDTFPFSAKAKPIQVLLNAKVACQTNVADIKSIFPKQDRNIPVLCMDLIYEYTL 403
QY 394 LLQGYHTADSWEHIFIGIKQSD-----AGWTLGYMLNL-----TNMI 433
DB 404 LVDDG--FGLNPKHEITVHDVQVKNYLVGAAPLGLCAIDLVSSTINKI 449

RESULT 13

T04439
hypothetical protein T18B16.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04439
R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15359
A;Accession: T04439
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
A;Cross-references: UNIPROT:O49676; EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
C;Genetics:
A;Map position: 4
A;Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150

Query Match 13.9%; Score 332; DB 2; Length 1052;
Best Local Similarity 26.9%; Pred. No. 1.9e-18;
Matches 104; Conservative 70; Mismatches 149; Indels 64; Gaps 16;

QY 60 PGISKPVQKNEIGIYLTDCMERAREVIPSQHOETPVVLGATAGWMLLR-MESELEADR 118
DB 578 PGFDKLVNRTGLTKTAIKPLIQWAEKQIPKNAHRTTSLFVYATAGVRRRLPADSSWILGN 637
QY 119 VLDVVERSLSNYPFDF--QGARIITQOEAGYGWITINY---LLGKFSQKTRWFSIVPEY 173
DB 638 VWSILAKS-----PFTCEREWKLIISTEAYFGWTALNQTSMLGALPKKA----- 684
QY 174 TNNQETFGALDGGASTQVTFPQNQTIESPONALQFLYKGVNVTHTSFLCYGKDKQA- 232
DB 685 ----TFGALDGGSSQLQVTF--ENEERTHNETNLRLIGSVNHHLSAYSLAGYGLNDAP 737
QY 233 -----LWQKLA---KDIQVANSNEILRDCPFPKPVKVVNVSDLYKTPCTKRFEMTLFPQ 843
DB 738 DRSVHLLKLLPNVNSDLEIEGKLEWKHPCNLNGYN-----QGYICQCASSVQGGKKGK 792
QY 284 ---QFETQIGNYQQCHQSILEFNSTCYPSQCAFNGIFLPPLOQDFGAFSAFYFMKPF 340
DB 793 SGVSIKLVGAPNWGEC-----SALAKNAPCALPDGY-PRPHQGFVAVSGFFVYVRF 842
QY 341 LNTSEKVSQEKVTEMMKFKCAQWPEIKTSYAGVKEKYLSEYCFSGTYLTLGLLQGYHF 400
DB 843 FNLSAE-ASLDDVLEKGREFCDAWQVARTSVS--PQPFIEQYCFRAPHYIVSLRLRELYI 899
QY 401 TADSWEHIFIGIKQSDAGWTILGYML 427
DB 900 T-----DKQIILG---SGSITWTLQVAL 919

RESULT 14

T23508
hypothetical protein K08H10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23508
R;Gardner, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19750
A;Accession: T23508
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-479 <WIL>
A;Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CA805544.1; GSPDB:GN00023; CESP:K0
A;Experimental source: clone K08H10
C;Genetics:
A;Gene: CESP:K08H10.4
A;Map position: 5
A;Introns: 36/3; 83/3; 189/1; 300/2; 412/3
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 13.8%; Score 328.5; DB 2; Length 479;

```

A:Map position: 5L
C:Function:
A:Description: hydrolase
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F:10-24/Domain: transmembrane #status predicted <TMM>
F:41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.5%; Score 322.5; DB 2; Length 518;
Best Local Similarity 26.5%; Pred. No. 4e-18;
Matches 122; Conservative 72; Mismatches 193; Indels 73; Gaps 20;

QY      8 STQNKALENVYKGIVLDAAGSSHTSYLIYKPAEKENDTGVVHQVSECRVKGPGISKFVQ 67
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
81 SQTSCSEHKVIMIDAGSTGRVHIYKFDVCTSPPTLL--DEKFDMLFPGLSF-- 135
QY      68 KUNEIGI--YLTDCMERAREVTPRSOQHPTPVYLGATAGNRLI--RMESEBELADRLVDVE 124
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 DTDVSGAANSLDPLLKVANVYPIKARSTCPVAVKATAGRLGLGDAKSSKILSAVRDHL 195
QY      125 RSLSNYPF--DFQGAIRITGOEAGYGMTINLLGKFSQKTRWSIVPYETNNQ--T 179
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 K--DTPFPVGEQGVISMGDEEGVAMITNNLGNIG-----ANGPKLPT 240
QY      180 FGALDGGASTQVTFVPQ---NQTIESPNALQFRLYKGDYNYVTHSFICYG-----K 229
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 AAVFDLGGSTQIVPEPTFINEKMDVGEHKFDLKFGENYTLYQFSLHGYGLKEGNKV 300
QY      230 DQALWQKLAKDTQVASNE-----ILRDPCHPGYKKVNVSDLYKTPTCTKRFEMTLFPQ 284
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 NSVLVENALKDGIKLGDNKTHTQLSSPCLPP---KVNATNEKVTLES-----ET 348
QY      285 FRIQIG---NYQQCHQSILELFN--TSVCPYSQCAFNGIFLPL-----QGDGFNFA 333
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
349 YTIIDFGPDPEGAQCRFLTDEILNKDAQCSPPCSFNGVHQPSLVRTPKESNDIYFSY 408
QY      334 FYFVVKFLNLTSEKVSQEKVEMKKFC--AQPWEIKTSYAGVKKYLSE--VCFSGTV 389
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
409 FVDRTRPLGNPLSFTLINE--LNDLIARIVCKGEETWNSVFGIAGSLDESDSHFCLDLSF 467
QY      390 ILSLLQLQGHYHTADSWEHIHFIFGIQGSAGWTLGYMLNL 429
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
468 QVSLHTGVDIPLQ--RELRTGKTKIANKEIGWCIGASLPL 505

Search completed: March 7, 2005, 13:25:02
Job time : 15.7943 secs

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 62.6216 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147A-29_COPY_27_473

Perfect score: 2385

Sequence: 1.KKTQLTSTQNKALPENVKY.....NLTNMPAEQLPLSHST 447

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	98.4	510	1 ENP1_HUMAN	P49961 homo sapien
2	1835	76.9	510	1 ENP1_MOUSE	P55772 mus musculus
3	1835	76.9	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1830	76.7	510	2 Q921Q6	Q921q6 mus musculus
5	1818	76.2	372	2 Q86VW3	Q86vw3 homo sapien
6	1794.5	75.2	511	1 ENP1_RAT	P97687 rattus norv
7	1715	71.9	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1690.5	70.9	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	66.0	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1450	60.8	508	2 Q6DFS1	Q6dfs1 xenopus tro
11	1418	59.5	508	2 Q6GP74	Q6gp74 xenopus lae
12	1308.5	54.9	492	2 Q8DC46	Q8dc46 brachydanio
13	1046	43.9	497	2 Q6UQ22	Q6uq22 mus musculus
14	1004	42.1	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	41.8	493	2 Q90X66	Q90x66 gallus gall
16	977	41.0	454	2 Q6ZM69	Q6zm69 brachydanio
17	971.5	40.7	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	40.4	495	1 ENP2_MOUSE	O5026 mus musculus
19	964.5	40.4	495	2 Q921R1	Q921r1 mus musculus
20	961	40.3	455	2 Q7T014	Q7t014 brachydanio
21	953	40.0	494	1 ENP2_CHICK	P79784 gallus gall
22	937.5	39.3	502	2 Q66L64	Q66l64 brachydanio
23	936	39.2	526	2 Q6GNA4	Q6gna4 xenopus lae
24	933	39.1	500	2 Q6NV19	Q6nv19 xenopus tro
25	913.5	38.3	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	38.2	529	1 ENP3_HUMAN	O75355 homo sapien
27	907.5	38.1	495	1 ENP2_HUMAN	Q9y513 homo sapien
28	906.5	38.0	458	2 Q6UVZ0	Q6uvz0 homo sapien
29	902.5	37.8	529	2 Q8BFW6	Q8bfw6 m mus mescu
30	854	35.8	453	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	34.6	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	27.6	544	2 Q7YTA4	Q7yta4 schistosoma
33	620.5	26.0	300	2 Q8K0L2	Q8k0l2 mus musculus
34	596.5	25.0	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	505	21.2	483	2 Q9XI62	Q9xi62 arabidopsis
36	504	21.1	488	2 Q6NQ48	Q6nq48 arabidopsis
37	491	20.6	503	2 Q94AP8	Q94ap8 arabidopsis
38	481	20.6	503	2 Q8H1D8	Q8h1d8 arabidopsis
39	485	20.3	537	2 Q6Z543	Q6z543 oryza sativ
40	483	20.3	634	2 Q6FRC2	Q6frc2 candida gla
41	482.5	20.2	336	2 Q8CCV2	Q8ccv2 mus musculus
42	471.5	19.8	555	2 Q94E22	Q94ez2 arabidopsis
43	469.5	19.7	405	2 Q9M977	Q9m9t7 arabidopsis
44	466	19.5	611	2 Q6DH30	Q6dh30 brachydanio
45	465.5	19.5	555	2 Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1

ID	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
AC	P49961; Q9UQ09; Q9Y3Q9;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)			
DE	(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).			
GN	Name=ENTPD1; Synonyms=CD39;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J.,			
RA	Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,			
RA	Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;			
RT	"The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization."			
RT	J. Immunol. 153:3574-3583(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RP	TISSUE=Umbilical vein;			
RX	MEDLINE=97149443; PubMed=8996251;			
RA	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Koziak K.,			
RA	Millan M., Hancock W.W., Bach F.H.;			
RT	"Loss of ATP diphosphohydrolase activity with endothelial cell activation."			
RT	J. Exp. Med. 185:153-163(1997).			
RL	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).			
RX	TISSUE=Placenta;			
RC	MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;			
RA	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,			
RA	Titani K., Fujimura Y., Narita N.;			
RT	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II."			
RT	FEBS Lett. 453:335-340(1999).			
RL	[4]			
RP	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96096723; PubMed=8529670;			
RA	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;			
RT	"Purification and properties of human placental ATP diphosphohydrolase."			
RL	Eur. J. Biochem. 234:66-74(1995).			
RN	[5]			
RP	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND			
RP	399-405 (ISOFORM PLACENTAL I).			
RC	TISSUE=Placenta;			

RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.,
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature
 RT distinct from CD39, localization and inhibition on shear-induced
 RT platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kazmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.,
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;
 RA Wang T.F., Guidotti G.,
 RT "CD39 is an ecto-(Ca²⁺,Mg²⁺)-ATPase.";
 RL J. Biol. Chem. 271:9898-9901(1996).
 RN [8]
 RP PALMITOYLATION.
 RX MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
 RA Kozlak K., Kazmarek E., Kittel A., Sevigny J., Blusztajn J.K.,
 RA Schulte Am Esch J. II, Imal M., Guckelberger O., Goepfert C., Qawi I.,
 RA Robson S.C.,
 RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
 RT caveolae.";
 RL J. Biol. Chem. 275:2057-2062(2000).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -!- COPACITOR: Requires calcium and magnesium.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Vascular;
 CC IsoId=P49961-1; Sequence=Displayed;
 CC Name=Placental I;
 CC IsoId=P49961-2; Sequence=VSP_003607;
 CC Name=Placental II;
 CC IsoId=P49961-3; Sequence=VSP_003608, VSP_003609;
 CC -!- TISSUE SPECIFICITY: Expressed primarily on activated lymphoid
 CC cells. Also expressed in endothelial tissues. The vascular isoform
 CC and the placental isoform II are present in both placenta and
 CC umbilical vein, whereas placental isoform I is present in placenta
 CC only.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and
 CC 7.5-8.0 with ADP.
 CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S73813; BAB32152.1; --
 CC EMBL; U87967; AAB47572.1; --
 CC EMBL; AJ133133; CAB41886.1; --
 CC EMBL; AJ133134; CAB41887.1; --
 CC PIR; I56242; I56242.
 CC DR Genew; HGNC:3363; ENTPD1.
 CC DR MIM; 601752; --

DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0007596; P:blood coagulation; TAS.
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39_1.
 DR PROSITE; PS01238; GDAL_CD39_NTPase, 1.
 KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
 KW Transmembrane.
 FT DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 510 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 457 457 MEDT -> MKGKDLTSQQ (in isoform Placental
 FT VARSPLIC 1 4 I and isoform Placental II).
 FT VARSPLIC 272 299 /FTId=VSP_003607.
 FT VARSPLIC 272 299 VASNEILRDCEPHGKVKVNVSDLYKT -> ASITQSRPA
 FT PFTSAPPATSCCFLEFQIQ (in isoform Placental
 FT II).
 FT VARSPLIC 300 510 /FTId=VSP_003608.
 FT Missing (in isoform Placental II).
 FT SS -> G (in Ref. 5).
 FT D -> K (in Ref. 4).
 FT T -> TGET (in Ref. 5).
 FT V -> Y (in Ref. 5).
 FT SEQUENCE 510 AA; 57964 MW; BAD87D249649159 CRC64;
 Query Match 98.4%; Score 2348; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 9.2e-176;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 TONKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTVGVHVEECRVKPGISFVQK 68
 DB 38 TONKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTVGVHVEECRVKPGISFVQK 97
 QY 69 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWELLRMESEELADVLDDVRSLS 128
 DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWELLRMESEELADVLDDVRSLS 157
 QY 129 NYPDFOGARIITGOEGAYGWTINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 188
 DB 158 NYPDFOGARIITGOEGAYGWTINVLGKFSQKTRWFSIVPYETNNQTFGALDLGGA 217
 QY 189 STQVTFVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEI 248
 DB 218 STQVTFVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEI 277
 QY 249 LRDFCFHPGKVKVNVSDLYKTPCTKFEFTLPPQOPEIQIGNYQOCHOSILELFNTSY 308
 DB 278 LRDFCFHPGKVKVNVSDLYKTPCTKFEFTLPPQOPEIQIGNYQOCHOSILELFNTSY 337
 QY 309 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 368
 DB 338 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 397
 QY 369 KTSVAGKVKVLSYCFSGVYLSLLLOGVHFTADSWEHIFHTKIQSGDAGWTLGYMLN 428
 DB 398 KTSVAGKVKVLSYCFSGVYLSLLLOGVHFTADSWEHIFHTKIQSGDAGWTLGYMLN 457
 QY 429 LTNMIPAEQPLSTPLSHST 447
 DB 458 LTNMIPAEQPLSTPLSHST 476
 RESULT 2
 ENP1_MOUSE

ID ENPI_MOUSE STANDARD; PRT; 510 AA.
 AC P55772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
 DE activation antigen) (ecto-apyrase) (CD39 antigen).
 GN Name=Entpdl; Synonym=Cd39;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95015846; PubMed=7930580;
 RA Maliszewski C.R., DeLespessé G.J.T., Schoenborn M.A., Armitage R.J.,
 RA Panslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
 RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
 RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
 RT structural characterization."
 RL J. Immunol. 153:3574-3583(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98399871; PubMed=9730622;
 RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
 RA Gayle R.B. III, Maliszewski C.R.;
 RT "Gene structure and chromosome location of mouse Cd39 coding for an
 RT ecto-apyrase."
 RL Cytogenet. Cell Genet. 81:287-289(1998).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 DR EMBL; AF037366; AAC82259.1; -;
 DR EMBL; AF041818; AAC83203.1; -;
 DR EMBL; AF041812; AAC83203.1; JOINED.
 DR EMBL; AF041813; AAC83203.1; JOINED.
 DR EMBL; AF041814; AAC83203.1; JOINED.
 DR EMBL; AF041815; AAC83203.1; JOINED.
 DR EMBL; AF041816; AAC83203.1; JOINED.
 DR EMBL; AF041817; AAC83203.1; JOINED.
 DR MGD; MGI:102805; Entpdl.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0004050; P:ATPase activity; IDA.
 DR GO; GO:0006200; P:ATP catabolism; IDA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
 DR GO; GO:0030168; P:platelet activation; IDA.
 DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF0150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 FT DOMAIN 1 36 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 510 Cytoplasmic (Potential).

FT CARBOHYD 73 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 226 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 291 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 333 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 428 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 457 N-linked (GlcNAc. .) (Potential).
 SQ SEQUENCE 510 AA; 57205 MW; 856A6113D2E13930 CRC64;
 Query Match 76.9%; Score 1835; DB 1; Length 510;
 Best Local Similarity 76.4%; Pred. No. 1.8e-135;
 Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;
 Qy 9 TONKALPENVKYIGVLDAGSSHTSLYTKYKPAEKENDTGVVQVLEQVKGPGISKYAKQ 68
 Db |||||
 Qy 38 TONKPLPENVKYIGVLDAGSSHTNLTYKWPAAEKENDTGVVQVLEQVKGPGISKYAKQ 97
 Db |||||
 Qy 69 VNEIGIYLTDCMERAREVPRSOHOETPVYLGATAGMRLRLMESEELADRLVDVVERSL 128
 Db |||||
 Qy 98 TDEIGAYLAECWELUSTELIPTSKKHQTPVYLGATAGMRLRLMESEQSADEVLAAVSTSLK 157
 Db |||||
 Qy 129 NYPDFQGARITQOBERGAYGWTINYLKGFSGKTRWFISIVPYETNNQETFGALDLGA 188
 Db |||||
 Qy 158 SYPDFQGAKITQOBERGAYGWTINYLKGFSGKTRWFISIVPYETNNQETFGALDLGA 216
 Db |||||
 Qy 189 STQVTFVQNTIESPNALQFRLYGKDYNNVYTHSFLCYGKQALWKAKLADIQVASNEI 248
 Db |||||
 Qy 217 STQITFVQNSTIESPNSLQFRLYGSDYTVYTHSFLCYGKQALWKAKLADIQVSSGV 276
 Db |||||
 Qy 249 LRDCPFHGYKVVNSDLYKTCFKFEMTLPPQOFEIQGIGNYQOCHQSILEFNTSY 308
 Db |||||
 Qy 277 LKDCPFNGYKVVNSDLYKTCFKFEMTLPPQOFEIQGIGNYQOCHQSILEFNTSY 336
 Db |||||
 Qy 309 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSK--VSOEKVTEMKKFCAQPWE 366
 Db |||||
 Qy 337 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSK--VSOEKVTEMKKFCAQPWE 396
 Db |||||
 Qy 367 EIKTSYAGVKEKYLSEYCFSGTYTLLSLLQGYHTFADSWEHIFGIQGSADGWTLYGM 426
 Db |||||
 Qy 397 ETKTSYVSVKEKYLSEYCFSGTYTLLSLLQGYHTFADSWEHIFGIQGSADGWTLYGM 455
 Db |||||
 Qy 427 LNLTNMIPASQPLSTPLSHST 447
 Db |||||
 Qy 456 LNLTNMIPASQPLSTPLSHST 476
 Db |||||
 RESULT 3
 Q8CDV7 PRELIMINARY; PRT; 539 AA.
 ID Q8CDV7
 AC Q8CDV7
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:492511C05 product:ectonucleoside triphosphate
 DE diphosphohydrolase 1, full insert sequence.
 GN Name=Entpdl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690 (2001).

[3] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RA The FANTOM Consortium,

RA "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RL Nature 420:563-573 (2002).

[4] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630 (2000).

[5] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771 (2000).

[6] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Kurihara C., Matsuyama T., Miyazaki R., Kondo S., Konno H., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Sakai K., Sakazume N., Sano H.,

RA Saito R., Saichoh H., Sakai K., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takawa A., Tanaka T., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK029512; BAC26486.1; -

DR MGD; MGI:102805; Entpdl.

DR GO; GO:0005605; C:basal lamina; IDA.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0004050; F:aprase activity; IDA.

DR GO; GO:0006200; P:ATP catabolism; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IDA.

DR GO; GO:0030158; P:platelet activation; IDA.

DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.

DR InterPro; IPR000407; GDAI_CD39_NTPase.

DR Pfam; PF01150; GDAI_CD39_1.

DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.

KW Hydrolase.

SQ SEQUENCE 539 AA; 60590 MW; 49565788313321F4 CRC64;

Query Match 76.9%; Score 1835; DB 2; Length 539;

Best Local Similarity 76.4%; Pred. No. 1.9e-135;

Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;

QY 9 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVHQVECRVKGFGISKVQK 68

DB 67 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVQLEECQVKGFGISKVQK 126

QY 69 VNEIGYLTDCMRAREVTPRQHQETPVYLGATAGNRLLRMESEBLADRLVDVRSLS 128

DB 127 TDSIGAYLACMELSTELIPTSKRHQTPVYLGATAGNRLLRMESEBLADVLAASVSLK 186

QY 129 NYFPDFQAGARIITGOEBGAYGWITINYLILGKFSQKTRWFSIVPYETNNQETFGALDLGA 188

DB 187 STPFDFQAGAKIITGOEBGAYGWITINYLILGRTQSQWMLSLIS-DSQKQETFGALDLGA 245

QY 189 STQVTFVPPQNTIESPDNALQRLYKGVNVTYTHSFLCYGKQDALWQKLAKDIQVANSNEI 248

DB 246 STQITFVPPQNTIESPENSQRLYGEDYTVYTHSFLCYGKQDALWQKLAKDIQVSSGGV 305

QY 249 LRDPCHFGYKVVNVDLYKTPCKRPEMTLPFOQFETQIGIGNYQOCHOSILELPTSY 308

DB 306 LKDPCHFGYKVVNVDLYKTPCKRPEMTLPFOQFETQIGIGNYQOCHOSILELPTSY 365

QY 309 CPYSQCAENGIFLPPLOQDGFAGFSAFYFVYKFLNLTSEK--VSQEKVTMMKKFCAQPWE 366

DB 366 CPYSQCAENGIFLPPLOQDGFAGFSAFYFVYKFLNLTSEK--VSQEKVTMMKKFCAQPWE 425

QY 367 EIKTSYAGVKEKYLSEYCFSGAYILS-LLQGYNFTDSSWEQHFHMGKIKDSNAGWTLGYM 426

DB 426 EIKTSYAGVKEKYLSEYCFSGAYILS-LLQGYNFTDSSWEQHFHMGKIKDSNAGWTLGYM 484

QY 427 LNLTNMIPAEQPLSTPLSHST 447

DB 485 LNLTNMIPAEQPLSTPLSHST 505

RESULT 4

Q921Q6 PRELIMINARY; PRT; 510 AA.

AC Q921Q6

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Entpdl protein.

GN Name=Entpdl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

MD MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2] SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011278; AAH11278.1; -

DR MGD; MGI:102805; Entpdl.

DR GO; GO:0005605; C:basal lamina; IDA.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0004050; F:aprase activity; IDA.

```
DR GO:0006400; P-ATP catabolism; IDA.
DR GO:0007186; P-g-protein coupled receptor protein signalin. . ; IDA.
DR GO:00030168; P-platelet activation; IDA.
DR GO:0009181; P-purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 76.7%; Score 1830; DB 2; Length 510;
Best Local Similarity 76.2%; Pred. No. 4.4e-135;
Matches 336; Conservative 45; Mismatches 56; Indels 4; Gaps 3;

QY 9 TONKALPENVKYGVLDAGSSHTSYLYKPAEKENDTGVHVQVECRVKGPGISKFVQK 68
DB 38 TONKALPENVKYGVLDAGSSHTSYLYKPAEKENDTGVVQQLBECQVKGPGISKYAQK 97
QY 69 VNEIGYILTDCHMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 128
DB 98 TDEICAYLAECNELTEIPIPSKHQTPVYLGATAGMRLRMESEESQSADEVLAAVSTSLK 157
QY 129 NYPPDFQGAIRITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 188
DB 158 GYPPDFQGAIRITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 216
QY 189 STQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGKQDAWLQAKLADIQVASNEI 248
DB 217 STQITVFQNSTIESPNSLOPRLYGEDYTVVTHSFLCYGKQDAWLQAKLADIQVSSGV 276
QY 249 LRDPCFHPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQTGNYQOCHQSTLELFTNTSY 308
DB 277 LKDPFCNPGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQTGNYQOCHQSTLELFTNTSY 336
QY 309 CPYSQCAFNGFLPLPLQDGFAGFAFYFVFMKFLNLTSEK--VSQKVTMMKKKCAQWPWE 366
DB 337 CPYSQCAFNGFLPLPLHSGFAGFAFYFVMDPFKKVAKNSVISQKTEITIKNFCKSWE 396
QY 367 EIKTSYAGVKEKYLEYCFSGTYILSLLLQGHFTADSWHEIHFTGKIQGSDAGWTLGYM 426
DB 397 ETKTSYPSVKEKYLEYCFSGTYILSLLLQGHFTADSWHEIHFTGKIQGSDAGWTLGYM 455
QY 427 LNLTNMIPAEOPLSPLSHST 447
DB 456 LNLTNMIPAEOPLSPLPHST 476

RESULT 5
Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356EB3 CRC64;

Query Match 76.2%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.6e-134;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 MESEELADRVLDVVERSLSNYPDFQGAIRITGOEGAYGWITINYLKGFQSKTRWFSI 169
DB 1 MESEELADRVLDVVERSLSNYPDFQGAIRITGOEGAYGWITINYLKGFQSKTRWFSI 60
QY 170 VPYETNNQETFGALDLGGAQSTQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGK 229
DB 61 VPYETNNQETFGALDLGGAQSTQVTFVQNTIESPDNALQRLYKDYNYVTHSFLCYGK 120
QY 230 DOALWQKLAKDIQVANSNEILRDPCHFGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQG 289
DB 121 DOALWQKLAKDIQVANSNEILRDPCHFGYKVVNSDLYKTPCTKRFEMTLPPQOFEIQG 180
QY 290 IGNYQOCHQSTLELFTNTSYCYPSQCAFNGFLPLPLQDGFAGFAFYFVFMKFLNLTSEKVS 349
DB 181 IGNYQOCHQSTLELFTNTSYCYPSQCAFNGFLPLPLQDGFAGFAFYFVFMKFLNLTSEKVS 240
QY 350 QEKVTMMKKKCAQWPWEIETKTSYAGVKEKYLEYCFSGTYILSLLLQGHFTADSWHEIH 409
DB 241 QEKVTMMKKKCAQWPWEIETKTSYAGVKEKYLEYCFSGTYILSLLLQGHFTADSWHEIH 300
QY 410 FIGIKQSDAGWTLGYMLNLTNMIAPQPLSTPLSHST 447
DB 301 FIGIKQSDAGWTLGYMLNLTNMIAPQPLSTPLSHST 338

RESULT 6
ENP1_RAT STANDARD; PRT; 511 AA.
ID ENP1_RAT
AC P97687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase)
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.; AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=9221928;
RA Wang T.-P., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]
```

Qy	189	STQTVFVFNQOTIESPDNALFRLYGKDYNVYTHSFLCYGKQDQALWQKLADIQVASNEI	248
Db	217	STQTVFVPLNQTLFAPETSLQFRLYGTDYTVYTHSFLCYGKQDQALWQKLADIQVSSGGI	276
Qy	249	LRDPCFHGQYKVKVNVSDLYTPTCKRHEMTLPQOFEIQIGINYQOCHOSILLENTSY	308
Db	277	LKDCPCFYPGYKVKVNVSLYGTPTCKRFEKLPNFQVQVGTGDBEQCHOSILKFFNNSH	336
Qy	309	CYPSOCAFNGIPLPLQDGFAGSAFYVMKFL- NLTSKV -SOEKVTMMKKFCAQPWE	366
Db	337	CYPSQCAFNGVPLPLQSGFGAFSAFYVMDFPKMANDSVSSQEKWTEITKNFCSKPWE	396
Qy	367	EIKTSYAGYKERYLSEYCFSGTYTLLSLLQGYHFTADSWEHIFGIKQSGDAGWTLCYM	426
Db	397	EVKASYPTVKEKYLSEYCFSGTYTLLSLLQGYHFTGTSWDQIHFMGKIKDSNAGWTLCYM	456
Qy	427	LNLTNNMIPAEPLSTPLSHST	447
Db	457	LNLTNNMIPAEQLSPPLPHST	477

RESULT 7

ENPI_PIG

ID

ENPI_PIG

STANDARD;

PRT;

510 AA.

AC

Q9MYU4;

DT

16-OCT-2001 (Rel. 40, Created)

DT

16-OCT-2001 (Rel. 40, Last sequence update)

DT

05-JUL-2004 (Rel. 44, Last annotation update)

DE

Entonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)

DE

(NTPdase) (ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).

GN

Name=ENTPD1; Synonyms=CD39;

OS

Sus scrofa (Pig)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX

NCBI_TaxID=9923;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Arctic endothelium;

RA

MEDLINE=20325090; PubMed=10866813;

RA

Leimens R., Vanduffel L., Kittel A., Benrezzak O.,

RA

Sevigny J.;

RT

"Distribution, cloning, and characterization of porcine nucleoside triphosphate diphosphohydrolase-1";

RL

Eur. J. Biochem. 267:4106-4114(2000).

RL

[2]

RP

SEQUENCE OF 202-220.

RC

TISSUE=Pancreas;

RX

MEDLINE=97115858; PubMed=8965160; DOI=10.1074/jbc.271.51.33116;

RA

Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,

RA

Beaudoin A.R., Bach P.H., Robson S.C.;

RT

"Identification and characterization of CD39/vascular ATP diphosphohydrolase.";

RL

J. Biol. Chem. 271:33116-33122(1996).

CC

!- FUNCTION: In the nervous system, could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation.

CC

Hydrolyzes ATP and ADP equally well.

CC

!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

CC

!- COFACTOR: Requires calcium and magnesium (By similarity).

CC

!- SUBUNIT: Homodimer; disulfide-linked (By similarity).

CC

!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC

!- TISSUE SPECIFICITY: Highest expression found in vascular endothelium, smooth muscle, spleen and lung.

CC

!- PTM: Cleaved into two polypeptides that seem to stay together by noncovalent interactions.

CC

!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

CC

CC

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EMBL: AJ133746; CAB95871.1; -
InterPro: IPR000407; GDAI_CD39_NTPase.
Pfam: PF01150; GDAI_CD39; 1.
PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
Antigen: Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Magnesium; Transmembrane.
CHAIN 1 510
FT Ectonucleoside triphosphate
FT diposphohydrolase 1.
FT Ectonucleoside triphosphate
FT diposphohydrolase 1 27 kDa subunit.
FT Ectonucleoside triphosphate
FT diposphohydrolase 1 54 kDa subunit.
FT Cytoplasmic (Potential).
FT Potential.
FT Extracellular (Potential).
FT Potential.
FT Cytoplasmic (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT N-linked (GlcNAc. .) (Potential).
FT G -> S (in Ref. 2).
SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;
Query Match 71.9%; Score 1715; DB 1; Length 510;
Best Local Similarity 70.7%; Pred. No. 4.8e-126;
Matches 311; Conservative 63; Mismatches 64; Indels 2; Gaps 2;
QY 9 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKNDTGVVHVQVEECRVKGGISKFVOK 68
DB 38 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKNDTGVSQVEECKLKGPISEFAK 97
QY 69 VNEIGYLTDCMERREVPVLSQHOETPVYLGATAGMRLRMESSELDRLVDVVERSL 128
DB 98 LGEIDYLEACMERARTVVPKSHAEPTVYLGATAGMRLRMKNLASKILSTVAESIT 157
QY 129 NYPPDFQAGRIITGOEAGYGMITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 188
DB 158 RYPDFQAGRIITGOEAGYGMITINLLDKIQSGWFLNPKRGDQTQETVYGALDLGA 217
QY 189 STQVTFVPOQNTIESPDNALQRLYGVKNVYTHSLCYGKQDQALWQKLAKDIQVASEI 248
DB 218 STQITFVPOQNVLESPEPTLHFLYGVKNVSVYTHSLCYGKQDQALLQKLTKDLK-NTNGT 276
QY 249 LRDPCFHCYKVVNVSDLYKTPCTKREPTMLPQOPEIQTGNYOCHOSILELFTNTSY 308
DB 277 IHEPCFHSYQRMVNSHLYEAPCTRRFTSLPFPPELEIQTGDPKQCOQSIRLPNTSY 336
QY 309 CYSQCAFNGLFPLPQDGFAGFAFYFVKFELNLTSEKVS-QEKVTEMKKFCAQWEE 367
DB 337 CYSRCSFGVPLPQDGFAGFAFYFVKFELNLTSEKVSQSKVSTLEAFCSRPAE 396
QY 368 IKTSYAGVKEKLYSCFSGTYLSLLQGYHFTADSWHHIFIKIQSGDAGWTLYML 427
DB 397 LQWYFGDVKEKLYSCFSGTYLTLSSGYHFTAEWKNHFMGKQVSTSGWTLYML 456
QY 428 NLTNMIPAEQPLSTPLSHST 447
DB 457 NLTNMIPSEPSSTPLSHST 476

RESULT 8

EN1_ENPI_BOVIN

ID ENPI_BOVIN

AC O18956;

DT 16-OCT-2001 (Rel. 40, Created)

STANDARD;

PRT;

513 AA.

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diposphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diposphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTPDL; Synonyms=CD39;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115958; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach P.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diposphohydrolase";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: AF005940; AAB62382.1; -
InterPro: IPR000407; GDAI_CD39_NTPase.
Pfam: PF01150; GDAI_CD39; 1.
PROSITE: PS01238; GDAI_CD39_NTPASE; 1.
Antigen: Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
Magnesium; Transmembrane.
DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 481
FT TRANSMEM 482 502
FT DOMAIN 503 513
FT CARBOHYD 73 73
FT CARBOHYD 227 227
FT CARBOHYD 245 245
FT CARBOHYD 307 307
FT CARBOHYD 336 336
FT CARBOHYD 373 373
FT CARBOHYD 460 460
FT CONFLICT 97 97
FT CONFLICT 101 103
FT CONFLICT 464 464
SEQUENCE 513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;
Query Match 70.9%; Score 1690.5; DB 1; Length 513;
Best Local Similarity 69.8%; Pred. No. 4e-124;
Matches 309; Conservative 64; Mismatches 65; Indels 5; Gaps 3;

QY 9 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKNDTGVVHVQVEECRVKGGISKFVOK 68

DB 38 TONKALPENKYGIVLDAGSSHTSLYIKVPAEKNDTGVTQIEESNVKGPISGFARK 97

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69 VNEIGIYLTDCWREAREVIPSQHOETPPVYLGCATGMRLLRMESEELADRVLDVVERSL 128
DB VNEINVLITACWERAQKQVIPSIOHMETPPVILGATAGMRLLRMESEELADRVLDVVERSL 157
129 NYPDFQCARLIITGEEGAYGWTITNYLLGKFSQKTRWFSIVPVETNNQETFFGALDVGGA 188
DB EYPDFQCARLIISQEEGAYGWTITNYLLGKFSQKTRWFSIVPVETNNQETFFGALDVGGA 217
189 STQVTFVQNOTIESPDNALQFRLYGKDYNYVTHSFYCYGKQDQALWOKLAKDIOVASNEI 248
DB STQITVFPQNETTESPNNLFRLYGKNYSVYTHSFYCYGKQDQALWOKLQGLQ-GTNGI 276
249 LRDPCFHGKGVKVVNSDLYKTPCKREMT---LPFOEFIOGKGVVQOCHOSILELEN 305
DB THEPCFHGRYMKIKMVSNEFGCTKRHELNSSFFVPLVDIEIRGAGNFQRCRQSLIQFN 336
306 TSYCFYSOCAFNGLFPLQDGFAGFAFYFVMPKFLNLTSEK-VSQEKVTEMMKKFCAQP 364
DB TSYCFYSSCSFNGVFLPLHGFAGFAFYFVMEFLNLTSESVSEVQLEKLEFCAQR 396
365 WEEIKTSYAGVCKYLSYCSFGTVLSLLQGVHFTADSWEHIFHFGIKOIGSDAGWTLG 424
DB WEEVQKNGFCKYLSYCSFGTVLSLLQGVHFTADSWEHIFHFGIKOIGSDAGWTLG 456
425 YMLNLTNNIPAPOLSTPLSHST 447
DB YMLNLTNNIPABEPMSPPLPHST 479
RESULT 9
Q8CEB1 PRELIMINARY; PRT; 420 AA.
AC Q8CEB1;
DC 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732419M6, product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence. (fragment).
GN Name=Entpdl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa K., Tanaka T., Matsura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1; -.
DR MGD; MGI:102805; Entpdl.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:ATP catabolism; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; 1.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
Query Match 66.0%; Score 1574; DB 2; Length 420;
Best Local Similarity 74.5%; Pred. No. 4.4e-115;
Matches 289; Conservative 42; Mismatches 53; Indels 4; Gaps 3;
QY 62 ISKVFQKVNIGIYLTDCWREAREVIPSQHOETPPVYLGCATGMRLLRMESEELADRVLD 121
DB 1 ISKVAQKQTEIGAYLACNELSTELIITSKHQTPVYLGCATGMRLLRMESEELADRVLD 60
QY 122 WVERSLNYPDFQCARLIITGEEGAYGWTITNYLLGKFSQKTRWFSIVPVETNNQETFFG 181
DB 61 AVSTSLKSYPDFQCARLIITGEEGAYGWTITNYLLGKFSQKTRWFSIVPVETNNQETFFG 119
QY 182 ALDGGASTQVTFVFPQNOTIESPDNALQFRLYGKDYNYVTHSFYCYGKQDQALWOKLAKDI 241
DB 120 ALDGGASTQVTFVFPQNOTIESPDNALQFRLYGKDYNYVTHSFYCYGKQDQALWOKLAKDI 179
QY 242 QVANSNEILRDCFPHPGKVVVNSDLYKTPCKREMTLPCTKFEFMTLPFQOFEIOGKGVVQOCHOSIL 301
DB 180 QVSSGCVLKDPCFHPGKVVVNSDLYKTPCKREMTLPCTKFEFMTLPFQOFEIOGKGVVQOCHOSIL 239
QY 302 ELFNSTCYCPSQCAFNGIFLPLQDGFAGFAFYFVMPKFLNLTSEK--VSQEKVTEMMKK 359
DB 240 ELFNSTCYCPSQCAFNGIFLPLQDGFAGFAFYFVMPKFLNLTSEK--VSQEKVTEMMKK 299
QY 360 FCAQWBEIKTSYAGVCKYLSYCSFGTVLSLLQGVHFTADSWEHIFHFGIKOIGSDA 419
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Db 300 FCSKSWETKTSYSPKBYLSEYCFSGAYTSL-LLQYNTGSGWEOIHFMGKIKOSNA 358
Qy 420 GWTGLYMLNLNMIPAEQPLSTPLSHST 447
Db 359 GWTGLYMLNLNMIPAEQPLSPPLPHST 386

RESULT 10
Q6DFS1
ID AC Q6DFS1 PRELIMINARY; PRT; 508 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
EN Entpdl-prov protein.
GN Name=entpdl-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076662; AAH76662.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR ProSITE; PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 60.8%; Score 1450; DB 2; Length 508;
Best Local Similarity 60.2%; Pred. No. 3.1e-105;
Matches 263; Conservative 75; Mismatches 97; Indels 2; Gaps 2;

Qy 10 QNKALPENYKIVLDAGSSHTSYLYYKWAPEKENDTGVVHQVECRVKGPGISKVFQKV 69
Db 39 QNKPLPKNIKIVLDAGSSHTSYLYYEWPAEKENDTGVVQINECKVEGNGISSYGHEP 98
Qy 70 NEIGLYLTDWNERAREVTPRSHQETPVYLGATAGMRLLRNMESELADRVLDVVVERSLN 129
Db 99 LKAGLSLQCKMKARQVTPERQORETPVYLGATAGMRLLRNMESELADRVLDVVVERSLN 158
Qy 130 YPFDFOGARITITQEEGAYGHITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLOGAS 189
Db 159 FPFDPQGARITITQEEGAYGHITINYLIGNFIQDSGNWFKYIP-NFKPTETSGALDLOGAS 217
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Qy 190 TQVTFVQNOTIESPDNALQFRLYGKDYNVYTHSFLCYGKQQAQWLAKDIQVANSIL 249
Db 218 TQITFESKRE-IBSQENSLHFLYKSYDIYTHSFLCYGKQQAQRLQATNSIKDATDSIL 276
Qy 250 RDCPFHGYKKVNVSDLYKTPCTKREFMTLPFOQFEIQGIGNYQQCHQSILELPNTSYC 309
Db 277 LDPFCNSGYRRNASTNDLYSSPCISKLURIPTAPSTLDIRGTNGYQLCKRNQVAFNRTHC 336
Qy 310 PYSQAFNGIFLPPLOGDGFAGFAFYFMKFLNLITSEKVSQEKVTEMMKKFCAQPWBEIK 369
Db 337 TYSHCSFNGVFPQSLDGTFCGAFSAFYFMVFNFLNLTNEQMSLDKVKETVERHCSRPMDEVK 396
Qy 370 TSYAGVKEKYLSEYCFSGTIVLSLLQGYHTADSWEHIPGIGKQSDAGWTGLGYMLNL 429
Db 397 KDFPKIKKYLSEYCFSGTIVLNLLEYGYGFSSENWMDIRFLGKIKQSDAGWTGLGYMLNL 456
Qy 430 TNMIPASOPLSTPLSHS 446
Db 457 TNMIPASLPYPPPLSHA 473
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RESULT 11

```
Q6GP74
ID Q6GP74 PRELIMINARY; PRT; 508 AA.
AC Q6GP74;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80631 protein.
GN Name=MGC80631;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
```

RESULT 13

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=liver;
RA Bigonnesse B., Levesque S.A., Kukulski F., Lecka J., Robson S.C.,
RL Fernandes M.J.G., Sevigny J.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY364442; AAQ84519.1; -;
DR GO; GO:0004050; F:aprase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase.
SQ SEQUENCE 497 AA; 54650 MW; 00DE822B6EEB1BDF CRC64;

Query Match 43.9%; Score 1046; DB 2; Length 497;
Best Local Similarity 47.9%; Pred. No. 1.6e-73;
Matches 210; Conservative 75; Mismatches 131; Indels 22; Gaps 10;

Qy 11 NKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISFVQKVN 70
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 NVLLPADTKFGIVDFDAGSSHTSLFYQWPANKEKDTGVVSQALTCQIEGPGISSYSDPT 93
Qy 71 EIGIVLTDCMERAREVIPSQHOETPVVLGATAGMRLLRMESEELADRLVDVVERSLNY 130
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
94 QAGESLKSCLBEALALIFQAOHPETPTFLGSTAGMRLLSQKNSQARDILAAVSQTUSKS 153
Qy 131 PFDFQAGRIITQOEBGAYGWITINLLG---KFSQKTRWFSIVPYETNNQETFGALDLGG 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 PVDFWGAKLAGQDEGAGFWITINVLGMLKYS-SGQW--ILPEE---GMLVGALDLGG 207
Qy 188 ASTQVTFVPQNTTESPDNALQFLRYGKDNVNYTHSFLCYGKQALMOKLAK-----DI 241
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
208 ASTQISFVQGPILDQ-STQVTFRLYGANSYVTHSYLCFGKQDQILNLLAKLAQDRLS 266
Qy 242 QVASNEILRDCPFHGPYKKNVNSDLYKTPCTKRFEMTLFPQOEIQIGNYQCHQSIL 301
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
267 QVAP---VRHPCYHSGYQAIIPLSLSDYSPCHTHTDLSLHNTQNTFVEGTGPGNCVALR 323
Qy 302 ELPTNTSYCP-YSCAFNGIFLPPQCGDFGSAFYVMKFLNLTSEKVSQKVTEMKKF 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
324 SLFPSSCKGQKCAFNQIYPPVHGQFYAFNSFYTHFLNLSRQ-SLNTVNDTVWKF 382
Qy 361 CAQPWEEKTSYAGVKEKYLESPGSPYIISLLQGHFTADSWEHIFTKIQGSDAG 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
383 CQKFWKLEVSYPG-QERWLRYCASGLYILVLLLEGYKFSEETWPNFQKQAGDTDIG 441
Qy 421 WTLGYMLNLTNMPAEQ 438
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
442 WTLGFMNLNLTGMIPAE 459

RESULT 14
ENPL_CHICK
ID_ENPL_CHICK STANDARD; PRT; 493 AA.
AC O93295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPbase) (Ecto-ATP diphosphohydrolase) (Arpbase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=ENTPD1; Synonyms=CD39;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE-Oviduct;
RX MEDLINE=98298108; PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RT "Molecular cloning of the chicken oviduct ecto-ATP-
```

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RT diphosphohydrolase.";
RL J. Biol. Chem. 273:16043-16049 (1998).
RN [2]
RP SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RX MEDLINE=97442428; PubMed=9295305; DOI=10.1074/jbc.272.38.23645;
RA Lewis-Carl S., Kirley T.L.;
RT "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-apyrase.";
RL J. Biol. Chem. 272:23645-23652 (1997).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
EMBL; AF041355; AAC26491.1; -;
InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Magnesium; Transmembrane.
FT DOMAIN 1 7 Cytoplasmic (Potential).
FT TRANSMEM 8 28 Potential.
FT DOMAIN 29 463 Extracellular (Potential).
FT TRANSMEM 464 486 Potential.
FT DOMAIN 487 493 Cytoplasmic (Potential).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 372 372 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
FT CONFLICT 16 16 C -> W (in Ref. 2).
FT CONFLICT 21 21 I -> G (in Ref. 1; AA sequence).
SQ SEQUENCE 493 AA; 54034 MW; F14FF43AA2F3603 CRC64;

Query Match 42.1%; Score 1004; DB 1; Length 493;
Best Local Similarity 45.7%; Pred. No. 3.1e-70;
Matches 196; Conservative 73; Mismatches 144; Indels 16; Gaps 7;

Qy 14 LPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISFVQKVNIG 73
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
35 LPPTKTKGLVDFDAGSTHTALVYQWPADKNGTGIQVQSVCTVNGSGISSYVADDPAG 94
Qy 74 IYLTDCMERAREVIPSQHOETPVVLGATAGMRLLRMESEELADRLVDVVERSLNYPFD 133
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
95 ASLKPCLDKAMAVIPVEQWQTPYTLGATAGMRLLRMESEELADRLVDVVERSLNYPFD 154
Qy 134 FQAGRIITQOEBGAYGWITINLLG---KFSQKTRWFSIVPYETNNQETFGALDLGGAST 190
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
155 FRGAQILTGNBEGSGFWITVNYLLTETLIKFSFAGKW-----EHPQNTFVLGALDLGGAST 209
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 73.022 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147a-29_COPY_27_473

Perfect score: 2385
Sequence: 1 KKTQLTSTQNKALPENVKY.....NLTNMIPARPLSPPLSHST 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2385	100.0	454	3 AAY70913	Aay70913 Human sol
2	2385	100.0	454	3 AAY70890	Aay70890 Protein e
3	2385	100.0	473	3 AAY70924	Aay70924 Human sol
4	2385	100.0	473	3 AAY70901	Aay70901 Protein e
5	2385	100.0	474	3 AAY70923	Aay70923 Human sol
6	2385	100.0	474	3 AAY70900	Aay70900 Protein e
7	2385	100.0	478	3 AAY70914	Aay70914 Human sol
8	2385	100.0	478	3 AAY70891	Aay70891 Protein e
9	2370.5	99.4	487	3 AAY70921	Aay70921 Human sol
10	2370.5	99.4	487	3 AAY70898	Aay70898 Protein e
11	2356	98.8	476	3 AAY70911	Aay70911 Human CD3
12	2356	98.8	476	3 AAY70888	Aay70888 Protein e
13	2354	98.7	463	3 AAY70925	Aay70925 Human sol
14	2354	98.7	463	3 AAY70902	Aay70902 Protein e
15	2353	98.7	464	3 AAY70922	Aay70922 Human sol
16	2353	98.7	464	3 AAY70899	Aay70899 Protein e
17	2348	98.4	439	4 AAB71918	Aab71918 Soluble h
18	2348	98.4	510	2 AAW04334	Aaw04334 Human lym
19	2348	98.4	510	2 AAW04264	Aaw04264 Human CD3
20	2348	98.4	510	3 AAY70910	Aay70910 Human sol
21	2348	98.4	510	3 AAY70887	Aay70887 Human sol
22	2348	98.4	510	4 AAB71917	Aab71917 Human CD3
23	2348	98.4	510	7 ADJ57262	Adj57262 Human CD3
24	2348	98.4	510	8 ADL24295	Adl24295 Human CD3
25	2348	98.4	510	8 ADQ99453	Adq99453 Human CD3

ALIGNMENTS

RESULT 1

AAY70913
ID AAY70913 standard; protein; 454 AA.

XX
AC AAY70913;

XX
DT 17-AUG-2000 (first entry)

XX
DE Human soluble CD39 and IL2 N-terminus comprising fusion construct.

XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; anginginal; cerebroprotective; antiarteriosclerotic; anticoagulant; KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Protein 1..15

FT /label= Mature human interleukin_2

FT /note= "N-terminal region"

FT Protein 16..454

FT /note= "Human soluble CD39 protein"

XX
WO200023459-A1.

XX
PD 27-APR-2000.

XX
PF 13-OCT-1999; 99WO-US022955.

XX
PR 16-OCT-1998; 98US-0104585P.

XX
PR 06-NOV-1998; 98US-0107466P.

XX
PR 13-AUG-1999; 99US-0149010P.

XX
PA (IMMV) IMMUNEX CORP.

XX
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX
WI WI: 2000-339644/29.

XX
PT N-PSDB; RAD00206.

XX
PT New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial

PT infarction, stroke, coronary artery disease or injury.

PS Claim 6a; Page 95-97; 122pp; English.

XX The present sequence is a fusion construct, comprising the N-terminal
XX amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39)
XX region, that has apyrase activity. This results in high levels of solCD39
XX expression and activity in the transfected cells. Soluble CD39 is
XX constructed by removing the N- and C-terminal transmembrane domains. It
XX retains the capacity to metabolise ATP and ADP at relevant concentrations
XX and the ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
XX embolism, platelet-associated ischaemic disorders including lung,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis, intracardiac and venous
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke

XX Sequence 454 AA;

Query Match 100.0%; Score 2385; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.5e-236;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 60
DB 8 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 67
QY 61 GISKFVQVKNVEIGIYLTDCMERAREVIPRSQHQETPPVYLGTATAGMRLRMESEELADRVL 120
DB 68 GISKFVQVKNVEIGIYLTDCMERAREVIPRSQHQETPPVYLGTATAGMRLRMESEELADRVL 127
QY 121 DVVERSLSNYPDFOGARIITCOEGAGYGVITINYLKGFSGKTWFSIVPYETNNQFTF 180
DB 128 DVVERSLSNYPDFOGARIITCOEGAGYGVITINYLKGFSGKTWFSIVPYETNNQFTF 187
QY 181 GALLDGGASTQTVTFPQNTIESPNALQFRLYGKDVNVTYHSFLCYGKDQALWQKLAKD 240
DB 188 GALLDGGASTQTVTFPQNTIESPNALQFRLYGKDVNVTYHSFLCYGKDQALWQKLAKD 247
QY 241 IQVASNEILRDPCHFPGYKKVNVNVDLYKTPTCKRFEMTLPPQFEIOGIGNYQCHOSI 300
DB 248 IQVASNEILRDPCHFPGYKKVNVNVDLYKTPTCKRFEMTLPPQFEIOGIGNYQCHOSI 307
QY 301 LEFNTSYCPYSOCAPNGIFLPLQDGFAGFAFVFMKFLNLTSEKVSQEKVTMMKKF 360
DB 308 LEFNTSYCPYSOCAPNGIFLPLQDGFAGFAFVFMKFLNLTSEKVSQEKVTMMKKF 367
QY 361 CAQWEEIKTSVAGVEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIKIGQSDAG 420
DB 368 CAQWEEIKTSVAGVEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIKIGQSDAG 427
QY 421 WTLGYMLNLTNMTAPQPLSTPLSHST 447
DB 428 WTLGYMLNLTNMTAPQPLSTPLSHST 454

RESULT 2

AAAY70890

ID AAAY70890 standard; protein; 454 AA.

XX

AC AAAY70890;

XX 17-AUG-2000 (first entry)

XX Protein encoded by fusion construct of human soluble CD39 cdna-1.

DE Soluble CD39; ADP-induced platelet activation; platelet aggregation;

XX

KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT 1..15
FT /label= Mature human interleukin_2
FT /note= "N-terminal region"
FT 16..454
FT Protein
XX W0200023094-A2.
XX 27-APR-2000.
XX 13-OCT-1999; 99WO-US023641.
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX (IMMV) IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.
XX Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
XX N-PSDB; AAD00201.
XX Inhibiting platelet activation and recruitment, useful for treating a
XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
XX Claim 6; Page 95-97; 118pp; English.

The present sequence is the protein encoded by a fusion construct of
sol (soluble)CD39 having apyrase activity. Fusion of 12 amino acids from
the N-terminus of mature human IL2 to the solCD39 coding region results
in high levels of both expression and activity in the supernatants of
transfected cells. This is used in the treatment of unstable angina,
myocardial infarction, stroke, coronary artery disease or injury,
atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
platelet-associated ischaemic disorder including lung ischaemia, coronary
ischaemia and cerebral ischaemia, thrombotic disorder including coronary
artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
peripheral artery thrombosis, venous thrombosis, thrombosis,
coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
transient ischaemic attack. Soluble CD39 is also useful for preventing
thrombus formation or reformation, occlusion, reocclusion, stenosis or
restenosis of blood vessels or stroke

Sequence 454 AA;

Query Match 100.0%; Score 2385; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.5e-236;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 60
DB 8 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 67
QY 61 GISKFVQVKNVEIGIYLTDCMERAREVIPRSQHQETPPVYLGTATAGMRLRMESEELADRVL 120

The present sequence is the protein encoded by a fusion construct of
sol (soluble)CD39 having apyrase activity. Fusion of 12 amino acids from
the N-terminus of mature human IL2 to the solCD39 coding region results
in high levels of both expression and activity in the supernatants of
transfected cells. This is used in the treatment of unstable angina,
myocardial infarction, stroke, coronary artery disease or injury,
atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
platelet-associated ischaemic disorder including lung ischaemia, coronary
ischaemia and cerebral ischaemia, thrombotic disorder including coronary
artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
peripheral artery thrombosis, venous thrombosis, thrombosis,
coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
transient ischaemic attack. Soluble CD39 is also useful for preventing
thrombus formation or reformation, occlusion, reocclusion, stenosis or
restenosis of blood vessels or stroke

Sequence 454 AA;

Query Match 100.0%; Score 2385; DB 3; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.5e-236;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 60
DB 8 KKTQLTSTONKALPENVKYGLVDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP 67
QY 61 GISKFVQVKNVEIGIYLTDCMERAREVIPRSQHQETPPVYLGTATAGMRLRMESEELADRVL 120

Db 68 GISKVQVKNVEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVL 127
Qy 121 DWVERSLSNYPDFQGARIIITQSEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETP 180
Db 128 DWVERSLSNYPDFQGARIIITQSEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETP 187
Qy 181 GALDLGGASTQVTFVPPQNQTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALMQLAKD 240
Db 188 GALDLGGASTQVTFVPPQNQTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALMQLAKD 247
Qy 241 IQVNASNEILRDPCHFPGYKVVVSDLYKTCRKFEMTLFPQOFEIQIGNYQOCHQSI 300
Db 248 IQVNASNEILRDPCHFPGYKVVVSDLYKTCRKFEMTLFPQOFEIQIGNYQOCHQSI 307
Qy 301 LEFNTSYCPYSQCAFNGIFLPLQGDGFAFVFMKFLNLSEKVSQKVTMMKKF 360
Db 308 LEFNTSYCPYSQCAFNGIFLPLQGDGFAFVFMKFLNLSEKVSQKVTMMKKF 367
Qy 361 CAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLQGYHFTADSWEHIFGKIQSDAG 420
Db 368 CAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLQGYHFTADSWEHIFGKIQSDAG 427
Qy 421 WTLGYMLNLTNMIPEQPLSTPLSHST 447
Db 428 WTLGYMLNLTNMIPEQPLSTPLSHST 454

RESULT 3
AA70924
ID AA70924 standard; protein; 473 AA.
XX
AC AA70924;
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, pIL20Trim4.
XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX /label= Leader_peptide
XX /note= "Derived from human interleukin 2 (hIL2)"
XX Cleavage-site 26..27
XX /note= "Cleavage site of leader sequence"
XX Protein 35..473
XX /note= "Human soluble CD39 protein"
XX
XX WO200023459-A1.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpe SD;
XX
XX

WPI; 2000-339644/29.
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 114-116; 122pp; English.
XX
XX The present sequence is the fusion protein construct, pIL20Trim4. This
XX construct comprises of the leader peptide from human interleukin 2 (hIL2)
XX and soluble CD39 (solCD39) protein region, having apyrase activity.
XX Soluble CD39 is constructed by removing the N- and C-terminal
XX transmembrane domains. It retains the capacity to metabolise ATP and ADP
XX at relevant concentrations and the ability to block and reverse ADP-
XX induced platelet activation and recruitment, including platelet
XX aggregation. Soluble CD39 polypeptides are useful for inhibiting
XX angiogenesis. It is useful for the treatment of unstable angina, stroke,
XX myocardial infarction, coronary artery disease or injury, embolism,
XX atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-
XX associated ischaemic disorders including lung, coronary and cerebral
XX ischaemia, thrombotic disorders including coronary, peripheral and
XX cerebral artery thrombosis, intracardiac and venous thrombosis,
XX coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
XX transient ischaemic attack. Soluble CD39 is also useful for preventing
XX thrombus formation or reformation, occlusion, reocclusion, stenosis or
XX restenosis of blood vessels or stroke
XX
XX Sequence 473 AA;
XX
XX Query Match 100.0%; Score 2385; DB 3; Length 473;
XX Best Local Similarity 100.0%; Pred. No. 2,7e-236;
XX Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KKTQLTSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 60
XX Db 27 KKTQLTSTQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGP 86
XX
XX Qy 61 GISKVQVKNVEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVL 120
XX Db 87 GISKVQVKNVEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVL 146
XX
XX Qy 121 DWVERSLSNYPDFQGARIIITQSEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETP 180
XX Db 147 DWVERSLSNYPDFQGARIIITQSEGAYGWITINVLGKFSQKTRWFSIVPYETNNQETP 206
XX
XX Qy 181 GALDLGGASTQVTFVPPQNQTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALMQLAKD 240
XX Db 207 GALDLGGASTQVTFVPPQNQTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDALMQLAKD 266
XX
XX Qy 241 IQVNASNEILRDPCHFPGYKVVVSDLYKTCRKFEMTLFPQOFEIQIGNYQOCHQSI 300
XX Db 267 IQVNASNEILRDPCHFPGYKVVVSDLYKTCRKFEMTLFPQOFEIQIGNYQOCHQSI 326
XX
XX Qy 301 LEFNTSYCPYSQCAFNGIFLPLQGDGFAFVFMKFLNLSEKVSQKVTMMKKF 360
XX Db 327 LEFNTSYCPYSQCAFNGIFLPLQGDGFAFVFMKFLNLSEKVSQKVTMMKKF 386
XX
XX Qy 361 CAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLQGYHFTADSWEHIFGKIQSDAG 420
XX Db 387 CAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLQGYHFTADSWEHIFGKIQSDAG 446
XX
XX 421 WTLGYMLNLTNMIPEQPLSTPLSHST 447
XX 447 WTLGYMLNLTNMIPEQPLSTPLSHST 473
XX
XX RESULT 4
XX AA70901
XX ID AA70901 standard; protein; 473 AA.
XX
XX AC AA70901;
XX
XX DT 17-AUG-2000 (first entry)

XX	Protein encoded by Trim 4 construct.	
DE	Soluble CD39; ADP-induced platelet activation; platelet aggregation;	
XX	unstable angina; myocardial infarction; stroke; coronary artery disease;	
XX	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;	
KW	platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;	
KW	cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;	
KW	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;	
KW	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;	
KW	PE; pulmonary embolism; transient ischaemic attack; thrombus formation;	
KW	occlusion; reocclusion; stenosis; restenosis; angiogenesis; DVT;	
KW	cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;	
KW	coronary ischaemia; vascular occlusion; pIL2Trim4 variant.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FH	Cleavage-site	26. .27
FT	Protein	35. .473
FT		/note= "Soluble portion of CD39"
FT		
XX		
PN	WO200023094-A2.	
XX		
XX	27-APR-2000.	
XX		
XX	13-OCT-1999; 99WO-US023641.	
XX		
PR	16-OCT-1998; 98US-0104585P.	
PR	06-NOV-1998; 98US-0107466P.	
PR	13-AUG-1999; 99US-0149010P.	
XX		
PA	(IMMV) IMMUNEX CORP.	
PA	(CORR) CORNELL RES FOUND INC.	
XX		
PI	Maliszewski CR, Gayle RB, Marcus AJ;	
XX		
XX	WPI; 2000-339518/29.	
XX		
XX	Inhibiting platelet activation and recruitment, useful for treating a	
PT	mammal suffering from unstable angina, myocardial infarction, stroke,	
PT	coronary artery disease or injury, comprises administering soluble CD39	
PT	polypeptides.	
XX		
PS	Example 11; Page 114-116; 118pp; English.	
XX		
XX	The present sequence is the protein encoded by Trim4 construct. pIL2Trim4	
CC	variant was constructed by removing the human IL2 residues from solCD39	
CC	fusion construct. Fusion of 12 amino acids from the N-terminus of mature	
CC	human IL2 to the solCD39 coding region results in high levels of both	
CC	expression and activity in the supernatants of transfected cells. SolCD39	
CC	is used in the treatment of unstable angina, myocardial infarction,	
CC	stroke, coronary artery disease or injury, atherosclerosis, peripheral	
CC	vascular occlusion, preclampsia, embolism, platelet-associated ischaemic	
CC	disorder including lung ischaemia, coronary ischaemia and cerebral	
CC	ischaemia, a thrombotic disorder including coronary artery thrombosis,	
CC	cerebral artery thrombosis, intracardiac thrombosis, peripheral artery	
CC	thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous	
CC	thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.	
CC	Soluble CD39 is also useful for preventing thrombus formation or	
CC	reformation, occlusion, reocclusion, stenosis or restenosis of blood	
CC	vessels or stroke	
XX		
SQ	Sequence 473 AA;	
	Query Match 100.0%; Score 2385; DB 3; Length 473;	
	Best Local Similarity 100.0%; Pred. No. 2.7e-236;	
	Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 KKTQLTSSTQNKALPENVKYGVLDAGSSHTSLIYIKVPAEKENDTGVVHVEECRVKGP 60	
Db	27 KKTQLTSSTQNKALPENVKYGVLDAGSSHTSLIYIKVPAEKENDTGVVHVEECRVKGP 86	

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX WPI; 2000-339644/29.
 XX
 XX New soluble CD39 polypeptides having apyrase activity, useful for
 PT inhibiting angiogenesis and treating unstable angina, myocardial
 PT infarction, stroke, coronary artery disease or injury.
 XX
 XX
 PS Claim 6; Page 113-114; 122pp; English.
 XX
 XX The present sequence is the fusion protein construct, pIL2LTrim3. This
 CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
 CC and soluble CD39 (solCD39) protein region, having apyrase activity.
 CC Soluble CD39 is constructed by removing the N- and C-terminal
 CC transmembrane domains. It retains the capacity to metabolise ATP and ADP
 CC at relevant concentrations and the ability to block and reverse ADP-
 CC induced platelet activation and recruitment, including platelet
 CC aggregation. Soluble CD39 polypeptides are useful for inhibiting
 CC angiogenesis. It is useful for the treatment of unstable angina, stroke,
 CC myocardial infarction, coronary artery disease or injury, embolism,
 CC atherosclerosis, peripheral vascular occlusion, pre-eclampsia, platelet-
 CC associated ischaemic disorders including lung, coronary and cerebral
 CC ischaemia, thrombotic disorders including coronary, peripheral and
 CC cerebral artery thrombosis, intracardiac and venous thrombosis,
 CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
 CC transient ischaemic attack. Soluble CD39 is also useful for preventing
 CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
 CC restenosis of blood vessels or stroke
 XX
 XX Sequence 474 AA;
 SQ

Query Match 100.0%; Score 2385; DB 3; Length 474;
 Best Local Similarity 100.0%; Pred. No. 2.7e-236;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKTQLTSTQNKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGP 60
 Db 28 KKTQLTSTQNKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGP 87
 Qy 61 GISKPVQKVEIGIYLTDCMERAREVTPRSQHOETPVVLGATAGNRLLRMESEELADRVL 120
 Db 88 GISKPVQKVEIGIYLTDCMERAREVTPRSQHOETPVVLGATAGNRLLRMESEELADRVL 147
 Qy 121 DVVERSLSNYPDFQGARIIITQBEAGYGMITINLLGKFSQKTRWFSIVPYETNNQET 180
 Db 148 DVVERSLSNYPDFQGARIIITQBEAGYGMITINLLGKFSQKTRWFSIVPYETNNQET 207
 Qy 181 GALDLGGASTQVTPVQNOTTESPDNALQFLYKGDYNNVYTHSLFCYKGDQALWQKLAKD 240
 Db 208 GALDLGGASTQVTPVQNOTTESPDNALQFLYKGDYNNVYTHSLFCYKGDQALWQKLAKD 267
 Qy 241 IQVASNEILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQQCHQSI 300
 Db 268 IQVASNEILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLFPQOFELQIGNYQQCHQSI 327
 Qy 301 LEFNTSYCPYSQCAFNGIFLPLQGDGFASAFYFVMKFLNLTSEKVSQEKVTMMKKF 360
 Db 328 LEFNTSYCPYSQCAFNGIFLPLQGDGFASAFYFVMKFLNLTSEKVSQEKVTMMKKF 387
 Qy 361 CAQPWEIKTSYAGKEXKLYSEYCFSGTYIISLLLOGHFTADSWEHIFTKIGQSDAG 420
 Db 388 CAQPWEIKTSYAGKEXKLYSEYCFSGTYIISLLLOGHFTADSWEHIFTKIGQSDAG 447
 Qy 421 WTLGYMLNLTNNIPAEQPLSTPLSHST 447
 Db 448 WTLGYMLNLTNNIPAEQPLSTPLSHST 474

RESULT 6
 AAY70900
 ID AAY70900 standard; protein; 474 AA.
 XX
 AC AAY70900;

17-AUG-2000 (first entry)
 Protein encoded by Trim 3 construct.
 Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 unstable angina; myocardial infarction; stroke; coronary artery disease;
 atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
 platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 occlusion; reocclusion; stenosis; restenosis; anti-anginal; cardiant;
 cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;
 coronary ischaemia; vascular occlusion; pIL2Trim3 variant.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers
 Cleavage-site 24..25
 Protein 36..474
 /note= "Soluble portion of CD39"
 WO200023094-A2.
 27-APR-2000.
 13-OCT-1999; 99WO-US023641.
 16-OCT-1998; 98US-0104585P.
 06-NOV-1998; 98US-0107466P.
 13-AUG-1999; 99US-0149010P.
 (IMMUNEX CORP.
 (CORR) CORNELL RES FOUND INC.
 Maliszewski CR, Gayle RB, Marcus AJ;
 WPI; 2000-339518/29.
 Inhibiting platelet activation and recruitment, useful for treating a
 mammal suffering from unstable angina, myocardial infarction, stroke,
 coronary artery disease or injury, comprises administering soluble CD39
 polypeptides.
 Example 11; Page 113-114; 118pp; English.
 The present sequence is the protein encoded by Trim3 construct. pIL2Trim3
 variant was constructed by removing the human IL2 residues from solCD39
 fusion construct. Fusion of 12 amino acids from the N-terminus of mature
 human IL2 to the solCD39 coding region results in high levels of both
 expression and activity in the supernatants of transfected cells. SolCD39
 is used in the treatment of unstable angina, myocardial infarction,
 stroke, coronary artery disease or injury, atherosclerosis, peripheral
 vascular occlusion, pre-eclampsia, embolism, platelet-associated ischaemic
 disorder including lung ischaemia, coronary ischaemia and cerebral
 ischaemia, a thrombotic disorder including coronary artery thrombosis,
 cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
 Soluble CD39 is also useful for preventing thrombus formation or
 reformation, occlusion, reocclusion, stenosis or restenosis of blood
 vessels or stroke
 SQ Sequence 474 AA;
 Query Match 100.0%; Score 2385; DB 3; Length 474;
 Best Local Similarity 100.0%; Pred. No. 2.7e-236;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKTQLTSTQNKALPENVKYGVILVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGP 60

DB	28	KTQLTSSQNKALPENVKYGVILDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKGP	87
QY	61	GISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVL	120
DB	88	GISKFKVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVL	147
QY	121	DVVERSLSNYPDFQGARIIITQOEGAGYCWITINLLGKFSQKTRWFSIVPYETNNQETF	180
DB	148	DVVERSLSNYPDFQGARIIITQOEGAGYCWITINLLGKFSQKTRWFSIVPYETNNQETF	207
QY	181	GALDLGGASTQVTFVFPQNTIESPNALQFRLYGKDYNNVYTHSLFCYKQDALWOKLAKD	240
DB	208	GALDLGGASTQVTFVFPQNTIESPNALQFRLYGKDYNNVYTHSLFCYKQDALWOKLAKD	267
QY	241	IQVANSNEILRDCPFHFGYKKNVNSDLYKTPCTKRFEMTLFPQOFEIOGIGNYQCHQSI	300
DB	268	IQVANSNEILRDCPFHFGYKKNVNSDLYKTPCTKRFEMTLFPQOFEIOGIGNYQCHQSI	327
QY	301	LELFNTSYCPYSQCAFNGIFLPLPQDGFAGSAFYVFMKFLNLTSEKVSQEKVTEMMKKF	360
DB	328	LELFNTSYCPYSQCAFNGIFLPLPQDGFAGSAFYVFMKFLNLTSEKVSQEKVTEMMKKF	387
QY	361	CAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOGVYHFTADSWEHIFHFIKIQGSDAG	420
DB	388	CAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLOGVYHFTADSWEHIFHFIKIQGSDAG	447
QY	421	WTGLGYMLNLTNMIPAEQPLSTPLSHST	447
DB	448	WTGLGYMLNLTNMIPAEQPLSTPLSHST	474
RESULT 7			
AAAY70914			
ID	AAAY70914 standard; protein; 478 AA.		
XX	AAAY70914;		
AC	AAAY70914;		
XX	17-AUG-2000 (first entry)		
DT	Human soluble CD39 fusion protein construct, pIL2LsolCD39.		
DE	Soluble CD39; solCD39; human; apyrase activity; platelet activation;		
KW	unstable angina; myocardial infarction; stroke; coronary artery disease;		
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;		
KW	platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;		
KW	coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;		
KW	thrombus formation; occlusion; stenosis; restenosis; angiogenesis;		
KW	antithrombotic; cerebroprotective; antiarteriosclerotic; anticoagulant;		
KW	cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.		
XX	Homo sapiens.		
OS	Synthetic.		
XX	Key		
FX	Location/Qualifiers		
FT	Peptide	/label= Leader peptide	
FT		/note= "Derived from human interleukin 2 (hIL2)"	
FT	Protein	/label= Mature human interleukin 2	
FT		/note= "Derived from N-terminal end of human IL2"	
FT	Region	/label= "Linker"	
FT		/note= "Human soluble CD39 protein"	
XX	WO200023459-A1.		
PD	27-APR-2000.		
XX	13-OCT-1999;		
XX	99WO-US022955.		
XX	16-OCT-1998:		
XX	98US-0104585P.		

CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
CC useful for preventing thrombus formation or reformation, occlusion,
CC reocclusion, stenosis or restenosis of blood vessels or stroke
XX
SQ Sequence 478 AA;

Query Match 100.0%; Score 2385; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.8e-236;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTQLTSTQNKALPENVKYGVILDGSSHTSLYIKWPAKENDTGVVHVEECRVKGP 60
DB 32 KKTQLTSTQNKALPENVKYGVILDGSSHTSLYIKWPAKENDTGVVHVEECRVKGP 91
QY 61 GISKFVKVNEIGIYLDTCMERAREVIPSQHQETPPVLTAGTWRLLRMESEELADRVL 120
DB 92 GISKFVKVNEIGIYLDTCMERAREVIPSQHQETPPVLTAGTWRLLRMESEELADRVL 151
QY 121 DVVERSLSNYPDFQGARIIITQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETP 180
DB 152 DVVERSLSNYPDFQGARIIITQEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETP 211
QY 181 GALLDGGASTQVTFVQNTIESPDNALQFRLYKDYNYVTHSFCLCYGKDQALWQKLAKD 240
DB 212 GALLDGGASTQVTFVQNTIESPDNALQFRLYKDYNYVTHSFCLCYGKDQALWQKLAKD 271
QY 241 IQVANSILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSI 300
DB 272 IQVANSILRDPCHPGYKVVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHOSI 331
QY 301 LEFNTSYCPYSQCAFNGIFLPLQGDGFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKF 360
DB 332 LEFNTSYCPYSQCAFNGIFLPLQGDGFGAFSAFYFVMKFLNLTSEKVSQEKVTEMKKF 391
QY 361 CAQPWEIKTSYAGVKESYLCSEYCFSGTYILSLQGYHFTADSEWHIHFHFKTGQSDAG 420
DB 392 CAQPWEIKTSYAGVKESYLCSEYCFSGTYILSLQGYHFTADSEWHIHFHFKTGQSDAG 451
QY 421 WTGLYMLNLTNMIPIAEQPLSTPLSHST 447
DB 452 WTGLYMLNLTNMIPIAEQPLSTPLSHST 478

RESULT 9
AA770921
ID AA770921 standard; protein; 487 AA.
XX AC AA770921;
XX DT 17-AUG-2000 (first entry)
XX DE Human soluble CD39 fusion protein construct, pIL2LFlagSolCD39.
XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiodysgenesis;
KW antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
OS Homo sapiens.
OS Synthetic.
XX Key 1. .24 Location/Qualifiers
XX Peptide /label= Leader peptide
XX FT /note= "Derived from human interleukin 2 (hIL2)"
XX FT 25. .36
XX FT /note= "Mature human interleukin 2 (hIL2) N-terminal end"
XX FT 37. .40
XX FT Region

RESULT 8
AA770891
ID AA770891 standard; protein; 478 AA.
XX AC AA770891;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by pIL2Lsol CD39.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antiangiinal; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion.
XX Homo sapiens.
OS Synthetic.
XX Key 1. .24 Location/Qualifiers
XX Peptide /note= "hIL2 leader sequence"
XX FT 25. .36
XX FT /note= "Mature human IL2"
XX FT 37. .39
XX FT /note= "Linker"
XX FT 40. .478
XX FT /note= "SolCD39 protein"
XX WO200023094-A2.
XX DT 27-APR-2000.
XX PD 13-OCT-1999; 99WO-US023641.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMVX) IMMUNEX CORP.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
XX DR N-FSDB; AAD00202.
XX PT Inhibiting platelet activation and recruitment, useful for treating a
XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
XX PS Disclosure; Page 99-101; 118pp; English.
XX
XX The present sequence is protein encoded by the coding region of
XX pIL2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase
XX activity. Fusion of 12 amino acids from the N-terminus of mature human
XX IL2 to the solCD39 coding region results in high levels of both
XX expression and activity in the supernatants of transfected cells. This is
XX used in the treatment of unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, atherosclerosis, peripheral vascular
XX occlusion, preclampsia, embolism, platelet-associated ischaemic disorder
XX including lung ischaemia, coronary ischaemia and cerebral ischaemia, a
XX thrombotic disorder including coronary artery thrombosis, cerebral artery
XX thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous

FT	Region	/note= "Linker sequence"	
FT		41. .48	
FT	Protein	/note= "FLAG Tag sequence"	
FT		49. .487	
FT		/note= "Human soluble CD39 protein"	
XX	WO200023459-A1.		
XX	27-APR-2000.		
XX	13-OCT-1999;	99WO-US022955.	
XX	16-OCT-1998;	98US-0104585P.	
PR	06-NOV-1998;	98US-0107466P.	
PR	13-AUG-1999;	99US-0149010P.	
XX	(IMV) IMMUNEX CORP.		
PA	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;		
XX	WPI; 2000-339644/29.		
XX	N-PSDB; AAD00209.		
DR	New soluble CD39 polypeptides having apyrase activity, useful for		
XX	inhibiting angiogenesis and treating unstable angina, myocardial		
XX	infarction, stroke, coronary artery disease or injury.		
XX	Disclosure; Page 109-111; 122pp; English.		
XX	The present sequence is the fusion protein construct pIL2L2FlagSolCD39,		
CC	comprising the leader peptide of human interleukin 2 (hIL2), 12 amino		
CC	acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and		
CC	soluble CD39 (solCD39) protein region, that has apyrase activity. This		
CC	produces high levels of solCD39 expression and activity in the		
CC	transfected cells. Soluble CD39 is constructed by removing the N- and C-		
CC	terminal transmembrane domains. It retains the capacity to metabolise ATP		
CC	and ADP at relevant concentrations and the ability to block and reverse		
CC	ADP-induced platelet activation and recruitment, including platelet		
CC	aggregation. Soluble CD39 polypeptides are useful for inhibiting		
CC	angiogenesis. It is useful for the treatment of unstable angina,		
CC	myocardial infarction, stroke, coronary artery disease or injury,		
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,		
CC	platelet-associated ischaemic disorders including lung, coronary and		
CC	cerebral ischaemia, thrombotic disorders including coronary, peripheral		
CC	and cerebral artery thrombosis, intracardiac and venous thrombosis,		
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), and		
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing		
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or		
CC	restenosis of blood vessels or stroke		
XX	Sequence 487 AA;		
SQ	Query Match	99.4%; Score 2370.5; DB 3; Length 487;	
	Best Local Similarity	98.0%; Pred. NO. 8.9e-235;	
	Matches 447; Conservative	0; Mismatches 0; Indels 9; Gaps 1;	
QY	1 KKTQLTSS-----TQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDGVVHQ 51		
Db	32 KKTQLTSSGDYKDDDKTQNKALPENVKYGI VLDAGSSHTSLYIYKPAEKENDGVVHQ 91		
QY	52 VEECRVKGPGISKVQKWEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRME 111		
Db	92 VEECRVKGPGISKVQKWEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRME 151		
QY	112 SEELADRVLDVVERSLSNYPFDQAGARIITQGEAGYGMWITINYLKGFESQKTRFVSIVP 171		
Db	152 SEELADRVLDVVERSLSNYPFDQAGARIITQGEAGYGMWITINYLKGFESQKTRFVSIVP 211		
QY	172 YETNNQETFGALDGGASTQVTFVQNQTIESP DNALQFRLYKQDYNVYTHSFLCYGKQD 231		
Db	212 YETNNQETFGALDGGASTQVTFVQNQTIESP DNALQFRLYKQDYNVYTHSFLCYGKQD 271		
QY	232 ALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIG 291		

Db	272	ALWQKLAKDIQVASNEILRDCPFHGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIG	331
QY	292	NYQOCHQSILELFTNTSYCPYSQAFNGIFLPLPQDGFCAFSAFYFVMKFLNLTSEKVSQE	351
Db	332	NYQOCHQSILELFTNTSYCPYSQAFNGIFLPLPQDGFCAFSAFYFVMKFLNLTSEKVSQE	391
QY	352	KVTENMKKFCAPWEEIKTSTVAGVKEKYLSEVCFSGTYILSLLLQGYHFTADSWEHIFI	411
Db	392	KVTENMKKFCAPWEEIKTSTVAGVKEKYLSEVCFSGTYILSLLLQGYHFTADSWEHIFI	451
QY	412	GKIQSDAGWTGLGYMLNLTNMPAPQPLSTPLSHST	447
Db	452	GKIQSDAGWTGLGYMLNLTNMPAPQPLSTPLSHST	487
RESULT 10			
AAV70898			
ID	AAV70898 standard; protein; 487 AA.		
AC	AAV70898;		
XX			
DT	17-AUG-2000 (first entry)		
XX	Protein encoded by soluble CD39 expression plasmid.		
XX	Soluble CD39; ADP-induced platelet activation; platelet aggregation;		
KW	unstable angina; myocardial infarction; stroke; coronary artery disease;		
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;		
KW	platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;		
KW	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;		
KW	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;		
KW	pulmonary embolism; transient ischaemic attack; thrombus formation;		
KW	occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiant;		
KW	cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;		
KW	coronary ischaemia; vascular occlusion; solCD39 expression plasmid.		
OS	Homo sapiens.		
OS	Synthetic.		
XX	Key	Location/Qualifiers	
PH	Peptide	1. .24	
FT		/note= "hull2 leader sequence"	
FT	Peptide	25. .36	
FT		/note= "First 12 amino acids of mature human IL2"	
FT	Region	37. .40	
FT		/label= linker	
FT	Region	41. .48	
FT		/note= "Flag tag"	
FT	Protein	49. .487	
FT		/note= "Soluble CD39"	
XX	WO200023094-A2.		
PN	27-APR-2000.		
XX	13-OCT-1999;	99WO-US023641.	
PF			
XX	16-OCT-1998;	98US-0104585P.	
PR	06-NOV-1998;	98US-0107466P.	
PR	13-AUG-1999;	99US-0149010P.	
XX	(IMV) IMMUNEX CORP.		
PA	(CORR) CORNELL RES FOUND INC.		
XX	Maliszewski CR, Gayle RB, Marcus AJ;		
PI	WPI; 2000-339518/29.		
DR	N-PSDB; AAD00204.		
XX	Inhibiting platelet activation and recruitment, useful for treating a		
PT	mammal suffering from unstable angina, myocardial infarction, stroke,		

coronary artery disease or injury, comprises administering soluble CD39 peptides.

Example 9; Page 109-111; 118pp; English.

The present sequence is encoded by soluble CD39(solCD39) expression plasmid. This was used for the transient expression of solCD39 protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 487 AA;

Query Match 99.4%; Score 2370.5; DB 3; Length 487;
Best Local Similarity 98.0%; Pred. No. 8.9e-235;
Matches 447; Conservative 0; Mismatches 0; Indels 9; Gaps 1

QY 1 KKTQTSS-----TONKALPENVKYGIVLDAGSSHTSLVIYKWPAEKENDTGVVHQ 51
| | | | |
Db 32 KKTQLTSSGDYDDDKTKONKALPENVKYGIVLDAGSSHTSLVIYKWPAEKENDTGVVHQ 91
| | | | |
QY 52 VVECRVKGPGISKFKVQKNEIGIYLTCMERAREVIPRSOHOETPVYLGATAGMRLLRME 111
| | | | |
Db 92 VVECRVKGPGISKFKVQKNEIGIYLTCMERAREVIPRSOHOETPVYLGATAGMRLLRME 151
| | | | |
QY 112 SEELADRVLDVVERSLSNYPDFOGARIITGOEBGAYGWITINVLLGKTSOKTRWFSIVP 171
| | | | |
Db 152 SEELADRVLDVVERSLSNYPDFOGARIITGOEBGAYGWITINVLLGKTSOKTRWFSIVP 211
| | | | |
QY 172 YETNNQETFGALDLGGASTQTVTFPQNQTIESPNALQFRLYGKDYNVYTHSPCLCYGKDQ 231
| | | | |
Db 212 YETNNQETFGALDLGGASTQTVTFPQNQTIESPDNALQFRLYGKDYNVYTHSPCLCYGKDQ 271
| | | | |
QY 232 ALWQKLAKDIQVASNEILRDCPFHPGKKVNVSDLYKTPCTKRFEMTLFPQQFEIQGIG 291
| | | | |
Db 272 ALWQKLAKDIQVASNEILRDCPFHPGKKVNVSDLYKTPCTKRFEMTLFPQQFEIQGIG 331
| | | | |
QY 292 NYQQCHQSILELNTSYCPYSOCAFNGIFLPPLQGDFGAFSAFYVMKFNLNLTSEKVSOE 351
| | | | |
Db 332 NYQQCHQSILELNTSYCPYSOCAFNGIFLPPLQGDFGAFSAFYVMKFNLNLTSEKVSOE 391
| | | | |
QY 352 KVTEMMKXFCAPWEIEIKTSYAGVKEKYLSYCFSGTYIISLLQGHFTADSWEHIHFI 411
| | | | |
Db 392 KVTEMMKXFCAPWEIEIKTSYAGVKEKYLSYCFSGTYIISLLQGHFTADSWEHIHFI 451
| | | | |
QY 412 GKIQSDAGWTGLGYMLNTNMIPAEQLSTPLSHST 447
| | | | |
Db 452 GKIQSDAGWTGLGYMLNTNMIPAEQLSTPLSHST 487
| | | | |

RESULT 11
AAY70911
ID AAY70911 standard; protein; 476 AA.
XX AC AAY70911;
XX DT 17-AUG-2000 (first entry)
XX DE Human CD39-L4-1 protein construct.
XX KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
XX KW unstable angina; myocardial infarction; stroke; coronary artery disease;
XX KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
XX KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
XX KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

KW	thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiac; vasotropic; thrombolytic.
KW	
KW	
XX	
OS	Homo sapiens.
OS	Synthetic.
PH	Key
FT	Region
FT	1. .37
FT	/note= "Human CD39-L4 protein N-terminal end"
FT	20. .21
FT	Cleavage-site
FT	/note= "Cleavage site of leader sequence"
FT	38. .476
FT	Region
FT	/note= "Human soluble CD39 protein"
XX	
XX	
PN	WO200023459-A1.
XX	
XX	
PD	27-APR-2000.
XX	
XX	
PP	13-OCT-1999; 99WO-US022955.
XX	
PR	16-OCT-1998; 98US-0104585P.
PR	06-NOV-1998; 98US-0107466P.
PR	13-AUG-1999; 99US-0149010P.
XX	
XX	(IMMV) IMMUNEX CORP.
XX	
PI	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX	
XX	WPI; 2000-339644/29.
DR	
XX	
PT	New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
PT	
PT	
XX	
XX	
PS	Claim 6; Page 89-91; 122pp; English.
XX	
XX	
CC	The present sequence is a fusion protein construct CD39-L4-1, comprising the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is a secreted apyrase, belonging to the CD39 family. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolize ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke
XX	
SO	Sequence' 476 AA:

	Query Match	98.8%	Score 2356;	DB 3;	Length 476;
	Best Local Similarity	100.0%;	Pred. NO. 2.7e-233;		
	Matches 441;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	7	SSTQNKALPENVKYGI	VLDAGSHTSI	LIYIKVPAEKENDTGVVHVEECRVKPGGISKEV	66
Db	36	SSTQNKALPENVKYGI	VLDAGSHTSI	LIYIKVPAEKENDTGVVHVEECRVKPGGISKEV	95
QY	67	QKWNIEGIYLTDCMERAREVI	PRSQHOETPVYLCATAGMRLRMESEELADRVLDVVERS	126	
Db	96	QKWNIEGIYLTDCMERAREVI	PRSQHOETPVYLCATAGMRLRMESEELADRVLDVVERS	155	
QY	127	LSNPYFPDQGARIITGQEEGAYGWITINYLGHFSQKTRWFISIVPVETNNQTFGALD	IG	186	
Db	156	LSNPYFPDQGARIITGQEEGAYGWITINYLGHFSQKTRWFISIVPVETNNQTFGALD	IG	215	

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RESULT 11
AAY70911
ID AAY70911 standard; protein; 476 AA.
XX
XX AAY70911;
XX AC
XX
XX
DT 17-AUG-2000 (first entry)
XX
XX
DE Human CD39-L4-1 protein construct.

```

Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
unstable angina; myocardial infarction; stroke; coronary artery disease;
atherosclerosis; peripheral vascular occlusion; presclampsia; embolism;
platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;

187 GASTQVTFVFNQTIESPNDALQRLYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASN 246
 216 GASTQVTFVFNQTIESPNDALQRLYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASN 275
 247 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYYQCHQSILELFTNT 306
 276 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYYQCHQSILELFTNT 335
 307 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 366
 336 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
 367 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 426
 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 455
 427 LNLTMIPAEQPLSTPLSHST 447
 456 LNLTMIPAEQPLSTPLSHST 476

RESULT 12
 AAY70888
 ID AAY70888 standard; protein; 476 AA.
 XX AC AAY70888;
 XX DT 17-AUG-2000 (first entry)
 XX DE
 XX DE Protein encoded by CD39-L4-1 construct.
 XX DE
 XX DE Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiact;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Region 1..37
 FT /note= "Derived from CD39-L4"
 FT Cleavage-site 20..21
 FT Region 38..476
 FT /note= "Soluble portion of CD39"
 FT
 XX WO200023094-A2.
 XX 27-APR-2000.
 XX 13-OCT-1999; 99WO-US023641.
 XX 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 XX Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39

polypeptides.
 Claim 6; Page 89-91; 118pp; English.
 The present sequence is a fusion construct of human soluble CD39 encoded by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the CD39 family. The fusion construct is used for the expression and activity of soluble CD39 in CHO (Chinese hamster ovary) cells. Soluble CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at physiologically relevant concentrations as well as the ability to block and reverse ADP-induced platelet activation and recruitment including platelet aggregation. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 476 AA;
 Query Match 98.8%; Score 2356; DB 3; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.7e-233;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SSTQNKALPENVKIGIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKVF 66
 Db 36 SSTQNKALPENVKIGIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKPGISKVF 95
 Qy 67 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDVVERS 126
 Db 96 QKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLESEELADRLDVVERS 155
 Qy 127 LSNYPDFQGARITTOEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG 186
 Db 156 LSNYPDFQGARITTOEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG 215
 Qy 187 GASTQVTFVFNQTIESPNDALQRLYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASN 246
 Db 216 GASTQVTFVFNQTIESPNDALQRLYGKDYNNVTHSFLCYGKQDQALWQKLAKDIOVASN 275
 Qy 247 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYYQCHQSILELFTNT 306
 Db 276 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPFQOFEIQIGNYYQCHQSILELFTNT 335
 Qy 307 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 366
 Db 336 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
 Qy 367 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 426
 Db 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTILGYM 455
 Qy 427 LNLTMIPAEQPLSTPLSHST 447
 Db 456 LNLTMIPAEQPLSTPLSHST 476

RESULT 13
 AAY70925
 ID AAY70925 standard; protein; 463 AA.
 XX AC AAY70925;
 XX DT 17-AUG-2000 (first entry)
 XX DE Human soluble CD39 fusion protein construct, IgkappalsolCD39.
 XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;

unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig; immunoglobulin kappa.

Homo sapiens.
OS
Synthetic.

Key Location/Qualifiers
Peptide 1..20
/label= "Leader peptide"
/note= "Derived from human immunoglobulin Ig kappa"
Cleavage-site 20..21
/note= "Cleavage site of leader sequence"
Region 21..24
/note= "Residues derived from human interleukin 2 (IL2)"
Protein 25..463
/note= "Human soluble CD39 protein"

WO200023459-A1.
27-APR-2000.

13-OCT-1999; 99WO-US022955.
16-OCT-1998; 98US-0104585P.
06-NOV-1998; 98US-0107466P.
13-AUG-1999; 99US-0149010P.

(IMMV) IMMUNEX CORP.

Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
WPI; 2000-339644/29.

New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.

Claim 6; Page 116-118; 122pp; English.

The present sequence is the fusion protein construct, IgkappaLsolCD39. This construct comprises of the leader peptide from human immunoglobulin Ig kappa, linked to the soluble CD39 (solCD39) protein region by few residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase activity and is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 463 AA;

Query Match 98.7%; Score 2354; DB 3; Length 463;
Best Local Similarity 99.1%; Pred. No. 4, 1e-233;
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

3 TOLTSSTQNKALPENVKYIVLDAGSSHTSYLYIKWPAEKENDTGTVHQQVEECRVKPGI 62
| :|||||

Db 19 TGAPTSTQNKALPENVKYIVLDAGSSHTSYLYIKWPAEKENDTGTVHQQVEECRVKPGI 78
Qy 63 SKFQKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDV 122
Db 79 SKFQKVNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDV 138
Qy 123 VERSLSNYPFPOQARIITGOEBGAYWITINYLKGFSSQKTRWFSIVPYETNNOETFGA 182
Db 139 VERSLSNYPFPOQARIITGOEBGAYWITINYLKGFSSQKTRWFSIVPYETNNOETFGA 198
Qy 183 LDLGASTQVTFVQNTIESPDNALQPRLYGKDVNVVTHSFLCYGKQDALWOKLAKDIQ 242
Db 199 LDLGASTQVTFVQNTIESPDNALQPRLYGKDVNVVTHSFLCYGKQDALWOKLAKDIQ 258
Qy 243 VASNEILLRDCPCFHPGYKKVNVVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILE 302
Db 259 VASNEILLRDCPCFHPGYKKVNVVSDLYKTPCTKRFEMTLPFQOFEIQIGNYQOCHQSILE 318
Qy 303 LFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCA 362
Db 319 LFNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCA 378
Qy 363 QPWEIKTSYAGVKEKYLSEYCFSGSTYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 422
Db 379 QPWEIKTSYAGVKEKYLSEYCFSGSTYLSLLQGYHFTADSWEHIFIGIKQSDAGWT 438
Qy 423 LGYMLNLTNMIPEAQPLSTPLSHST 447
Db 439 LGYMLNLTNMIPEAQPLSTPLSHST 463

RESULT 14
AAV70902
ID AAV70902 standard; protein; 463 AA.
XX
AC AAV70902;
XX
DT 17-AUG-2000 (first entry)
XX
DE Protein encoded by IgkappaLsolCD39 construct.
XX
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antiangiinal; cardiac; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; IgkappaLsolCD39 construct.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
Peptide 1..20
/note= "Igkappa leader sequence"
FT Cleavage-site 20..21
FT Region 21..24
/note= "Derived from IL-2"
FT Region 25..463
/note= "Soluble portion of CD39"
FT Region 25..32
/note= "Derived from solCD39"

WO200023094-A2.
27-APR-2000.
13-OCT-1999; 99WO-US023641.
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PR	16-OCT-1998;	98US-0104585P.
PR	06-NOV-1998;	98US-0107466P.
PR	13-AUG-1999;	99US-0149010P.
XX	(IMMV) IMMUNEX CORP.	
PA	(CORR) CORNELL RES FOUND INC.	
PA		
XX		
PI	Maliszewski CR, Gayle RB, Marcus AJ;	
DR	WPI; 2000-339518/29.	
XX		
PT	Inhibiting platelet activation and recruitment, useful for treating a	
PT	mammal suffering from unstable angina, myocardial infarction, stroke,	
PT	coronary artery disease or injury, comprises administering soluble CD39	
PT	polypeptides.	
XX		
PS	Claim 6; Page 116-118; 118pp; English.	
CC	The present sequence is the protein encoded by IGKappaIaSolCD39 construct	
CC	This is used for transient expression of soluble(sol)CD39 in recombinant	
CC	cells for determining enzymatic activity and platelet inhibitory activity	
CC	for each protein product. SolCD39 is used in the treatment of unstable	
CC	angina, myocardial infarction, stroke, coronary artery disease or injury,	
CC	atherosclerosis, peripheral vascular occlusion, pre-eclampsia, embolism,	
CC	platelet-associated ischemic disorder including lung ischemia, coronary	
CC	ischemia and cerebral ischemia, thrombotic disorder including coronary	
CC	artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,	
CC	peripheral artery thrombosis, venous thrombosis, thrombolysis,	
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE);	
CC	transient ischemic attack. Soluble CD39 is also useful for preventing	
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or	
CC	restenosis of blood vessels or stroke	
XX		
SQ	Sequence 463 AA;	
Query Match		
Best Local Similarity 98.7%; Score 2354; DB 3; Length 463;		
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		
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DB	: :	
DG	19 TGATFSTQNKAIPENVKYGIVLDAGSSHTSLYYIKWPAAEKENDTGVVHQQVEECRVKGPGI 78	
QY	63 SKFYQKVNEIGIYLTDCHMERAREVIPRSQHQTTPVYLGCATAGMRLLRMESELADRVLDV 122	
DB	:	
DG	79 SKFYQKVNEIGIYLTDCHMERAREVIPRSQHQTTPVYLGCATAGMRLLRMESELADRVLDV 138	
QY	123 VERSLSNYPFPFGQARIITGOEGAYGWITTNYLLGKFESQTRWFSPVPYEINNETFEA 182	
DB	:	
DG	139 VERSLSNYPFPFGQARIITGOEGAYGWITTNYLLGKFESQTRWFSPVPYEINNETFEA 198	
QY	183 LDLGASTQVTTFVPONQTIESPNDALQFLRYGKDYNVTHSFCLCYGKQDALWKLAKDIQ 242	
DB	:	
DG	199 LDLGASTQVTTFVPONQTIESPNDALQFLRYGKDYNVTHSFCLCYGKQDALWKLAKDIQ 258	
QY	243 VASNEILLDPCHFPGYKKVNVDLYKTCPCKRFEMTLPPFOQFEIQGIGNYQCQSILIE 302	
DB	:	
DG	259 VASNEILLDPCHFPGYKKVNVDLYKTCTKEFKFTMTLPFOQFEIQGIGNYQCQSILIE 318	
QY	303 LFNTSYCYPSCAFNGIFLPLPQGDFGAFAFYFMVKFNLTSEKYQBKVTEMKKKPCA 362	
DB	:	
DG	319 LFNTSYCYPSCAFNGIFLPLPQGDFGAFAFYFMVKFNLTSEKYQBKVTEMKKKPCA 378	
QY	363 QPWEEKITSYAGVKEKIYSEYCFSGTYIIISLLQGHFTADSWEHIHFICKIQGSDAGWT 422	
DB	:	
DG	379 QPWEEKITSYAGVKEKIYSEYCFSGTYIIISLLQGHFTADSWEHIHFICKIQGSDAGWT 438	
QY	423 LGYMNLNTNMIPAEQPLSTPLSHST 447	
DB	:	
DG	439 LGYMNLNTNMIPAEQPLSTPLSHST 463	

Query Match 98.7%; Score 2353; DB 3; Length 464;
Best Local Similarity 99.8%; Pred. No. 5.3e-233;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy	67	QKVNIEGILY	TDCHMERAREV	IPRSQHQETPVY	LGATAGMRLLRMESE	ELADRVLDVVERS 126
Db	84	QKVNIEGILY	TDCHMERAREV	IPRSQHQETPVY	LGATAGMRLLRMESE	ELADRVLDVVERS 143
Qy	127	LSNYPFDFOGARI	ITQBEGAYCHIT	INYLKGFQKTRWFS	IVPYETNNOETFGAL	DLG 186
Db	144	LSNYPFDFOGARI	ITQBEGAYCHIT	INYLKGFQKTRWFS	IVPYETNNOETFGAL	DLG 203
Qy	187	GASTQVTFVPQNO	TIESPDNALQRLY	GKDYNVVYTHSFL	CYGKQOALWQKLAKD	IQVASN 246
Db	204	GASTQVTFVPQNO	TIESPDNALQRLY	GKDYNVVYTHSFL	CYGKQOALWQKLAKD	IQVASN 263
Qy	247	EILRDCPCHPGY	KKVNVSDLYKTP	CTKRFEMLTLPFO	QFEIQGIGNYQQCHQ	SILELFNT 306
Db	264	EILRDCPCHPGY	KKVNVSDLYKTP	CTKRFEMLTLPFO	QFEIQGIGNYQQCHQ	SILELFNT 323
Qy	307	SYCPYSQCAFNGI	FLPPLQDGFAGF	SAFYFMKFLNLTSE	KVSQEKVTMMKKFCA	QPWE 366
Db	324	SYCPYSQCAFNGI	FLPPLQDGFAGF	SAFYFMKFLNLTSE	KVSQEKVTMMKKFCA	QPWE 383
Qy	367	EIKTSYAGVKEKY	LSEYCFSGTYIL	SLALQGYHFTADS	WEHIFIGKIQGS	DAGWTLGYM 426
Db	384	EIKTSYAGVKEKY	LSEYCFSGTYIL	SLALQGYHFTADS	WEHIFIGKIQGS	DAGWTLGYM 443
Qy	427	LNLTNMIPAEQ	PLSTPLSHST	447		
Db	444	LNLTNMIPAEQ	PLSTPLSHST	464		

Search completed: March 7, 2005, 13:13:11
Job time : 74.1332 secs

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GenCore version 5.1.6
: Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 52.4401 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-29_COPY_27_473
Perfect score: 2385
Sequence: 1 KKTQTSSTQNKALPENVKY.....NLTNMPAEQLSTPLSHST 447

Scoring table: BLOSUM62
dapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES											
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2	2385	100.0	473	9	US-09-835-147-29	Sequence 29, Appl					
3	2385	100.0	474	9	US-09-835-147-28	Sequence 28, Appl					
4	2385	100.0	478	9	US-09-835-147-8	Sequence 8, Appli					
5	2370.5	99.4	487	9	US-09-835-147-26	Sequence 26, Appl					
6	2356	98.8	476	9	US-09-835-147-3	Sequence 3, Appli					
7	2354	98.7	463	9	US-09-835-147-30	Sequence 30, Appl					
8	2353	98.7	464	9	US-09-835-147-27	Sequence 27, Appl					
9	2348	98.4	439	9	US-09-374-586-2	Sequence 2, Appli					
10	2348	98.4	502	13	US-10-092-063-38	Sequence 38, Appl					
11	2348	98.4	510	9	US-09-835-147-2	Sequence 2, Appli					
12	2348	98.4	510	9	US-09-374-586-1	Sequence 1, Appli					
13	2348	98.4	510	10	US-09-781-796B-1	Sequence 1, Appli					

14	2348	98.4	510	16	US-10-646-308-30	Sequence 30, Appli
15	2294	96.2	476	9	US-09-835-147-4	Sequence 4, Appli
16	1009	42.3	495	9	US-09-823-356-4	Sequence 4, Appli
17	910.5	38.2	529	9	US-09-923-304-4	Sequence 4, Appli
18	906.5	38.0	458	13	US-10-052-586-496	Sequence 496, App
19	906.5	38.0	458	14	US-10-174-590-496	Sequence 496, App
20	906.5	38.0	458	14	US-10-176-758-496	Sequence 496, App
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31	906.5	38.0	458	14	US-10-176-757-496	Sequence 496, App
32	906.5	38.0	458	14	US-10-176-913-496	Sequence 496, App
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34	906.5	38.0	458	14	US-10-180-557-496	Sequence 496, App
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37	906.5	38.0	458	14	US-10-174-579-496	Sequence 496, App
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42	906.5	38.0	458	14	US-10-175-743-496	Sequence 496, App
43	906.5	38.0	458	14	US-10-176-488-496	Sequence 496, App
44	906.5	38.0	458	14	US-10-176-492-496	Sequence 496, App
45	906.5	38.0	458	14	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 100.0% Score 2385; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-210; Indels 0; Gaps 0;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	8	KTQLTSTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP	67
QY	61	GISKVQKNEIGIYILTDCEMERAREVIPRSQHOETFPVYLGTAGMRLRMESEELADRVL	120
DB	68	GISKVQKNEIGIYILTDCEMERAREVIPRSQHOETFPVYLGTAGMRLRMESEELADRVL	127
QY	121	DVVERSLSNYPDFOGARIITGOEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETP	180
DB	128	DVVERSLSNYPDFOGARIITGOEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETP	187
QY	181	GALDGGASTQVTFVQNOTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKD	240
DB	188	GALDGGASTQVTFVQNOTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKD	247
QY	241	IQVASNEILRDCPFHPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIIGIGNYQCHQSI	300
DB	248	IQVASNEILRDCPFHPGYKVVNVSDLYKTPCTKRFEMTLPPQOFEIIGIGNYQCHQSI	307
QY	301	LELFNTSYCPYSCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKF	360
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; Sequence 29, Application US/09835147			
; Patent No. US2002002277A1			
GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; CURRENT FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 29			
; LENGTH: 473			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-29			
Query Match 100.0%; Score 2385; DB 9; Length 473;			
Best Local Similarity 100.0%; Pred. No. 1.8e-210;			
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	1	KTQLTSTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP	60
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; Sequence 28, Application US/09835147			
; Patent No. US2002002277A1			
GENERAL INFORMATION:			
; APPLICANT: Maliszewski, Charles R.			
; APPLICANT: Gayle III, Richard B.			
; APPLICANT: Price, Virginia L.			
; APPLICANT: Gimpel, Steven D.			
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
; FILE REFERENCE: 2879-US			
; CURRENT APPLICATION NUMBER: US/09/835,147			
; CURRENT FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: US 60/104,585			
; PRIOR FILING DATE: 1998-10-16			
; PRIOR APPLICATION NUMBER: US 60/107,466			
; PRIOR FILING DATE: 1998-11-06			
; PRIOR APPLICATION NUMBER: US 60/149,010			
; PRIOR FILING DATE: 1999-08-13			
; PRIOR APPLICATION NUMBER: PCT/US99/22955			
; PRIOR FILING DATE: 1999-10-13			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 28			
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; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Fusion			
; OTHER INFORMATION: construct of human CD39			
US-09-835-147-28			
Query Match 100.0%; Score 2385; DB 9; Length 474;			
Best Local Similarity 100.0%; Pred. No. 1.8e-210;			
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
US-09-835-147-28			
QY	1	KTQLTSTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP	60
DB	28	KTQLTSTONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKGP	87
QY	61	GISKVQKNEIGIYILTDCEMERAREVIPRSQHOETFPVYLGTAGMRLRMESEELADRVL	120
DB	88	GISKVQKNEIGIYILTDCEMERAREVIPRSQHOETFPVYLGTAGMRLRMESEELADRVL	147

QY 121 DVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVPVETNNQETFF 180
DB 148 DVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVPVETNNQETFF 207
QY 181 GALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQDALWOKLAKD 240
DB 208 GALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQDALWOKLAKD 267
QY 241 IQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQOCHOSI 300
DB 268 IQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQOCHOSI 327
QY 301 LELENTSYCPYSCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKF 360
DB 328 LELENTSYCPYSCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKF 387
QY 361 CAQPEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIKIQGSDAG 420
DB 388 CAQPEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIKIQGSDAG 447
QY 421 WTGYMLNLTNMIPEOPLSTPLSHST 447
DB 448 WTGYMLNLTNMIPEOPLSTPLSHST 474

RESULT 4

US-09-835-147-8

; Sequence 8, Application US/09835147
; Patent No. US20020002277A1

GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; TYPE: PRT

; LENGTH: 478

; ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39

US-09-835-147-8

Query Match 100.0%; Score 2385; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.9e-210; Indels 0; Gaps 0;
Matches 447; Conservative 0; Mismatches 0

QY 1 KKTQLTSSNQKALPENVKYGVLDAGSSHTSLYIKVPAEKENDTGVVHQVEECRVKGP 60
DB 32 KKTQLTSSNQKALPENVKYGVLDAGSSHTSLYIKVPAEKENDTGVVHQVEECRVKGP 91
QY 61 GISKFKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRYL 120
DB 92 GISKFKVQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRYL 151
QY 121 DVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVPVETNNQETFF 180
DB 152 DVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVPVETNNQETFF 211

QY 181 GALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQDALWOKLAKD 240
DB 212 GALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQDALWOKLAKD 271
QY 241 IQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQOCHOSI 300
DB 272 IQVASNEILRDCPFHPGKVVVNSDLYKTPCTKRFEMTLPFQOPEIQGIGNYQOCHOSI 331
QY 301 LELENTSYCPYSCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKF 360
DB 332 LELENTSYCPYSCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVSQEKVTMMKKF 391
QY 361 CAQPEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIKIQGSDAG 420
DB 392 CAQPEEIKTSYAGVKEKYLSEYCSGTIYLSLLQGYHFTADSWEHIFIKIQGSDAG 451
QY 421 WTGYMLNLTNMIPEOPLSTPLSHST 447
DB 452 WTGYMLNLTNMIPEOPLSTPLSHST 478

RESULT 5

US-09-835-147-26

; Sequence 26, Application US/09835147

; Patent No. US20020002277A1

GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 487

; TYPE: PRT

; ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39

US-09-835-147-26

Query Match 99.4%; Score 2370.5; DB 9; Length 487;
Best Local Similarity 98.0%; Pred. No. 4.1e-209;
Matches 447; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 KKTQLTSS-----TONKALPENVKYGVLDAGSSHTSLYIKVPAEKENDTGVVHQ 51
DB 32 KKTQLTSSGVYKDDDKTONKALPENVKYGVLDAGSSHTSLYIKVPAEKENDTGVVHQ 91
QY 52 VEECRVKGPISKFQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRME 111
DB 92 VEECRVKGPISKFQKNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRME 151
QY 112 SEELADRYLDVVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVP 171
DB 152 SEELADRYLDVVVERSLSNYPDFQAGARIITGOEGAYGWIITINYLKGFQKTRWFSIVP 211
QY 172 YETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQD 231
DB 212 YETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFCLCYGKQD 271

QY 232 ALWOKLAKDIOVASNEILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIG 291
DB 272 ALWOKLAKDIOVASNEILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIG 331
QY 292 NYQOCHQSILELNTSYCPYSCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQE 351
DB 332 NYQOCHQSILELNTSYCPYSCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQE 391
QY 352 KVTMMKFCAPWBEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWHEHIHFI 411
DB 392 KVTMMKFCAPWBEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWHEHIHFI 451
QY 412 GKIQSDAGWTGLGYMLNTNMIPASQPLSTPLSHST 447
DB 452 GKIQSDAGWTGLGYMLNTNMIPASQPLSTPLSHST 487

RESULT 6

US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-3

Query Match 98.8%; Score 2356; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 8,6e-208;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 SSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPGI 66
DB 36 SSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPGI 95
QY 67 QKNEIGIVLTDGWERAREVIPSQHOETPVYLGATAGMRLRMSEELADRLVDVRS 126
DB 96 QKNEIGIVLTDGWERAREVIPSQHOETPVYLGATAGMRLRMSEELADRLVDVRS 155
QY 127 LSNYPDFQARITGQEEGAYGWIITNYLLGKFSQKTRWFSIVPYETNNQETFGALD 186
DB 156 LSNYPDFQARITGQEEGAYGWIITNYLLGKFSQKTRWFSIVPYETNNQETFGALD 215
QY 187 GASTQVTFVQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWOKLAKDIOVASN 246
DB 216 GASTQVTFVQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWOKLAKDIOVASN 275
QY 247 EILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIGNYQOCHQSILELNT 306
DB 276 EILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIGNYQOCHQSILELNT 335

QY 307 SYCPYSCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQEKVTEMMKFCAPWE 366
DB 336 SYCPYSCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQEKVTEMMKFCAPWE 395
QY 367 EIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWHEHIHFIKIQSDAGWTGLGYM 426
DB 396 EIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWHEHIHFIKIQSDAGWTGLGYM 455
QY 427 LNLNMIIPASQPLSTPLSHST 447
DB 456 LNLNMIIPASQPLSTPLSHST 476

RESULT 7

US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 98.7%; Score 2354; DB 9; Length 463;
Best Local Similarity 99.1%; Pred. No. 1.3e-207;
Matches 441; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 TQLTSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPGI 62
DB 19 TQLTSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVECRVKGPGI 78
QY 63 SKFQVQKNEIGIVLTDGWERAREVIPSQHOETPVYLGATAGMRLRMSEELADRLVDV 122
DB 79 SKFQVQKNEIGIVLTDGWERAREVIPSQHOETPVYLGATAGMRLRMSEELADRLVDV 138
QY 123 VERSLSNYPDFQARITGQEEGAYGWIITNYLLGKFSQKTRWFSIVPYETNNQETFGA 182
DB 139 VERSLSNYPDFQARITGQEEGAYGWIITNYLLGKFSQKTRWFSIVPYETNNQETFGA 198
QY 183 LDLGASTQVTFVQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWOKLAKDIO 242
DB 199 LDLGASTQVTFVQNOTIESPDNALQFRLYKGDYNYVTHSFLCYGKDQALWOKLAKDIO 258
QY 243 VASNEILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIGNYQOCHQSILE 302
DB 259 VASNEILRDCPHGKYKVVNSDLYKTPCTKRPEMTLPFOQFEIOIGNYQOCHQSILE 318
QY 303 LFNSTCYCPSQCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQEKVTEMMKFCAP 362
DB 319 LFNSTCYCPSQCAFNGIFLPPLOQDGFAGFAFYVPMKFLNLTSEKVSQEKVTEMMKFCAP 378

QY 363 QWEEIKTSYAGVKGKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWT 422
DB 379 QWEEIKTSYAGVKGKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWT 438
QY 423 LCVMLNLTNMIPAEQPLSTPLSHST 447
DB 439 LCVMLNLTNMIPAEQPLSTPLSHST 463

RESULT 8
US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 98.7%; Score 2353; DB 9; Length 464;
Best Local Similarity 99.8%; Pred. No. 1.6e-207;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSTQNKALPENVKYIGVLDAGSSHTSLYIKVPAEKENDTGVVHVEECRVKGPISKPV 66
DB 24 SATQNKALPENVKYIGVLDAGSSHTSLYIKVPAEKENDTGVVHVEECRVKGPISKPV 83
QY 67 QKVNIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 126
DB 84 QKVNIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 143
QY 127 LSNYPDFOGARIITQOEGAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 186
DB 144 LSNYPDFOGARIITQOEGAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLG 203
QY 187 GASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASN 246
DB 204 GASTQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASN 263
QY 247 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPPQOPEIQIGNYQQCHQSILELFTNT 306
DB 264 EILRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPPQOPEIQIGNYQQCHQSILELFTNT 323
QY 307 SYCPYSQCAFNGIFLPPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMWE 366
DB 324 SYCPYSQCAFNGIFLPPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMWE 383
QY 367 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTIGYMLN 426
DB 384 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTIGYMLN 443

QY 427 LNLTMIPAEQPLSTPLSHST 447
DB 444 LNLTMIPAEQPLSTPLSHST 464

RESULT 9
US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 98.4%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 4.2e-207;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TQNKALPENVKYIGVLDAGSSHTSLYIKVPAEKENDTGVVHVEECRVKGPISKPVOK 68
DB 1 TQNKALPENVKYIGVLDAGSSHTSLYIKVPAEKENDTGVVHVEECRVKGPISKPVOK 60
QY 69 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 128
DB 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 120
QY 129 NYPDFOGARIITQOEGAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLGA 188
DB 121 NYPDFOGARIITQOEGAGYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDGLGA 180
QY 189 STQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNEI 248
DB 181 STQVTFVPQNTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNEI 240
QY 249 LRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPPQOPEIQIGNYQQCHQSILELFTNTSY 308
DB 241 LRDPCHFPGYKKVNVSDLYKTPCTKRFEMTLPPQOPEIQIGNYQQCHQSILELFTNTSY 300
QY 309 CPYSQCAFNGIFLPPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMWEI 368
DB 301 CPYSQCAFNGIFLPPQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPMWEI 360
QY 369 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTIGYMLN 428
DB 361 KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFGKIQSDAGWTIGYMLN 420
QY 429 LTNMIPAEQPLSTPLSHST 447
DB 421 LTNMIPAEQPLSTPLSHST 439

RESULT 10
US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265

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; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-092-063-38

Query Match
Best Local Similarity 98.4%; Score 2348; DB 13; Length 502;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFPVK 68
DB 38 TONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFPVK 97

QY 69 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 128
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 157

QY 129 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 188
DB 158 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 217

QY 189 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 248
DB 218 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 277

QY 249 LRDPCHPHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGICNYQOCHQSILELFTSY 308
DB 278 LRDPCHPHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGICNYQOCHQSILELFTSY 337

QY 309 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 368
DB 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397

QY 369 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 428
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 457

QY 429 LTNNIPAEQPLSTPLSHST 447
DB 458 LTNNIPAEQPLSTPLSHST 476

RESULT 11
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2079-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-835-147-2

Query Match
Best Local Similarity 98.4%; Score 2348; DB 9; Length 510;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 38 TONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFPVK 97

QY 69 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 128
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 157

QY 129 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 188
DB 158 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 217

QY 189 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 248
DB 218 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 277

QY 249 LRDPCHPHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGICNYQOCHQSILELFTSY 308
DB 278 LRDPCHPHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGICNYQOCHQSILELFTSY 337

QY 309 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 368
DB 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397

QY 369 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 428
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 457

QY 429 LTNNIPAEQPLSTPLSHST 447
DB 458 LTNNIPAEQPLSTPLSHST 476

RESULT 12
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
; US-09-374-586-1

Query Match
Best Local Similarity 98.4%; Score 2348; DB 9; Length 510;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-092-063-38

Query Match
Best Local Similarity 98.4%; Score 2348; DB 13; Length 502;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TONKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFPVK 68
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QY 69 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 128
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERSL 157

QY 129 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 188
DB 158 NYPDFOGARIITQOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 217

QY 189 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 248
DB 218 STQVTFVQNOTIESPDNALQFLRYGKDYNYVTHSFLCYGKQDQALWQKADIQVASNEI 277

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DB 278 LRDPCHPHGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGICNYQOCHQSILELFTSY 337

QY 309 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 368
DB 338 CPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWEEI 397

QY 369 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 428
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLLQGVHFTADSWEHIFIGIKQSDAGWTLYGMLN 457

QY 429 LTNNIPAEQPLSTPLSHST 447
DB 458 LTNNIPAEQPLSTPLSHST 476

RESULT 11
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2079-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
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Qy	189	S	T	Q	V	T	F	P	O	N	G	T	I	E	S	P	D	N	A	L	O	F	R	L	G	K	D	N	Y	T	H	S	F	L	C	V	G	K	D	O	A	L	W	O	K	I	D	I	O	V	A	S	N	E	I	248			
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RESULT 13
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No: US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-781-796B-1

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; Sequence 30, Application US/10646308			
; Publication No. US20040136992A1			
; GENERAL INFORMATION:			
; APPLICANT: BURTON, Paul B. J.			
; APPLICANT: DEISHER, Theresa A.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE			
; FILE REFERENCE: 3432-B			
; CURRENT APPLICATION NUMBER: US/10/646,308			
; CURRENT FILING DATE: 2003-08-21			
; PRIOR APPLICATION NUMBER: --to be assigned--			
; PRIOR FILING DATE: 2003-08-12			
; PRIOR APPLICATION NUMBER: 60/406,418			
; PRIOR FILING DATE: 2002-08-28			
; NUMBER OF SEQ ID NOS: 36			
; SOFTWARE: Patent in version 3.2			
; SEQ ID NO 30			
; LENGTH: 510			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
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Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	158	NYPDFQGARIITQEGEGAYGWIITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA	217
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QY	369	KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHITPCTKLGQSDAGWTLGYMLN	428
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RESULT 15
US-09-835-147-4
; Sequence 4, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: VARIANT
; LOCATION: (39)
; OTHER INFORMATION: Any amino acid, preferably Cys or Ser
US-09-835-147-4

	Query Match	96.2%	Score 2294;	DB 9;	Length 476;
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Db	280	DPCFPHGXYKKVNVSDLYKTP	CTKRFEMTLFPQOF	EIQGIGNYQQCHSILE	339

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:32 ; Search time 19.0492 Seconds
(without alignments)
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Title: US-09-835-147a-29_COPY_27_473

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2348	98.4	502	4	US-09-370-625A-38
3	2348	98.4	510	3	US-08-930-921-1
4	2348	98.4	510	3	US-09-781-796C-1
5	910.5	38.2	529	3	US-09-240-639-4
6	910.5	38.2	529	4	US-09-908-510A-4
7	910.5	38.2	529	4	US-09-905-744B-4
8	910.5	38.2	529	4	US-10-107-660-4
9	910.5	38.2	529	4	US-10-107-576-4
10	910.5	38.2	529	4	US-09-905-732B-4
11	910.5	38.2	529	4	US-09-923-304-4
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34	442.5	18.6	153	4	US-10-107-660-15	Sequence 15, Appl
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43	417.5	17.5	150	4	US-10-107-660-16	Sequence 16, Appl
44	417.5	17.5	150	4	US-10-107-576-16	Sequence 16, Appl
45	417.5	17.5	150	4	US-09-905-732B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-557-800C-55
; Sequence 55, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-55

Query Match 98.4%; Score 2348; DB 4; Length 502;

Best Local Similarity 100.0%; Pred. No. 3.5e-243;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKPGISKPVQK 68

Db 38 TONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGWHQVEECRVKPGISKPVQK 97

Qy 69 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVVERSL 128

Db 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRLVDVVERSL 157

Qy 129 NYPDFQARIITQBEQAYGWIITNYLLGKFSOKTRWFSIVPYETNNQETFGALDLGGA 188

QY	309	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	368
Db	338	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	397
QY	369	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	428
Db	398	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	457
QY	429	LTNMIPAEQPLSTPLSHST	447
Db	458	LTNMIPAEQPLSTPLSHST	476
RESULT 3			
US-08-930-921-1			
; Sequence 1, Application US/08930921B			
; Patent No. 6287837			
; GENERAL INFORMATION:			
; APPLICANT: BEAUDOIN, Adrien R.			
; APPLICANT: SEVIGNY, Jean			
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION			
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT			
; TITLE OF INVENTION: TECHNOLOGY			
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN			
; CURRENT FILING DATE: 1998-01-02			
; EARLIER APPLICATION NUMBER: PCT/CA96/00223			
; EARLIER FILING DATE: 1996-04-10			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 510			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: Description of Unknown Organism: unknown			
; US-08-930-921-1			
Query Match 98.4%; Score 2348; DB 3; Length 510;			
Best Local Similarity 100.0%; Pred. No. 3.6e-243;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	9	TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKGPISKFVQK	68
Db	38	TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKGPISKFVQK	97
QY	69	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	128
Db	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	157
QY	129	NYPDFQGARIIITQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA	188
Db	158	NYPDFQGARIIITQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA	217
QY	189	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	248
Db	218	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	277
QY	249	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	308
Db	278	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	337
QY	309	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	368
Db	338	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	397
QY	369	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	428
Db	398	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	457
QY	429	LTNMIPAEQPLSTPLSHST	447
Db	458	LTNMIPAEQPLSTPLSHST	476

Db	158	NYPDFQGARIIITQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA	217
QY	189	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	248
Db	218	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	277
QY	249	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	308
Db	278	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	337
QY	309	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	368
Db	338	CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMKKKFCQAPWEEI	397
QY	369	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	428
Db	398	KTSYAGVKEKYLSEYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSDAGWTGMYLN	457
QY	429	LTNMIPAEQPLSTPLSHST	447
Db	458	LTNMIPAEQPLSTPLSHST	476
RESULT 2			
US-09-370-625A-38			
; Sequence 38, Application US/09370625A			
; Patent No. 6600032			
; GENERAL INFORMATION:			
; APPLICANT: Ford, John			
; APPLICANT: Mulero, Julio			
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES			
; FILE REFERENCE: 28110735908			
; CURRENT APPLICATION NUMBER: US/09/370,625A			
; CURRENT FILING DATE: 1999-08-09			
; PRIOR APPLICATION NUMBER: PCT/US99/16180			
; PRIOR FILING DATE: 1999-07-16			
; PRIOR APPLICATION NUMBER: 09/350,836			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR APPLICATION NUMBER: 09/273,447			
; PRIOR FILING DATE: 1999-03-19			
; NUMBER OF SEQ ID NOS: 39			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 38			
; LENGTH: 502			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-09-370-625A-38			
Query Match 98.4%; Score 2348; DB 4; Length 502;			
Best Local Similarity 100.0%; Pred. No. 3.5e-243;			
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	9	TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKGPISKFVQK	68
Db	38	TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVMHVEECRVKGPISKFVQK	97
QY	69	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	128
Db	98	VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL	157
QY	129	NYPDFQGARIIITQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA	188
Db	158	NYPDFQGARIIITQEBGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALDLGGA	217
QY	189	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	248
Db	218	STQVTFVQNTIESPDNALQFRLYKDYNNVTHSFLCYGKDQALWOKLAKDIQVASNEI	277
QY	249	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	308
Db	278	LRDPCFHPGKVVVNSDLYKTPCTKRFEMTLPPQOFEIQIGNYQQCHOSILELFNTSY	337

RESULT 4
US-09-781-796C-1
; Sequence 1, Application US/09781796C
; Patent No. 680284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEROF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796C-1

Query Match 98.4%; Score 2348; DB 4; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.6e-243;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TONKALPENVKYGIIVLDAGSSHTSLYYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQK 68
Db 38 TONKALPENVKYGIIVLDAGSSHTSLYYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQK 97
Qy 69 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLMESBELADRLDVVVERSL 128
Db 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLMESBELADRLDVVVERSL 157
Qy 129 NYPDFQAGIITGOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 188
Db 158 NYPDFQAGIITGOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGA 217
Qy 189 STQVTFVQNTIESPDNALQFRLYGKDYNYTHSFQCYGKQDQALWQKLAKDIOVASNEI 248
Db 218 STQVTFVQNTIESPDNALQFRLYGKDYNYTHSFQCYGKQDQALWQKLAKDIOVASNEI 277
Qy 249 LRDPCHFPGYKVVVNSDLYKTPCT--KRPETMLPFOQFEIQGNYQOCHQSILELFTSY 308
Db 278 LRDPCHFPGYKVVVNSDLYKTPCTKRPETMLPFOQFEIQGNYQOCHQSILELFTSY 337
Qy 309 CPYSQAFNGIFLPLPQDGFCAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEI 368
Db 338 CPYSQAFNGIFLPLPQDGFCAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEI 397
Qy 369 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLGYMLN 428
Db 398 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLGYMLN 457
Qy 429 LTNMIPASQPLSTPLSHST 447
Db 458 LTNMIPASQPLSTPLSHST 476

RESULT 5
US-09-240-639-4
; Sequence 4, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-4

APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 529
TYPE: PRT
ORGANISM: Homo sapiens
US-09-240-639-4

Query Match 38.2%; Score 910.5; DB 3; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 10 QNKALPENVKYGIIVLDAGSSHTSLYYIKWPAEKENDTGVVHVQVEECRVKPGISKVFQKV 69
Db 47 KQEVLPPLKLYGIIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKCSVKSGSISSYGNP 106
Qy 70 NEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLMESBELADRLDVVVERSLN 129
Db 107 QDVPRAFECQKVKGVQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYPKS 166
Qy 130 YPDFQAGIITGOEGAYGMITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGAS 189
Db 167 QPDFRGAQLISGQEGYGVWITANYLMGNFLEKNLHMWV--HPHGVETTTGALDLGAS 224
Qy 190 TQVTFVQNTIESPDNALQFRLYGKDYNYTHSFQCYGKQDQALWQKLAKDIOVA-SNEI 248
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYLYTHSFQCYGRNAEKKFLAMLQNSPTKVH 284
Qy 249 LRDPCHFPGYKVVVNSDLYKTPCT--KRPETMLPFOQFEIQGNYQOCHQSILELFT 306
Db 285 LTNPCYPRDYSISTMTGMHGFVDSLCTVQRPESYNPNVDITFEGTDPCLCKEKVASI 344
Qy 307 SYC--PYSCAFNGIFLPLPQDGFCAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWP 365
Db 345 KACHDQCTCFDGVYQKIKGPFVAFAGFYTASALNL--SGSFSLDTFNSSTWFCSQNW 403
Qy 366 BEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWEHIFIGIKQSDAGWTLGY 425
Db 404 SOLPLLLPKPDEVVARSYCFSANIYIHLFVNGYKFTETWPOIHFEKEVGNSSIAWSLGY 463
Qy 426 MLNLTNMPASQPL 439
Db 464 MSLTINQIPAESPL 477

RESULT 6
US-09-908-510A-4
; Sequence 4, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-510A-4

[illegible]

QY 366 EEIKTSYAGVKEKYLSEYCFSGTYSILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 425
DB 404 SOLPLLLPKPDEVVARSYCFSANYYIHLFVNGYKFTETWPIQIHFKEVGNSSIAWSLGY 463
QY 426 MLNLTMIPAEQPL 439
DB 464 MSLTNQIPAESPL 477

RESULT 9

US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4

Query Match 38.2%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 10 QNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGCVHVQVEECRVKGPISKFVQKV 69
DB 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVWSQTFKCSYKSGSISSYGNP 106
QY 70 NEIGYILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 129
DB 107 QDVPAPEECQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS 166
QY 130 YPPDFQAGRIITQGEAGYGHITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 189
DB 167 QPEDFRGAQIISGQEEGYGMITANYLNGNLFLEKNLHMWV--HPHGVTETTGALDLGGAS 224
QY 190 TQVTFVPOQNTIESPDNALQFRLYKGVNVTYHSGFLCYGKDQALWQKLAKDIOVA-SNEI 248
DB 225 TQISFVAGEKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284
QY 249 LRDCPFHFGYKVVNVDLYKTPCT--KRPEMTLPFOQFEIQGIGNYQOCHQSILELNT 306
DB 285 LTNPCTPRDYSISFTMGHVFDLSCTVDQRPESYNPNVDVITTEGTGDPSLCKEKVASIFDF 344
QY 307 SYC-PYSQCAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCQAPW 365
DB 345 KACHDOETCSFDGYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
QY 366 EEIKTSYAGVKEKYLSEYCFSGTYSILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 425
DB 404 SOLPLLLPKPDEVVARSYCFSANYYIHLFVNGYKFTETWPIQIHFKEVGNSSIAWSLGY 463
QY 426 MLNLTMIPAEQPL 439
DB 464 MSLTNQIPAESPL 477

RESULT 10

US-09-905-732B-4
; Sequence 4, Application US/09905732B
; Patent No. 6787328

; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-732B-4

Query Match 38.2%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

QY 10 QNKALPENVKYGIIVLDAGSSHTSLYIYKPAEKENDTGCVHVQVEECRVKGPISKFVQKV 69
DB 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVWSQTFKCSYKSGSISSYGNP 106
QY 70 NEIGYILTCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 129
DB 107 QDVPAPEECQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETAANEVLESIQSYFKS 166
QY 130 YPPDFQAGRIITQGEAGYGHITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGAS 189
DB 167 QPEDFRGAQIISGQEEGYGMITANYLNGNLFLEKNLHMWV--HPHGVTETTGALDLGGAS 224
QY 190 TQVTFVPOQNTIESPDNALQFRLYKGVNVTYHSGFLCYGKDQALWQKLAKDIOVA-SNEI 248
DB 225 TQISFVAGEKMDLNTSDIMQVSLYGVYVTLTHSFQCYGRNEAEKKFLAMLLQNSPTKNH 284
QY 249 LRDCPFHFGYKVVNVDLYKTPCT--KRPEMTLPFOQFEIQGIGNYQOCHQSILELNT 306
DB 285 LTNPCTPRDYSISFTMGHVFDLSCTVDQRPESYNPNVDVITTEGTGDPSLCKEKVASIFDF 344
QY 307 SYC-PYSQCAFNGIFLPLQDGFAGFSAFYFVMKFLNLTSEKVSQEKVTEMMKFCQAPW 365
DB 345 KACHDOETCSFDGYQPKIKGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNFCSQNW 403
QY 366 EEIKTSYAGVKEKYLSEYCFSGTYSILSLLOQYHFTADSWEHIFIGIKQSDAGWTGLY 425
DB 404 SOLPLLLPKPDEVVARSYCFSANYYIHLFVNGYKFTETWPIQIHFKEVGNSSIAWSLGY 463
QY 426 MLNLTMIPAEQPL 439
DB 464 MSLTNQIPAESPL 477

RESULT 11

US-09-923-304-4
; Sequence 4, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UTSC:658US
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-4

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Query Match      38.2%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 10 QNKALPENVKYGVILVDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKGPISKFQKV 69
Db 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVQTFKCSVKSGSISSYGNP 106

Qy 70 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 129
Db 107 QDVPRAFECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166

Qy 130 YPFDFOGARIITGOEAGYGNWITINYLKGFQOKTRWFSIVPYETNNQETFGALDLGGAS 189
Db 167 QPFDPRGAQIISGOEAGYGNWITANVLMGNFLEKNLHMWV--HPHGVEITGALDLGGAS 224

Qy 190 TVQTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALMOKLAKDQVA--SNEI 248
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284

Qy 249 LRDPCHFPGYKVVNVDLYKTPCT--KRFEMTLPFQOFEIQGIGNYQOCHQSILELNT 306
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGPDLCKEKVASIFDF 344

Qy 307 SYC-PYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 365
Db 345 KACHDETCSFDGVQPKIGPVAFAGFYTASALNL--SGSFSLDTFNSSTWNFCSQNW 403

Qy 366 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOGHFTADSWEHIFGKIQGSDAGWTIGY 425
Db 404 SOLPLLLPKFDEVYARSYCFSANIYIHLFVNGYKFTTEETWQIHFPEKEVGNSSIAWSLGY 463

Qy 426 MLNLTNMPAEOPL 439
Db 464 MSLTNTQIPAESPL 477

RESULT 12
US-09-949-016-6049
; Sequence 6049, Application US/09949016
; Patent No. 6812839
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6049
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6049

Query Match      38.2%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 10 QNKALPENVKYGVILVDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKGPISKFQKV 69
Db 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVQTFKCSVKSGSISSYGNP 106

Qy 70 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 129
Db 107 QDVPRAFECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166

Qy 130 YPFDFOGARIITGOEAGYGNWITINYLKGFQOKTRWFSIVPYETNNQETFGALDLGGAS 189
Db 167 QPFDPRGAQIISGOEAGYGNWITANVLMGNFLEKNLHMWV--HPHGVEITGALDLGGAS 224

Qy 190 TVQTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALMOKLAKDQVA--SNEI 248
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284

Qy 249 LRDPCHFPGYKVVNVDLYKTPCT--KRFEMTLPFQOFEIQGIGNYQOCHQSILELNT 306
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGPDLCKEKVASIFDF 344

Qy 307 SYC-PYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 365
Db 345 KACHDETCSFDGVQPKIGPVAFAGFYTASALNL--SGSFSLDTFNSSTWNFCSQNW 403

Qy 366 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOGHFTADSWEHIFGKIQGSDAGWTIGY 425
Db 404 SOLPLLLPKFDEVYARSYCFSANIYIHLFVNGYKFTTEETWQIHFPEKEVGNSSIAWSLGY 463

Qy 426 MLNLTNMPAEOPL 439
Db 464 MSLTNTQIPAESPL 477
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Qy 130 YPFDFOGARIITGOEAGYGNWITINYLKGFQOKTRWFSIVPYETNNQETFGALDLGGAS 189
Db 167 QPFDPRGAQIISGOEAGYGNWITANVLMGNFLEKNLHMWV--HPHGVEITGALDLGGAS 224

Qy 190 TVQTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALMOKLAKDQVA--SNEI 248
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284

Qy 249 LRDPCHFPGYKVVNVDLYKTPCT--KRFEMTLPFQOFEIQGIGNYQOCHQSILELNT 306
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGPDLCKEKVASIFDF 344

Qy 307 SYC-PYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 365
Db 345 KACHDETCSFDGVQPKIGPVAFAGFYTASALNL--SGSFSLDTFNSSTWNFCSQNW 403

Qy 366 EEIKTSYAGVKEKYLSEYCFSGTYILSLLOGHFTADSWEHIFGKIQGSDAGWTIGY 425
Db 404 SOLPLLLPKFDEVYARSYCFSANIYIHLFVNGYKFTTEETWQIHFPEKEVGNSSIAWSLGY 463

Qy 426 MLNLTNMPAEOPL 439
Db 464 MSLTNTQIPAESPL 477

RESULT 13
US-09-905-743B-4
; Sequence 4, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-905-743B-4

Query Match      38.2%; Score 910.5; DB 4; Length 529;
Best Local Similarity 41.5%; Pred. No. 1.3e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 10 QNKALPENVKYGVILVDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKGPISKFQKV 69
Db 47 KQEVLPGLKYGIVLDAGSSRTTVYVQWPAEKENNTGVVQTFKCSVKSGSISSYGNP 106

Qy 70 NEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSLN 129
Db 107 QDVPRAFECMQKVGQVPSHLHGSTPIHLGATAGMRLLRQNETAANEVLESIQSYFKS 166

Qy 130 YPFDFOGARIITGOEAGYGNWITINYLKGFQOKTRWFSIVPYETNNQETFGALDLGGAS 189
Db 167 QPFDPRGAQIISGOEAGYGNWITANVLMGNFLEKNLHMWV--HPHGVEITGALDLGGAS 224

Qy 190 TVQTFVFPQNTIESPDNALQFRLYKDYNNVYTHSFCLYCKDQALMOKLAKDQVA--SNEI 248
Db 225 TQISFVAGEKMDLNTSDIMQVSLYGVVYTLTHSFQCYGRNEAEKKFLAMLQNSPTKNH 284

Qy 249 LRDPCHFPGYKVVNVDLYKTPCT--KRFEMTLPFQOFEIQGIGNYQOCHQSILELNT 306
Db 285 LTNPCTPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDITFEGTGPDLCKEKVASIFDF 344

Qy 307 SYC-PYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPW 365
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Db 345 KACHDQETCSFDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNPFCSONW 403
Qy 366 BEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWHEHIFGKIQSDAGWTGLGY 425
Db 404 SOLPLLLPKFDEYVARSYCFSANYYIHLFVNGYKFTETWQIHFKEVGNSSIAWSLGY 463
Qy 426 MLNLNMIPIAEQPL 439
Db 464 MSLTNQIPAESPL 477

RESULT 14
US-09-949-016-11328
; Sequence 11328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11328
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11328

Query Match 38.2%; Score 910.5; DB 4; Length 556;
Best Local Similarity 41.5%; Pred. No. 1.4e-88;
Matches 180; Conservative 79; Mismatches 168; Indels 7; Gaps 5;

Qy 10 QNKALPENVKYIGVLDAGSSHTSLYIYKPAEKENDTGVVHVQVEECRVKGFSGKVFQV 69
Db 74 KQELPPLKLYIGVLDAGSSRTVYVYQWPAEKENNTGVSTFKCVKSGSGISYGNP 133
Qy 70 NEIGYILDCMERAREVTPRSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN 129
Db 134 QDVPRAFEECKQVKGVQFPHLHGSTPIHLGATAGMRLRLQNETAANEVLIESIQSYPKS 193
Qy 130 YPFDFOGARIITGOEGAYGWITINLLGKFSOKTRWFSIVPYETNNQETFGALDLGGAS 189
Db 194 QPFDFRGAQLISGQEGYGYGITANYLMGNFLEKLMWV--HPHGVETTTGALDLGGAS 251
Qy 190 TQVTFVQNTIESPDNALQFLRYGKYNVYTHSFLCYGKQDALMOKLAKDIQVA-SNEI 248
Db 252 TQISPVAGEKMDLNTSDIMQVSLYGVVYVLYTHSFCYGRNEAEKKFLAMLLQNSPTKNH 311
Qy 249 LRDPCHFGYKVVNVDLYKTPCT--KRPFMTLPFQOFGIYQOCHQSIIELENT 306
Db 312 LTNPCYPRDYSISFTMGHVFDSLCVTVDQRPESYNPDVITTEGTDGDSLCKEKVASIEDF 371
Qy 307 SYC-PYSOCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTEMMKFCAPW 365
Db 372 KACHDQETCSFDGVYQPKIGPFVAFAGFYTASALNL-SGSFSLDTFNSSTWNPFCSONW 430
Qy 366 BEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWHEHIFGKIQSDAGWTGLGY 425
Db 431 SOLPLLLPKFDEYVARSYCFSANYYIHLFVNGYKFTETWQIHFKEVGNSSIAWSLGY 490
Qy 426 MLNLNMIPIAEQPL 439
Db 491 MSLTNQIPAESPL 504
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RESULT 15
US-09-949-016-11559
; Sequence 11559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11559

Query Match 36.3%; Score 865; DB 4; Length 479;
Best Local Similarity 41.3%; Pred. No. 8.3e-84;
Matches 183; Conservative 69; Mismatches 137; Indels 54; Gaps 9;

Qy 9 TQNKALPENVKYIGVLDAGSSHTSLYIYKPAEKENDTGVVHVQVEECRVKGFSGKVFQV 68
Db 36 TRDVRREPALKYIGVLDAGSSHTSMFIYKWPADKENDTGVVGHSSCDVPGGSISSYADN 95
Qy 69 VNEIGYILDCMERAREVTPRSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSLN 128
Db 96 PSGASQSLVGLCEALQDVPKERRHAGTPLYLGATAGMRLNLNTPASTSVLMAYTHLT 155
Qy 129 NYPDFOGARIITGOEGAYGWITINLLG--KFSQKTRWFSIVPYETNNQETFGALDL 185
Db 156 QYPDFRGAQLISGQEGYGYGITANYLMGNFLEKLMWV--RPRKGTGLGAMD 209
Qy 186 GGASTQVTFVQNTIESPDNA--LQFLRYGKYNVYTHSFLCYGKQDALMOKLAKDIQV 243
Db 210 GGASTQITF---ETTSPAEDRASEVQLHLYGQHYRVYTHSFLCYGRDQVLRLLASALQT 266
Qy 244 ASNEILRDPCHFGYKVVNVDLYKTPCTKRFEMTLPFQOF-----EIOGIGNYQOCH 297
Db 267 HGPH----PCWPRGFSTQVLLGDVYQSPCT----MAQRPNQFNESARVSLSGSSDPHL 318
Qy 298 QSILELNTSYCPYSQCAFNGIFLPLQDGFAGSAFYVMKFL--NLTSEKVSQEKVTE 355
Db 319 DLVSGLSFSSCPSPSCFNGVFPQPVAGNFVAFSAFYVDFLRTSMGLPVTALQQL 378
Qy 356 MMKIFCAQPMWEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWHEHIFGKI 415
Db 379 AAVNVNQTWQA-----QLLSRGYGDFERAFGCVIFQKAA 414
Qy 416 GSDAGWTGLGYMLNLTNMIPIAEQ 438
Db 415 DTAVGWALGYMLNLTNLIPIADPP 437

Search completed: March 7, 2005, 13:28:00
Job time : 20.0492 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:59:07 ; Search time 13.6708 Seconds
(without alignments)
3117.881 Million cell updates/sec

Title: US-09-835-147a-30_COPY_21_463
Perfect score: 2368
Sequence: 1 APTSTQNKALPENVKYIVL.....NLTNMIPAEQLSTPLSHST 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 791.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	99.2	510	2 I56242	Lymphoid cell, acti
2	505	21.3	483	2 D86276	hypothetical prote
3	469.5	19.8	405	2 E86276	hypothetical prote
4	453	19.1	630	2 S50463	hypothetical prote
5	416	17.6	572	2 T40856	probable nucleotid
6	406.5	17.2	516	2 G84442	probable nucleosid
7	402.5	17.0	485	2 T34147	hypothetical prote
8	394.5	16.7	508	2 C86276	7A19.33 protein -
9	386.5	16.3	557	2 T16696	hypothetical prote
10	381.5	16.1	556	2 T39109	probable guanosine
11	376	15.9	455	2 S48859	nucleoside triphos
12	334	14.1	454	2 J4616	aprase (EC 3.6.1.
13	332	14.0	1052	2 T04439	hypothetical prote
14	328.5	13.9	479	2 T23508	hypothetical prote
15	323.5	13.7	518	2 T40732	guanosine-diphosph
16	167	7.1	628	2 A55421	nucleoside-triphos
17	106	4.5	369	2 S77299	C4-dicarboxylase-b
18	101.5	4.3	716	2 T21516	hypothetical prote
19	100	4.2	307	2 T27332	hypothetical prote
20	99	4.2	1951	2 B43963	RNA viral polymera
21	98.5	4.2	590	2 A81411	autolysin, N-acety
22	98.5	4.2	797	2 D86247	hypothetical prote
23	98.5	4.2	989	2 B84532	hypothetical prote
24	98.5	4.2	1509	2 B89985	hypothetical prote
25	98	4.1	371	2 T05213	hypothetical prote
26	98	4.1	665	2 T18979	hypothetical prote
27	98	4.1	3848	2 T17414	Tipc protein - sli
28	97.5	4.1	392	2 A96738	hypothetical prote
29	97	4.1	494	2 T03774	probable histidine

RESULT 1

I56242
Lymphoid cell activation antigen - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56242

R/Maliszewski, C.R.; Dellespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.;
J. Immunol. 153, 3574-3583, 1994
A/Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural cha
A/Reference number: I56242; MUID:95015846; PMID:7930580
A/Accession: I56242
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-510 <RES>

A/Cross-references: UNIPROT:P49961; GB:S73813; NID:G75255; PIDN:AAB32152.1; PID:G765255
C/Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 99.2%; Score 2348; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.2e-182;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	5	TQNKALPENVKYIGVLDAGSSHTSLYIKYKPAEKENDTGVVHVQVEECRVKPGISKVQK	64
Db	38	TQNKALPENVKYIGVLDAGSSHTSLYIKYKPAEKENDTGVVHVQVEECRVKPGISKVQK	97
Qy	65	VNEIGIYLTDCMERAREVIRSRQHOETPVYLGATAGHRLRMESEELADRLDVVERSL	124
Db	98	VNEIGIYLTDCMERAREVIRSRQHOETPVYLGATAGHRLRMESEELADRLDVVERSL	157
Qy	125	NYPDFQGARITGOEERGAYGVITINLLGKFSOKTRWFSIVPYETNNQETFGALDLGGA	184
Db	158	NYPDFQGARITGOEERGAYGVITINLLGKFSOKTRWFSIVPYETNNQETFGALDLGGA	217
Qy	185	STQVTFVFPQNTIESPDNALQFLRYGKDYNNYTHSFCLCYGKQDALQWLAKDIQVASNEI	244
Db	218	STQVTFVFPQNTIESPDNALQFLRYGKDYNNYTHSFCLCYGKQDALQWLAKDIQVASNEI	277
Qy	245	LRDPCFHPGKVVNVSDLYKTPCTKPFEMTLPPQOFEIQIGIGNYQOCHQSILELFNTSY	304
Db	278	LRDPCFHPGKVVNVSDLYKTPCTKPFEMTLPPQOFEIQIGIGNYQOCHQSILELFNTSY	337
Qy	305	CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	364
Db	338	CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTENMKKFCQAPWEEI	397
Qy	365	KTSYAGVKEKYLSYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSGDAGWTLYGMLN	424
Db	398	KTSYAGVKEKYLSYCFSGTGYLSLLQGYHFTADSWEHIFIGIKIQSGDAGWTLYGMLN	457
Qy	425	LTNMPAEQPLSTPLSHST	443
Db	458	LTNMPAEQPLSTPLSHST	476

probable fibrin
myosin I beta - bu
(R)-2-hydroxygluta
hypothetical prote
sarine/threonine k
spore germination
Mg2+ transporter h
probable permease
hypothetical prote
hypothetical prote
lactacin 481/lacto
hypothetical 51.7
hypothetical prote
probable dnak prot
probable dnak-type
probable fad-depen

QY 13 NVKGVILVLDAGSHTSLYIKWP-----REKENDTGV-----VHQVECRVK-GRGI 58
 Db 7 NDRFGIVLDAGSSGRIRHVFVKQDTESLHATNQDSQSILOSVPHIHQEKDWTFLKNFL 66
 QY 59 SKFVQKNE-IGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLD 117
 Db 67 SSFEKKPODAYKSHIKPLDFAKNIIPESHWSCEVFQIQTAGMRL-----PDQIQQSILD 123
 QY 118 VVERSLSNYPDF-----QGARITGOEGAGYGMITINYLKGFSPQKTRWFSIVPYETN 171
 Db 124 GLCQGL-KHPAEFLVEDCSAQIQVIDGETEGYGLWGLNLYLVGHENDYNP-----EVS 175
 QY 172 NOETFGALDGGASTQVTFVQNO-----TIESPDNALQRLYKDYNYVTH 218
 Db 176 DHFTFGFMDMGAGTQIAFAPHDSGEIARHDDIATIFLRSVNGDLQ-----KWDVFS 229
 QY 219 SFLCYGKQALWOKLAKIOVA-----SNEILRDPCHFPGYKVVNVSDLYKT 266
 Db 230 TWLGFAGNARRYLQAQILNLPENTYENDDFSTRNLNDPCMPRG-----SSTDF--- 281
 QY 267 PCKRFEMLTPOQFEIOGIGNYQCHOSILE-LFNTSYCPYSQCAFNGIFLPLQGD- 324
 Db 282 ---EFKDTI---PHIAGSGNYEQTKSIYVPLLLKNMPCDDEPCLFNGVHAPRI--DFA 331
 QY 325 ---GAPSAFYVFMKFLNLTSEKVSQKTEMKMKFCAQWEEI-----KTSYAGVKEK 374
 Db 332 NDKTIGTSEYVITANDVPKAGE-YNFKDKSKLREFCNSNWTQILANSKGVNSIPEN 390
 QY 375 YLSVEYCRSTYLSLLQGY---HPTADSWEH---FIGIQSGDAGWTGLGYML 423
 Db 391 FLKQACFGNVLNLTGHEGDMPRIDVDA-ENVNDRPLFQSVKEVERELSWTLGRIL 447

RESULT 5
 T40856
 Probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40856
 R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: Z21952
 A:Accession: T40856
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <RAM>
 A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:
 A:Experimental source: strain 972h.; cosmid C11E10
 C:Genetics:
 A:Gene: SPDB:SPCC11E10.05c
 A:Map position: 3

Query Match 17.6%; Score 416; DB 2; Length 572;
 Best Local Similarity 27.3%; Pred. NO. 1.1e-25;
 Matches 131; Conservative 69; Mismatches 156; Indels 124; Gaps 19;
 QY 15 KYGIVLDAGSHTSLYIKWPAEKEN-----DTGVHGVHQBECRVKGPQISKFV 62
 Db 4 KYGIFIDAGSGSRLLIISWDYDTSLSLSDKVKLPLIETIGDGGKWSLKVQGISFPA 63
 QY 63 QKVNIG-IYITDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVER 121
 Db 64 NNPKHVGGKHLKELLDFAAHPKDVHETPVFLSATAGMRLGVDAQ---NKLISHACR 120
 QY 122 SL-SNYPDF---QGARITGOEGAGYGMITINYLKGFSPQKTRWFSIVPYETNQTFF 176
 Db 121 YIKKNYDFDIPNCNSIRIVIDKAGMGYGLATNYLLKTLTEK-----DTSV 168
 QY 177 GALLDGGASTQVTF-VPONQTIESP-----NALQRLYKDYNYVTHSFLCYGK 225
 Db 169 GFLDMGGASVQIAFLPFSQKYNKXDSISTVHIGLQNGQQL-----EYPLFTWLGFGA 223
 QY 226 DOALWOKLAKIOVASNEI---LRDPCFHPGYKVVNVSDLYKTPCTKRFEMTLFPOQFE 282

Db 224 NEAYRYLGLLIESENGKVGNTLSDPCSLRG-----RTYDIDGIE 263
 QY 283 IQGIGNYQCHOSILELFTNSY-CPYSQCAFNGIFLPLQGDGFAFSAFYVFMKFLNLT 341
 Db 264 FAGTGDILKQCLKLTYNLLNKDKPCMDPCPDGSIIPV--DF-ANTEFVGVSEFWYTN 320
 QY 342 EKVSQ-----EKVTEMKMKFCAQWEEI-----KTSYAGVKEKYLSEYCFSGTY 385
 Db 321 DVFMGGSYHFPNFKKVD-----YCGTEWETMLSRNLKELTPTDENKLEKLCFKASW 376
 QY 386 ILSLLLOG-----YHFTADSWEHIFIGIKQSGDAGWTGLGYML 423
 Db 377 ALNVLHGFDPVKNTSSNAKOGSLVIPAYHSPFTSLE-----KIERTVSWTLGQVL 430

RESULT 6
 G84442
 Probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84442
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84442
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: UNIPROT:O80612; GB:AB002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g02970
 A:Map position: 2
 C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.2%; Score 406.5; DB 2; Length 516;
 Best Local Similarity 27.5%; Pred. No. 5.5e-25;
 Matches 117; Conservative 68; Mismatches 187; Indels 53; Gaps 13;
 QY 13 NVKGVILVLDAGSHTSLYIKWPAEKENDTGVHQBECRVK-GPGISKFVQKVEIGIY 71
 Db 65 SLRYSVVIDGGSTGTRIHVFGYRIESGKPVFEFGANVASLKLHPLGSAPADDDPGASVS 124
 QY 72 LTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL--SNYPFD 129
 Db 125 LTELVEFAKGRVPGKMMIETEVRLMATAGMRLLELPVQE---KILGVARRVLKSSGFLFR 181
 QY 130 FOGARIITGOEGAGYGMITINYLKGFSPQKTRWFSIVPYETNNOETFGALDGGASTQVT 189
 Db 182 DEWASVLSGSDGEGYAVVAVNFAFGSLG-----GDPLKTTGIVELGASAQVT 229
 QY 190 FVPONQTIESPDNALQRLYKDYNYVTHSFLCYGKQQA---LW-QKLAKD-----IQVAS 241
 Db 230 FVSSEPW--PPEFRTISFGNVTYNSHGFHPGQNAADKLWGLSLLSRDHNSAVEPTR 287
 QY 242 NEILRDPCHFPGYKVVNVSDLYKTPCTKRFEMTLFPOQFEIOGIGNYQCHOSILELFN 301
 Db 288 EKIFTDPCAPKGYNLNDANTQKLSLLAESRLSDSF-----QAGGNYSQCRSAALTILQ 342
 QY 302 TSYCPYSQCAFNGIFLPLQGDGFAFSAFYVFMKFLNLTSEKVSQKTEMKMKFCAQW 361
 Db 343 DG-----NGRILLIAG----FSFLPGL-----GEKAWLSNMSIAGERFCGEDW 383
 QY 362 EEIKTSYAGVKEKYLSEYCFSGTYLSLLQGYHFTADSWEHIFIGIKQSGDAGWTGLY 421
 Db 384 SKLRVKDPSLHEEDLLRYCFSSAYIVSLLHDTLGLPLDD-ERIGYANQAGDIPLDWALGA 442
 QY 422 MLNLT 426
 Db 443 FIQOT 447

Qy	190	FVPO-----NOTIESPDNALQRLYKDYNNVYTHSFCLGVGKQOALWOKLAKDIOVASNEIL	245
		::: : : : : : : : : : : : :	
Db	294	FEPRFASDGESLVDGDHKYILDYNGEQVELYQHSGLGYGLKEA--RKLHKFVLNNAEAL	351
		: : : : : : : : : : : : : :	
Qy	246	RD-----PCFHPGYKKVNVSDLYKTPCTKRFEM-----TLPFQOPEIQGIG	287
		::: : : : : : : : : : : : :	
Db	352	KESLELGDSTSIHPCUH-----LNASLTHPDSKSEASEVVFVGPSLAHLSLOCGRGA	405
		: : : : : : : : : : : : : :	
Qy	288	NYOQCHOSIILEFNYSYCPYSQCAFNGIFLPPLODGF-----AFSAFYFVKMFLNLTS	342
		: : : : : : : : : : : : : :	
Db	406	E-----KALYKDKNCVPRPCSFNGVHQPKFTETFDSPYILYSYFYDMISLGMPS-	456
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Qy	343	KVSOEKVTMMKFCAP--WEBEIKTSYAGVKE-KYLSEYCFSGTYIISLLQGHFTAD	399
		: : : : : : : : : : : : : :	
Db	457	TFTIEDMKYLANSVCSGPTYMQDAFSLTDALKELKEPWCWCLDLYNMYISLISLVGYEIPNN	516
		: : : : : : : : : : : : : :	
Qy	400	SWEHIHPGKIQSDAGWTILGYMLNL	425
		: : : : : : : : : : : :	
Db	517	--RQLHTAKKIDNKELGWCLGASLSM	540
		: : : : : : : : : : : :	
RESULT 11			
S48859			
nucleoside triphosphatase precursor, chromatin-associated - garden pea			
C;Species: Pisum sativum (garden pea)			
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004			
C;Accession: S65147; S48859			
R;Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.			
Plant Mol. Biol. 30, 135-147, 1996			
A;Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated,			
A;Reference number: S65141; MUID: S6197404; PMID: 8616230			
A;Accession: S65147			
A;Molecule type: mRNA			
A;Residues: 1-455 <HS2>			
A;Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:G563611; PIDN:CAA83655.1;			
C;Superfamily: nucleoside triphosphatase chromatin-associated			
C;Keywords: nucleus			

Query Match	15.9%	Score 376;	DB 2;	Length 455;																						
Best Local Similarity	24.9%	Pred. No. 1.4e-22;																								
Matches 120;	Conservative 83;	Mismatches 176;	Indels 102;	Gaps 19																						
Qy	2	PTSTQNKALPENV-----	KYGI	VL	DAG	SHT	SL	Y	Y	K	W	P	A	E	K	N	D	T	G	V	V	H	-	46		
Db	16	PAITSSOYLGNLLTSRKIFLKEBIEISSYAVF	DAG	TG	SR	H	V	Y	H	F	-----	N	Q	N	D	L	L	H	I	71						
Qy	47	--OV	E	C	R	V	K	G	P	G	I	S	K	F	V	Q	N	E	I	G	I	L	T	104		
Db	72	GK	G	E	Y	N	K	T	P	G	L	S	S	Y	A	N	N	P	E	Q	A	K	S	131		
Qy	105	R	M	S	E	E	L	A	D	R	V	L	D	V	E	R	S	L	N	-	Y	P	F	D	161	
Db	132	N	G	D	A	S	E	-	-	K	I	L	Q	S	R	D	M	L	S	R	T	F	N	186		
Qy	162	W	F	S	I	P	Y	E	T	N	N	O	E	T	F	G	A	L	D	I	G	G	A	S	213	
Db	187	-----	Y	T	K	T	G	V	I	D	L	G	G	S	V	O	M	A	V	S	K	T	A	K	236	
Qy	214	N	V	T	H	S	F	L	C	Y	G	K	Q	A	L	W	K	L	A	D	I	O	V	A	S	267
Db	237	D	L	V	H	S	Y	L	H	F	G	R	-----	E	A	S	R	A	E	I	K	L	T	P	R	279
Qy	268	C	T	R	K	E	M	T	L	P	Q	F	E	I	G	I	G	N	O	O	C	H	O	S	I	325
Db	280	--	B	E	F	K	A	T	-----	A	Y	T	S	G	A	N	F	N	K	C	K	N	T	I	R	327
Qy	326	-----	A	F	S	A	F	Y	F	V	M	K	F	N	L	T	S	E	K	-	-	-	-	-	-	374
Db	328	G	Q	K	N	L	F	A	S	S	E	F	F	Y	L	P	E	D	T	G	M	V	D	A	S	387
Qy	375	Y	L	S	E	Y	-	C	F	S	G	T	Y	I	L	S	L	L	Q	H	F	T	A	D	S	429
Db	388	N	V	A	S	Y	C	M	D	I	Y	O	V	L	L	V	D	G	-	-	F	O	L	D	P	445

QY	430 P 430	Db	363 YLNAAKVACQTNVADIKSIFPKTODRNIPLYCMLDIYEYTLVLDG--FGLNPHKEITVIH 420
Db	446 P 446	QY	409 KIQSGD---AGWTLGYMLNL-----TNMI 429
Db		Db	421 DVOYKNYLVGAAWPLGCAIDLVSSTINKI 449
RESULT 12			
JC4616			
apyrase (EC 3.6.1.5) precursor - potato			
A:Alternate names: adenylpyrophosphatase; ATP-diphosphohydrolase			
C:Species: Solanum tuberosum (potato)			
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			
C:Accession: J04616; PC4147			
R:Handa, M.; Guidotti, G.			
A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato			
A:Reference number: J04616; PMID:8579614			
A:Accession: J04616			
A:Molecule type: mRNA			
A:Residues: 1-454 <HAN>			
A:Cross-references: UNIPROT:P80595; GB:U58597; NID:gl381632; PID:AA02720.1; PID:gl3816			
A:Accession: PC4147			
A:Molecule type: protein			
A:Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>			
A:Experimental source: tubers			
A:Note: The authors translated the codon GCA for residue 215 as Gly			
C:Comment: This enzyme belongs to a family of E-type Apyrases, and it catalyzes the hydrolysis of ATP to ADP and inorganic phosphate. It has a high substrate specificity, and insensitive to inhibition by vanadate, and insensitive to inhibition by vanadate.			
C:Genetics:			
A:Gene: tropl			
C:Superfamily: nucleoside triphosphatase chromatin-associated			
C:Keywords: glycoprotein; hydrolase; transmembrane protein			
F:1-30/Domain: signal sequence #status predicted <SIG>			
F:8-25/Domain: transmembrane #status predicted <TM>			
F:31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>			
F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding			
F:192-212/Region: nucleotide binding #status predicted			
F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding			
F:390-410,427-446/Region: hydrophobic carboxyl end			
F:151,262/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 14.1%; Score 334; DB 2; Length 454;			
Best Local Similarity 24.9%; Pred. No. 3.5e-19;			
Matches 112; Conservative 80; Mismatches 185; Indels 72; Gaps 17;			
QY	12 ENVKYGIVLDAGSSHTLSYIYKPAEKENDTGCVHVEECRVKPGISKFKVQKNEIGIY 71	Db	56 PGISKFKVQKNEIGIYVITDCMERAREVIPSQHOETPVLGATAGMRLLR-MESEELADR 114
Db	42 ESEHVAVIDAGSTGSRVHVRFD-EKGLLPIGNNIEYFMATEPGLSSYAEDPKAAANS 100	Db	578 PGFDKLVNRTGLKTAIKPLIQWAERQIPKNAHRTTSLFYATAGVRLRPADSSWILGN 637
QY	72 LTDCMERAREVIPSQHOETPVLGATAGMRLLRMESELADRVLDVVE---RSLSNYPF 128	QY	115 VLDVVERSLSNYPDF--QGARIITGOEGAGVWITIN---LLGKFSOKTRWFSIVPYE 169
Db	101 LBPFLDGAEGVVPQELQSETPLELGATAGRLMKGDA---AEKILQAVRNLVKNOSTFHS 157	Db	638 VMSLAKS-----PFCRRWVKLITGEAYFGWTALNTQSMGLPKKA-----684
QY	129 DFGARIITGOEGAGVWITINVLCKFSQKTRWFSIVPYETNNQETFGALDLGGASTQV 188	QY	170 TNNQETFGALDLGGASTQVTFVFPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDA- 228
Db	158 KQWVTLIDQTQSGTWAAINVLGNLCK-----DYKSTTATIDLGGSVQM 205	Db	685 -----TFGALDLGSSLQVTF--ENERTHNETNLNLRLIGSVNHLISAYSLAGYGLNDAF 737
QY	189 TFPQON-QTIESPDN-----ALQFRLYGKDYNNVYTHSFLCYGKQDAALWQKLAKDIQVAS 241	QY	229 -----LWQKLA---KDIQVASEILRDCFHFGYKKNVNSDLYKTPCTKRFEMLTFQ 279
Db	206 AVAISNEQPAKAPQNEDEGPYVQKHLMSKDYNLVHVSILNYGQ-LAGRAEIFFKASRNES 264	Db	738 DRSVVHLLKLLPNWNKSDLIEGKLEMKHPCNLNGYN-----GQYICQACASSVQGGKKG 792
QY	242 NEILRDPCHPGYKVVNVSDLYKTPCTKRFEMLTFPQFEIQQIGNYQOCHQSILELNFN 301	QY	280 ---QFEIQIGNYQOCHQSILELNFNTSYCPYSCAFNGIFLPLPQDGFAGSAFYFMKF 336
Db	265 NPCALEGC--DGYYISYGGVD--YKVPKPKG-----SSWKRCLRLTRHALK 306	Db	793 SGVSIKLVGAPNWGEC-----SALAKNAFCALPDGY-PRPHGQFYAVSGFFVYRF 842
QY	302 -TSYCPYSCAFNGIFLPLQSGDFG-----AFSAFYFMKFLNLTSEKVSQE-----K 348	QY	337 LNLTSKVSQEKVTEMMKFCAPQWBEIKTSYAGVKEKLYSEYCFSGTYILSLILQYHF 396
Db	307 INAKNIEECTFNGVW---NGGGDGQXNIHASSFFYDGAQGVIVDTKFPFSALAKPIQ 362	Db	843 FNLSAE-ASLDDVLEKRGREFCDRAWQVARTSVS--PQPFIEQYCFRAPHYIVSLRLGLYI 899
QY	349 VTEMKKFKCAQWBEIKTSYAGVKEKLYSEYCFSGTYILSLILQYHFTADSWEHIFIG 408	QY	397 TADSWEHIFIGIKQSGDAGWTLGYML 423
RESULT 14			
T23508			
hypochemical protein K08H10.4 - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004			
C:Accession: T23508			
R:Gardner, A.			
submitted to the EMBL Data Library, November 1996			
A:Reference number: Z19750			
A:Accession: T23508			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-479 <WII>			
A:Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; CESP:K			

A;Description: The sequence of *S. cerevisiae* cosmids 8199, 8334, and 9871.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:51 ; Search time 62.0612 Seconds
(without alignments)
3655.279 Million cell updates/sec

Title: US-09-835-147a-30_COPY_21_463

Perfect score: 2368

Sequence: 1 APTSTONKALPENVKYIVL.....NLTNMPAEQLSTPLSHST 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2348	99.2	510	1 ENP1_HUMAN	P49961 homo sapien
2	1835	77.5	510	1 ENP1_MOUSE	P57772 mus musculus
3	1835	77.5	539	2 Q8CDV7	Q8cdv7 mus musculus
4	1830	77.3	510	2 Q92106	Q92106 mus musculus
5	1818	76.8	372	2 Q86V3	Q86v3 homo sapien
6	1794.5	75.8	511	1 ENP1_RAT	P97687 rattus norv
7	1715	72.4	510	1 ENP1_PIG	Q9myu4 sus scrofa
8	1630.5	71.4	513	1 ENP1_BOVIN	O18956 bos taurus
9	1574	66.5	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1450	61.2	508	2 Q8DFS1	Q8dfs1 xenopus tro
11	1418	59.9	508	2 Q8GPF4	Q8gp74 xenopus lae
12	1306.5	55.2	492	2 Q8DC46	Q8dc46 brachydanio
13	1046	44.2	497	2 Q8UQ22	Q8uq22 mus musculus
14	1004	42.4	493	1 ENP1_CHICK	Q93295 gallus gall
15	997	42.1	493	2 Q90X66	Q90x66 gallus gall
16	975	41.2	454	2 Q8ZM69	Q8zm69 brachydanio
17	971.5	41.0	495	1 ENP2_RAT	O35795 rattus norv
18	964.5	40.7	495	1 ENP2_MOUSE	O35026 mus musculus
19	964.5	40.7	495	2 Q921R1	Q921r1 mus musculus
20	961	40.6	455	2 Q7T014	Q7t014 brachydanio
21	953	40.2	494	1 ENP2_CHICK	P79784 gallus gall
22	937.5	39.6	502	2 Q66L64	Q66l64 brachydanio
23	936	39.5	526	2 Q6GNA4	Q6gna4 xenopus lae
24	933	39.4	500	2 Q6GNV19	Q6gnv19 xenopus tro
25	913.5	38.6	529	2 Q80Z26	Q80z26 rattus norv
26	910.5	38.5	529	1 ENP3_HUMAN	O75355 homo sapien
27	907.5	38.3	495	1 ENP2_HUMAN	O9y513 homo sapien
28	906.5	38.3	458	2 Q6UVZ0	Q6uvz0 homo sapien
29	902.5	38.1	529	2 Q8BFW6	Q8bfw6 m mus muscu
30	854	36.1	453	2 Q6ZM68	Q6zm68 brachydanio
31	825.5	34.9	452	2 Q8N6K2	Q8n6k2 homo sapien

32	658	27.8	544	2 Q7YTA4	Q7yta4 schistosoma
33	620.5	26.2	300	2 Q8K0L2	Q8k0l2 mus musculus
34	596.5	25.2	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	505	21.3	483	2 Q9XI62	Q9xi62 arabidopsis
36	504	21.3	488	2 Q6NQ48	Q6nq48 arabidopsis
37	491	20.7	503	2 Q94AP8	Q94ap8 arabidopsis
38	491	20.7	503	2 Q8H1D8	Q8h1d8 arabidopsis
39	485	20.5	537	2 Q6Z543	Q6z543-oryza sativ
40	483	20.4	634	2 Q6FCR2	Q6frc2 candida gla
41	482.5	20.4	336	2 Q8CCV2	Q8ccv2 mus musculus
42	471.5	19.9	555	2 Q94E22	Q94ez2 arabidopsis
43	469.5	19.8	405	2 Q9M9T7	Q9m9t7 arabidopsis
44	469	19.8	611	2 Q6DHJ0	Q6dhj0 brachydanio
45	465.5	19.7	555	2 Q80612	Q80612 arabidopsis

ALIGNMENTS

RESULT 1

ID	ENP1_HUMAN	STANDARD;	PRT;	510 AA.
AC	P49961: Q9UQ09; Q9Y3Q9;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)			
DE	(NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPbase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).			
GN	Name=ENTPD1; Synonyms=CD39;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Nakajima T., Schoenborn M.A., Armitage R.J., Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;			
RT	"The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization."			
RT	J. Immunol. 153:3574-3583(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM VASCULAR).			
RP	TISSUE=Umbilical vein;			
RC	MEDLINE=97149443; PubMed=8996251;			
RX	Robson S.C., Kaczmarek E., Siegel J.B., Candinas D., Kozlak K., Millan M., Hancock W.W., Bach F.H.;			
RA	"Loss of ATP diphosphohydrolase activity with endothelial cell activation."			
RT	J. Exp. Med. 185:153-163(1997).			
RL	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).			
RP	TISSUE=Placenta;			
RC	MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;			
RX	Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T., Titani K., Fujimura Y., Narita N.;			
RA	"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II."			
RT	FEBS Lett. 453:335-340(1999).			
RL	[4]			
RP	SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.			
RP	TISSUE=Placenta;			
RC	MEDLINE=96096723; PubMed=8529670;			
RX	Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;			
RA	"Purification and Properties of human placental ATP diphosphohydrolase."			
RT	Eur. J. Biochem. 234:66-74(1995).			
RL	[5]			
RP	SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND 399-405 (ISOFORM PLACENTAL I).			
RP	TISSUE=Placenta;			

RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki K., Fujimura Y.,
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature
 RT distinct from CD39, localization and inhibition on shear-induced
 RT platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 RN [6]
 RP FUNCTION.
 RP MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 RN [7]
 RP CHARACTERIZATION.
 RP MEDLINE=96213267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;
 RA Wang T.F., Guidotti G.;
 RT "CD39 is an ecto-(Ca²⁺,Mg²⁺)-ATPase.";
 RL J. Biol. Chem. 271:9898-9901(1996).
 RN [8]
 RP PALMITOYLATION.
 RP MEDLINE=20102721; PubMed=10635909; DOI=10.1074/jbc.275.3.2057;
 RA Kozlak K., Kaczmarek E., Kittel A., Sevigny J., Blustajn J.K.,
 RA Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,
 RA Robson S.C.;
 RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
 RT caveolae.";
 RL J. Biol. Chem. 275:2057-2062(2000).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=Vascular;
 CC IsoId=p49961-1; Sequence=Displayed;
 CC Name=Placental I;
 CC IsoId=p49961-2; Sequence=VSP_003607;
 CC Name=Placental II;
 CC IsoId=p49961-3; Sequence=VSP_003608, VSP_003609;
 CC TISSUE SPECIFICITY: Expressed primarily on activated lymphoid
 CC cells. Also expressed in endothelial tissues. The vascular isoform
 CC and the placental isoform II are present in both placenta and
 CC umbilical vein, whereas placental isoform I is present in placenta
 CC only.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and
 CC 7.5-8.0 with ADP.
 CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; S73813; AAB32152.1; -;
 CC EMBL; U87967; AAB47572.1; -;
 CC EMBL; AJ133133; CAB41886.1; -;
 CC EMBL; AJ133134; CAB41887.1; -;
 CC PIR; I56242; I56242.
 CC Genbank; HGNC:3363; ENTPD1.
 CC MIM; 601752; -;

DR GO:0005887; C:integral to plasma membrane; TAS.
 DR GO:0007596; P:blood coagulation; TAS.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39; 1.
 DR PROSITE; PS01238; GDAI_CD39_NTPase; 1.
 KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;
 KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
 KW Transmembrane.
 KW DOMAIN 1 16 Cytoplasmic (Potential).
 FT TRANSMEM 17 37 Potential.
 FT DOMAIN 38 478 Extracellular (Potential).
 FT TRANSMEM 479 499 Potential.
 FT DOMAIN 500 510 Cytoplasmic (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 4 MSDT -> MKGTGKDLTSQQ (in isoform Placental
 FT I and isoform Placental II).
 FT FTID=VSP_003607.
 FT VASNEILRDFCFRPGYKKVNVSDLYKT -> ASIQSRPA
 FT PFTSAPPAPTSCCFUFIQ (in isoform Placental
 FT II).
 FT FTID=VSP_003608.
 FT Missing (in isoform Placental II).
 FT FTID=VSP_003609.
 FT SS -> G (in Ref. 5).
 FT D -> K (in Ref. 4).
 FT T -> TGET (in Ref. 5).
 FT V -> Y (in Ref. 5).
 SQ SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;
 Query Match 99.2%; Score 2348; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 5.8e-174;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFVQK 64
 DB 38 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKFVQK 97
 QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 124
 DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSL 157
 QY 125 NYPDFQGARIITGOEGAYGWTINVLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 184
 DB 158 NYPDFQGARIITGOEGAYGWTINVLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217
 QY 185 STQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDALMOKLAKDIQVASNEI 244
 DB 218 STQVTFVPPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDALMOKLAKDIQVASNEI 277
 QY 245 LRDCPFHPGKVVNVSDLYKTKCFEMTLFPOQFEIOGIGNYQOCHOSILELFTSY 304
 DB 278 LRDCPFHPGKVVNVSDLYKTKCFEMTLFPOQFEIOGIGNYQOCHOSILELFTSY 337
 QY 305 CPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 364
 DB 338 CPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEI 397
 QY 365 KTSYAGVKRYLSYCFSGTYLSLLLOGHYFTADSWEHIFTKIQGSDAGWTGLYN 424
 DB 398 KTSYAGVKRYLSYCFSGTYLSLLLOGHYFTADSWEHIFTKIQGSDAGWTGLYN 457
 QY 425 LTNNIPAEQPLSTPLSHST 443
 DB 458 LTNNIPAEQPLSTPLSHST 476
 RESULT 2
 ENP1_MOUSE

```

ID ENPI MOUSE STANDARD; PRT; 510 AA.
AC P55772;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase1) (Ecto-ATP diphosphohydrolase) (Arpbase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R.; Delepesse G.J.T.; Schoenborn M.A.; Amitage R.J.;
RA Fauslow W.C.; Nakajima T.; Baker E.; Sutherland G.R.; Poindexter K.;
RA Birks C.; Albert A.; Friend D.; Gimpel S.D.; Gayle R.B. III;
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization.";
RL J. Immunol. 153:3574-3583(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=98399871; PubMed=9730622;
RA Schoenborn M.A.; Jenkins N.A.; Copeland N.G.; Gilbert D.J.;
RA Gayle R.B. III; Maliszewski C.R.;
RT "Gene structure and chromosome location of mouse Cd39 coding for an
RT ecto-apyrase.";
RL Cyogenet. Cell Genet. 81:287-289(1998).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF037366; AAB92259.1; -
DR EMBL; AF041818; AAC83203.1; -
DR EMBL; AF041812; AAC83203.1; JOINED.
DR EMBL; AF041813; AAC83203.1; JOINED.
DR EMBL; AF041814; AAC83203.1; JOINED.
DR EMBL; AF041815; AAC83203.1; JOINED.
DR EMBL; AF041816; AAC83203.1; JOINED.
DR EMBL; AF041817; AAC83203.1; JOINED.
DR MGP; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0004050; P:apyrase activity; IDA.
DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR PROSITE; PS01238; GDA1_CD39; 1.
DR Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
KW DOMAIN 1 16 Cytoplasmic (Potential).
FT TRANSMEM 17 37 Potential.
FT DOMAIN 38 478 Extracellular (Potential).
FT TRANSMEM 479 499 Potential.
FT DOMAIN 500 510 Cytoplasmic (Potential).

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FT CARBOHYD 73 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 226 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 291 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 333 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 428 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 457 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 510 AA; 57205 MW; 856A6113D2E13930 CRC64;
Query Match 77.5%; Score 1835; DB 1; Length 510;
Best Local Similarity 76.4%; Pred. No. 4.5e-134;
Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;
Qy 5 TONKALPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGVVHQVEECRVKPGSGSKFVQK 64
Db TONKPLPENVKYIGIVLDAGSSHTSLYIYKPAEKENDTGVVQLEECQVKPGSGSKVAQK 97
Qy 65 VNEIGIYLTOMERARVIPSQHOETPVYLGATAGMRLRMSESEELADRLVDVVERSL 124
Db TDEIGAYLAECMELSTELIPTSRKHQTPVYLGATAGMRLRMSESEQSADEVLAAVSTLK 157
Qy 125 NYPDFQCARIIITGOERGAYGWITINYLKFSOKTRWFSIVPYETNNQETFGALDLGGA 184
Db SYPPDFQAKIITGOERGAYGWITINYLGRFTQEQSWLSLIS-DSQKETFGALDLGGA 216
Qy 185 STQVTFVQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQALWOKLAKDIQVASNEI 244
Db STQITFVQNSTIESPENSILQFRLYGEDYTVYTHSFLCYGKQALWOKLAKDIQVSSGGV 276
Qy 245 LRDPCHFPGYKVVVNSDLKYTPCTKRFEMTLPPQOFEIQIGIGNYQOCHQSILELFWTSY 304
Db LKDPCHFPGYKVVVNSDLKYTPCTKRFEMTLPPQOFRIQGTGTYEQCHQSILELFWNSH 336
Qy 305 CPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLMLTSEK--VSOEKVTEMMKFCQAOPWE 362
Db CPYSQCAFNGVFLPPLHSGFAGSAFYVMDFFKKVANSVISOEKTEITKFNCSKWE 396
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSGDAGMTLGYM 422
Db ETKTSYPSVKEKYLSEYCFSGAYILS-LLQGYNFTDSSWEQIHFMGKIKDSNAGMTLGYM 455
Qy 423 LNLTNMIPASQPLSTPLSHST 443
Db LNLTNMIPASQPLSPPLPHST 476
RESULT 3
Q8CDV7 ID Q8CDV7 PRELIMINARY; PRT; 539 AA.
AC Q8CDV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:492151C05 product:ectonucleoside triphosphate
DE diphosphohydrolase 1, full insert sequence.
GN Name=Entpd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P.; Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";

```

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT preparing full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK029512; BAC26486.1; -;
 DR MGD; MGI:102805; Entpd1.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004050; F:apoptosis; IDA.
 DR GO; GO:0006200; P:ATP catabolism; IDA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IDA.
 DR GO; GO:0003158; P:platelet activation; IDA.
 DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39_1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 DR Hydroxylase.
 SQ SEQUENCE 539 AA; 60590 MW; 49565788313321F4 CRC64;
 Query Match 77.5%; Score 1835; DB 2; Length 539;
 Best Local Similarity 76.4%; Pred. No. 4.8e-134;
 Matches 337; Conservative 45; Mismatches 55; Indels 4; Gaps 3;
 5 TQNKALPENVKYGIIVLDAGSSHTSYIYKWPAAKENDTGTVHQQVEECRVKGFSGKVFQK 64
 67 TQNKALPENVKYGIIVLDAGSSHTSYIYKWPAAKENDTGTVHQQVEECRVKGFSGKVFQK 126
 65 VNEIGIYLTDCMERAREVPRCHQETPVYLGATAGMILLRMESEELADRLVDVVERSL 124
 127 TDEIGAYLAECMELSTIPTSKHQTVPYLGATAGMILLRMESEELADRLVDVVERSL 186

QY 125 NYPDFQAGRIITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLGA 184
 DB 187 SYPPDFQAGRIITGOEGAYGWITINYLKGRTRQSGWLSLIS-DSQKQETFGALDLGA 245
 QY 185 STQVTFVPPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQOALWQKLAKDIQVANSNEI 244
 DB 246 STQITVPPQNTIESPDNALQRLYKGVNVTHTSFLCYGKQOALWQKLAKDIQVANSNEI 305
 QY 245 LRDPCEHPGKVVNVNVDLYKTPCTKRPEMTLPFOQFELQIGIYQOCHQSILELFTSY 304
 DB 306 LKDPCEHPGKVVNVNVDLYKTPCTKRPEMTLPFOQFELQIGIYQOCHQSILELFTSY 365
 QY 305 CPYSQCAFNGIFLPPLOQDGFAGFAFYFVYKFLNLTSEK--VSQEKVTEMKKFCAQPW 362
 DB 366 CPYSQCAFNGIFLPPLOQDGFAGFAFYFVYKFLNLTSEK--VSQEKVTEMKKFCAQPW 425
 QY 363 EIKTSYAGVKEKYLSEYCFSGYVILSLILQGHVTPADSWEHIFHFIQKIQSDAGWTLGYM 422
 DB 426 EIKTSYAGVKEKYLSEYCFSGYVILSLILQGHVTPADSWEHIFHFIQKIQSDAGWTLGYM 484
 QY 423 LNLTNMIPAEQPLSTPLSHST 443
 DB 485 LNLTNMIPAEQPLSTPLSHST 505
 RESULT 4
 Q921Q6 PRELIMINARY; PRT; 510 AA.
 ID Q921Q6
 AC Q921Q6
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Entpd1 protein.
 GN Names:Entpd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011278; AAH11278.1; -;
 DR MGD; MGI:102805; Entpd1.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004050; F:apoptosis; IDA.

DR GO; GO:0006200; P:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 510 AA; 57176 MW; E77BB644AE1413A0 CRC64;

Query Match 77.3%; Score 1830; DB 2; Length 510;
Best Local Similarity 76.2%; Pred. No. 1.1e-133;
Matches 336; Conservative 45; Mismatches 56; Indels 4; Gaps 3;

QY 5 TONKALPENKYGIVLDAGSSHTSYIYKPAEKNDTGTVHQPVECKVKGFGISKFVQK 64
DB TONKPLPENKYGIVLDAGSSHTSYIYKPAEKNDTGTVHQPVECKVKGFGISKFAQK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMELLRWSEELADRVLDVVERSL 124
DB TDEIGAYLAECHELSTELIPTSKHQTPTVYLGATAGMELLRWSEESQSADEVLAAVSTSLK 157
QY 125 NYPDFQAGARIITGQEGAYGMITINYLKGFQSKTRWFSIVPYTNNQETFGALDLGGA 184
DB GYPDFQAGARIITGQEGAYGMITINYLKGFQSKTRWFSIVPYTNNQETFGALDLGGA 216
QY 185 STQTVFQONQTIESPNDALQRLYKGYNYVTHSFLCYGKQALWQKLAKDIQVASNEI 244
DB STQITVFQNSTIESPNSLOPRLYGEDYTVVTHSFLCYGKQALWQKLAKDIQVSSGGV 276
QY 245 LRDCFFHGYKXVNVSDLYKTPCTKREMTLPFOQFEIQTGNYQOCHQSIIELEFNTSY 304
DB LKDCFFHGYKXVNVSDLYKTPCTKREMTLPFOQFEIQTGNYQOCHQSIIELEFNTSY 336
QY 305 CPYSQAFNGIFLPLQDGFAGFAFYFVWKFLNLTSEK--VSQKVTMMKKFCAQOPWE 362
DB CPYSQAFNGIFLPLQDGFAGFAFYFVWKFLNLTSEK--VSQKVTMMKKFCAQOPWE 396
QY 363 EIKTSYAGVKKYLSEYCFSGTYILSLLLQGHFTADSWHEHFTGKTQSDAGWTGGM 422
DB EIKTSYAGVKKYLSEYCFSGTYILSLLLQGHFTADSWHEHFTGKTQSDAGWTGGM 455
QY 423 LNLNTMIPAEQPLSTPLSHST 443
DB LNLNTMIPAEQPLSTPLSHST 476

RESULT 5
Q86VV3 PRELIMINARY; PRT; 372 AA.
ID Q86VV3
AC Q86VV3
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENTPD1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; ABB1DE1366356EE3 CRC64;

Query Match 76.8%; Score 1818; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.3e-133;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 MESEELADRVLDVVERSLSNYPDFQAGARIITGQEGAYGMITINYLKGFQSKTRWFSI 165
DB 1 MESEELADRVLDVVERSLSNYPDFQAGARIITGQEGAYGMITINYLKGFQSKTRWFSI 60
QY 166 VPYTNNOETFGALDLGGASTQNTVFQONQTIESPNDALQRLYKGYNYVTHSFLCYGK 225
DB VPYTNNOETFGALDLGGASTQNTVFQONQTIESPNDALQRLYKGYNYVTHSFLCYGK 120
QY 226 DQALWQKLAKDIQVASNEILRDCFFHGYKXVNVSDLYKTPCTKREMTLPFOQFEIQG 285
DB DQALWQKLAKDIQVASNEILRDCFFHGYKXVNVSDLYKTPCTKREMTLPFOQFEIQG 180
QY 286 IGYNQOCHQSIIELEFNTSYCFYSQAFNGIFLPLQDGFAGFAFYFVWKFLNLTSEKVS 345
DB IGYNQOCHQSIIELEFNTSYCFYSQAFNGIFLPLQDGFAGFAFYFVWKFLNLTSEKVS 240
QY 346 QEKVTMMKKFCAQOPWEIETKTSYAGVKKYLSEYCFSGTYILSLLLQGHFTADSWHEH 405
DB QEKVTMMKKFCAQOPWEIETKTSYAGVKKYLSEYCFSGTYILSLLLQGHFTADSWHEH 300
QY 406 FIGKIQSDAGWTGLGYMLNLTNMLIPAEQPLSTPLSHST 443
DB FIGKIQSDAGWTGLGYMLNLTNMLIPAEQPLSTPLSHST 338

RESULT 6
ENPL RAT
ID ENPL RAT
AC P97687; STANDARD; PRT; 511 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase)
DE activation antigen (Ecto-apyrase) (CD39 antigen).
GN Name=Entpd1; Synonyms=Cd39;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX PubMed=9221928;
RA Wang T.-P., Rosenberg P.A., Guidotti G.;
RT "Characterization of brain ecto-apyrase: evidence for only one ecto-
RT apyrase (CD39) gene.";
RL Brain Res. Mol. Brain Res. 47:295-302(1997).
RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Cochlea; DOI=10.1016/S0169-328X(99)00244-2;
 RX MEDLINE=20050856; PubMed=9664474; DOI=10.1016/S0028-3908(97)00115-9;
 RA Vlakovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
 RT "Evidence for alternative splicing of ecto-ATPase associated with
 RT termination of purinergic transmission.";
 RL Brain Res. Mol. Brain Res. 73:85-92(1999).
 RN [3]
 RP SEQUENCE OF 432-511 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=36031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
 RT "An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
 RT rat brain.";
 RL Neuropharmacology 36:1189-1200(1997).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
 CC kidney, liver, muscle, thymus, lung and spleen.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NPase family.
 CC
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 CC
 CC EMBL; U81295; AAC53195.1; -;
 CC EMBL; Y15685; CAA75730.1; -;
 CC RGD; 69265; Entd1
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
 FT DOMAIN 1 16
 FT TRANSMEM 17 37
 FT POTENTIAL 37
 FT EXTRACELLULAR (Potential).
 FT POTENTIAL 38 478
 FT TRANSMEM 479 499
 FT POTENTIAL 500 511
 FT CYTOPLASMIC (Potential).
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 73 73
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 226 226
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 291 291
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 333 333
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 374 374
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 429 429
 FT N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 458 458
 FT N-linked (GlcNAc. .) (Potential).
 FT CONFLICT 332 332
 FT F > L (in Ref. 2).
 SQ SEQUENCE 511 AA; 57408 MW; 4CC123D3B5644C193 CRC64;
 Query Match 75.8%; Score 1794.5; DB 1; Length 511;
 Best Local Similarity 74.4%; Pred. No. 6.3e-131;
 Matches 328; Conservative 51; Mismatches 59; Indels 3; Gaps 3;
 QY 5 TONKALPENVKYGVLDAGSSHTSLIYKPAEKENDTGVVHOVECRVKGPGISKVOK 64
 DB 38 THNKLPLPENVKYGVLDAGSSHTSLIYKPAEKENDTGVVQLLEECQVKGPGISKVAK 97
 QY 65 VNEIGIYLTDCWREAREVIPSQHSQTPVYLGCATAGMELLMSEELADRVLDVVERSL 124
 DB 98 TDELAAYLAECWKWSTERIPASKQHPVYLGCATAGMELLMSEELADRVLDVVERSL 157
 QY 125 NYPFDQGARITQGEAGYWTINYLKFKPSQKTRWFSIVPVTNNQTFGALDGG 184
 DB 158 SYPDFQGAKITQGEAGYWTINYLKFKPSQKTRWFSIVPVTNNQTFGALDGG 216

QY 185 STQVTFVQNTTIESPDNALQFRLYKDYNNVYTHSLCYGKQALMOKLAKDIQVASNEI 244
 DB 217 STQVTFVPLNQTLEAPETSLQFRLYGTDTYVYTHSLCYGKQALMOKLAKDIQVSSGGI 276
 QY 245 LRDPCHPHGKVKVNVSDLYKTPCTCTKRFEMTLFPQFETQIGNYOCHOSILELFTSY 304
 DB 277 LKDPFCFPGYKVKVNVSELYGTCTKRFKELPFNQVQGTGDEYEQCHOSILKFFNNH 336
 QY 305 CPYSQCAFNGIFLPLQGDGAFSAFVFMKEL-NLTSEKV-SOEKVTEMKKFCAOPWE 362
 DB 337 CPYSQCAFNGFVLPPLQGSFSAFVFMDFPKMANDSVSSQEKMTETIRKFCSPWE 396
 QY 363 EIKTSVAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 422
 DB 397 EVKASPTVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 456
 QY 423 LNLTNMIPAEQPLSTPLSHST 443
 DB 457 LNLTNMIPAEQPLSPPLPHST 477
 RESULT 7
 ENPI_PIG ID ENPI_PIG STANDARD; PERT; 510 AA.
 AC Q9MYU4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 03-JUL-2004 (Rel. 44, Last annotation update)
 DE Ectonucleoside triphosphatase diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell
 DE activation antigen) (Ecto-apyrase) (CD39 antigen).
 GN Name=ENTPD1; Synonyms=CD39;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic endothelium;
 RX MEDLINE=20325090; PubMed=10866813;
 RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezaak O.,
 RA Sevigny J.;
 RT "Distribution, cloning, and characterization of porcine nucleoside
 RT triphosphate diphosphohydrolase-1.";
 RL Eur. J. Biochem. 267:4106-4114(2000).
 RN [2]
 RP SEQUENCE OF 202-220.
 RC TISSUE=Pancreas;
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
 RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well.
 CC -1- CATALYTIC ACTIVITY: ATP + 2 H₂O = AMP + 2 phosphate.
 CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Highest expression found in vascular
 CC endothelium, smooth muscle, spleen and lung.
 CC -1- PTM: Cleaved into two polypeptides that seem to stay together by
 CC noncovalent interactions.
 CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NPase family.
 CC
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DR	EMBL; AJ133746; CAB95871.1; -. InterPro; IPR000407; GDAL CD39_NTPase.
DR	Pfam; PF01150; GDAL CD39; 1.
DR	PROSITE; PS01238; GDAL CD39_NTPASE; 1.
KW	Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
KW	Magnesium; Transmembrane.
CHAIN	1 510
FT	Ectonucleoside triphosphate
FT	diphosphohydrolase 1.
FT	Ectonucleoside triphosphate
FT	diphosphohydrolase 1 27 kDa subunit.
FT	Ectonucleoside triphosphate
FT	diphosphohydrolase 1 54 kDa subunit.
FT	Cytoplasmic (Potential).
FT	Potential..
FT	Extracellular (Potential).
FT	Potential.
FT	Cytoplasmic (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	N-linked (GLCNAC. . .) (Potential).
FT	G -> S (in Ref. 2).
FT	CONFLICT 203 203
FT	SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;
SQ	

Query Match	72.4%;	Score 1715;	DB 1;	Length 510;
Best Local Similarity	70.7%;	Pred. No. 9.6e-125;		
Matches 311;	Conservative 63;	Mismatches 64;	Indels 2;	Gaps 2;

Qy	5	TQKALPENVKYIGIVLDAGSHSTSLYIKWPAEKENDTGVVHQVEBCRVKGPISKFVQK	64
Db	38	TQKPLPENVKFIVLDAGSHSTSLYIKWPAEKENDTGVVSOVEECKLXGPISFEPAK	97
Qy	65	VNHIGIVLTCMERAREVIPSQHOETPPVYLGATAGMRLLRMESEELADRVLDVVERSL	124
Db	98	LGBIDIYLECMERARTVPSQHAETPPVYLGATAGMRLLRMKNENLASKILSTVAESIT	157
Qy	125	NYPPDFQGARIIITQOBEGAYGWITINYLKGFQKTRWFSIVPYETNNQFTFGALDILGGA	184
Db	158	RYPPDFQGARIIITQOBEGAYGWITINYLKDFIQKSGWFNLKPRKGTQBTYTGALDILGGA	217
Qy	185	STQVTPVQNOTTESPDNALQPLRYGKDVNYTHSFLCYKQDQALWQKLAKDIQVASNEI	244
Db	218	STQITVQVQNVLSPENTUHFRLYGNYSVYTHSFLCYKQDQALLQKLTDLK-NTNGT	276
Qy	245	LRDPCFHPGKYKVVNSDLYKTCRKFEMTLPPFQOFEIOGINYOCHOOSIILEFNTSY	304
Db	277	IHEPCFHSQVRRMNVSHLYEAPCTRFRFLTSLFPPELEIOGTGDFQCKQOSIRPLFNTSY	336
Qy	305	CPYSQCAFNGIFLPPLOQDPRGASAFYFWKMFNLNLTSSEKUS-0EKVTEMKKKCPAQDWEE	363
Db	337	CPYSRCSFDPGVFLPQGDPAAFSAFYVNGFLNLTSSEGSFQSKVTSITLEAFCSRPAE	396
Qy	364	IKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTFTADSWEHIFGKIQGSADGWTLYGML	423
Db	397	LQWYFGDVKEKYLSEYCFSGTYILTLLLSGYHTAETWKNHFWPKQVOSTSVGWTLYGML	456
Qy	424	NLTNMIAPBOPLTSTPLSHST	443
Db	457	NLTNMIPSBEPSTRLSHST	476

RESULT 8

ENP1 BOVIN

ENP1_BOVIN	ENP1_BOVIN	STANDARD:	PRT:
ID	ENP1_BOVIN		513 AA

AC 018956;

DT 16-OCT-2001 (Rel. 40, Created)

```
Qy 65 VNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLMRSEELADRVLDVRSLS 124
Db 98 VNEINVLTACMERAKVIPSIOHMETPVYLGATAGMRLMRSEELADRVLDVRSLS 157
Qy 125 NYPDFOGARIITGOBEGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFGALDILGGA 184
Db 158 EYPDFOGARIISQEBEGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFGALDILGGA 217
Qy 185 STQVTFPQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALQKADQVANSNEI 244
Db 218 STQVTFPQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALQKADQVANSNEI 276
Qy 245 LRDCFCFHCYKVVNVSDLYKTPCTKEPMT--LPQOEIIOGIGNVQOCHOSILEFN 301
Db 277 IHEPCFHSRVRKTKMNSVNLGFCRHELMNSFYPLVDEIRGAGNFQRCRQSIILFN 336
Qy 302 TSYCPYSCAFNGIFLPLPLOGDFGAFSAFYVMKFLNLTSEK-VSQBKVTMMKKFCAQP 360
Db 337 TSYCPYSCSFGVFLPLPHQFGAFSAFYVMKFLNLTSEK-VSQBKVTMMKKFCAQP 396
Qy 361 WEEIKTSVAGVEKYLSEYCSGTYVYLSLLQGHVFTADSWEHIFTKIGQSDAGWTIG 420
Db 397 WEEVQKNGEYKYLSEYCSGTYVYLSLLQGHVFTADSWEHIFTKIGQSDAGWTIG 456
Qy 421 YMLNLTNMPAEQPLSTPLSHST 443
Db 457 YMLNLTNMPAEQPLSTPLSHST 479
RESULT 9
Q8CEB1
ID Q8CEB1 PRELIMINARY; PRT; 420 AA.
AC 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:473241916 product:ectonucleoside triphosphate
DE diposphonhydrolase 1, full insert sequence. (Fragment).
GN Name=Entpd1;
OS Mus musculus;
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 409:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka Y., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai I., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akanira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK028625; BAC26037.1; -.
DR MGD; MGI:102805; Entpd1.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004050; F:ATP catabolism; IDA.
DR GO; GO:0006200; F:ATP catabolism; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P:platelet activation; IDA.
DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
FT NON TER 1 1
SQ SEQUENCE 420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
Query Match 66.5%; Score 1574; DB 2; Length 420;
Best Local Similarity 74.5%; Pred. No. 6.8e-114;
Matches 289; Conservative 42; Mismatches 53; Indels 4; Gaps 3;
Qy 58 ISKPVQKVNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLMRSEELADRVLD 117
Db 1 ISKPVQKVNEIGIYLTDCMERAREVTPRSQHOETPVYLGATAGMRLMRSEELADRVLD 60
Qy 118 VVERSLSNYPDFOGARIITGOBEGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFG 177
Db 61 AVSTSLKSYPPDFOGARIITGOBEGAYGWTINVLGKFSOKTRWFSIVPVETNNQSTFG 119
Qy 178 ALDLGGASTQVTFPQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALQKAD 237
Db 120 ALDLGGASTQVTFPQNOTIESPDNALQFRLYGKDYNNVYTHSFLCYGKQDQALQKAD 179
Qy 238 QVANSNEILRDPCEHPGKVVNVSDLYKTPCTKEPMTLPFOOEIIOGIGNVQOCHOSIL 297
Db 180 QVSSGGVLPDCEHPGKVVNVSELYGTCTKEPMTLPFOOEIIOGIGNVQOCHOSIL 239
Qy 298 ELFNYSYCPYSCAFNGIFLPLPLOGDFGAFSAFYVMKFLNLTSEK--VSEQKVTMMKK 355
Db 240 ELFNYSYCPYSCAFNGIFLPLPLOGDFGAFSAFYVMKFLNLTSEK--VSEQKVTMMKK 299
Qy 356 FCAQWPEIKTSVAGVEKYLSEYCSGTYVYLSLLQGHVFTADSWEHIFTKIGQSDA 415
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Db 300 PCSKWEETKTSYSPVSEKYLSEYCFSGAYTSL-LLQYNFTGSSWEQIHFMGKIDNSA 358
Qy 416 GWTILGYMLNLTNMIAPAOPLSTPLSHST 443
Db 359 GWTILGYMLNLTNMIAPAOPLSPPLPHST 386

RESULT 10
Q6DFS1 Q6DFS1 PRELIMINARY; PRT; 508 AA.
AC Q6DFS1 Q6DFS1 PRELIMINARY; PRT; 508 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Entpdl-protov-prov.
GN Name=entpdl-prov.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Gerhard D.S.;
RL EMBL; BC076662; AAH76662.1; -;
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
SQ SEQUENCE 508 AA; 57322 MW; 12CAEAC05BEABDEB CRC64;

Query Match 61.2%; Score 1450; DB 2; Length 508;
Best Local Similarity 60.2%; Pred. No. 3.8e-104;
Matches 263; Conservative 75; Mismatches 97; Indels 2; Gaps 2;.

Qy 6 QNKALPENVKYGVLDAGSSHTSYLYIKWPAEKENDTGVHVEECRVKPGTSKFKVKV 65
Db 39 QNKELPNKIKYGVLDAGSSHTSYLYIYEWPAEKENDTGVVQINECKVEGNGISSYGH 98
Qy 66 NEIGYILTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLN 125
Db 99 LKAGLSLQCKNKAQVPEKQRETVPYLGATAGMRLLRMTNATMAEVLSSVENTLRS 158
Qy 126 YPFDFQGARITQEGAGYMITNLYLLGKPSQKTRWFSIVPYETNNQETFGALDLGAS 185
Db 159 YPFDFQGARITQEGAGYMITNLYLLGKPSQKTRWFSIVPYETNNQETFGALDLGAS 217
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[illegible]

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Qy 187 QVTFVPMQNTIESPDNALQFRLYGKYNVYTHSFCLYCKDQA---LWOKLAKDIQVASNE 243
Db 210 QITFQP-GVTIEDKNTSVLFRLYGNTYSLYTHSYLCYGOIQASKRLMAALHQDGSYYQN- 267
Qy 244 ILRDPCHPHGKVKVNSDLYKTPCTKRFEMTLFPQOFBIOGIGNYQOCHOSILEFNLS 303
Db 268 -ISHPCYPKGYRRITIAEIVDSPVTPSMLSPAQILTVTGTGNPAACPTAILKLFNLT 326
Qy 304 YCPYSQCAFNGIFLPPLOQDGFASAFYFMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 363
Db 327 CGANRTCGFDGVYQPPVRGQFFAFAGFYTFSLNLTGQQ-SLSHVNATWDFCNKNWSE 385
Qy 364 IKTSYAGVKYKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYML 423
Db 386 LVETFPQNKKE-HLHTYCVVGLYILTLVLDGKFKDEHTWSNIHFSQKAGNADIGWTLGFML 444
Qy 424 NLTNMIPAE 432
Db 445 NLTNMIPTE 453

RESULT 15
Q90X66 PRELIMINARY; PRT; 493 AA.
AC Q90X66;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Ecto-ATP-diphosphohydrolase (EC 3.6.1.5).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OC NCBI_FaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21982040; PubMed=11985621;
RA Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
RT "Purification, characterization, cloning, and expression of the
RL chicken liver ecto-ATP-diphosphohydrolase."
DR Eur. J. Biochem. 269:2373-2382(2002).
DR EMBL; AF426405; AAL25086.1;
DR GO; GO:0004050; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
KW Hydrolase.
SQ SEQUENCE 493 AA; 54063 MW; 0380449E86167B70 CRC64;
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Query Match 42.1%; Score 997; DB 2; Length 493;
Best Local Similarity 45.7%; Pred. No. 6.1e-69;
Matches 196; Conservative 72; Mismatches 145; Indels 16; Gaps 7;

Qy 10 LPENVKGVILVDAGSSHTSLYIKWPAKENDTGVHGVVECRVKGPISKFVQKVNIEG 69
Db 35 LPPGTGYLVFDAGSTHTALYVQWPAKENGTVGVSQVCTVNGSGISSYADDPAAG 94
Qy 70 IYLTDCMERAREVTPRSQHTPVYLGATAGMRLLRMESEBELADRLDVVERSLSNYPFD 129
Db 95 ASLXPCLDKAMAVIPVEQWQOTPTVYLGATAGMRLLRMESEBELADRLDVVERSLSNYPFD 154
Qy 130 FQGARITQGEAGYGTITNYLLG---KFSQKTRWFSIVPYETNNQETFGALDGGAST 186
Db 155 FRGAQILTGNEEGSGFGLTVNLYLLTLTKFSFAGK-----EHPQNTFVLGALDGGAST 209
Qy 187 QVTFVPMQNTIESPDNALQFRLYGKYNVYTHSFCLYCKDQA---LWOKLAKDIQVASNE 243
Db 210 QITFQP-GVTIEDKNTSVLFRLYGNTYSLYTHSYLCYGOIQASKRLMAALHQDGSYYQN- 267
Qy 244 ILRDPCHPHGKVKVNSDLYKTPCTKRFEMTLFPQOFBIOGIGNYQOCHOSILEFNLS 303
Db 268 -ISHPCYPKGYRRITIAEIVDSPVTPSMLSPAQILTVTGTGNPAACPTAILKLFNLT 326
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Qy 304 YCPYSQCAFNGIFLPPLOQDGFASAFYFMKFLNLTSEKVSQEKVTMMKKFCAQPWEE 363
Db 327 CGANRTCGFDGVYQPPVRGQFFAFAGFYTFSLNLTGQQ-SLSHVNATWDFCNKNWSE 385
Qy 364 IKTSYAGVKYKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFIGIKIQGSDAGWTLGYML 423
Db 386 LVETFPQNKKE-HLHTYCVVGLYILTLVLDGKFKDEHTWSNIHFSQKAGNADIGWTLGFML 444
Qy 424 NLTNMIPAE 432
Db 445 NLTNMIPTE 453
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Search completed: March 7, 2005, 13:22:51
Job time : 63.0612 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 12:50:01 ; Search time 72.3686 Seconds
(without alignments)
2367.530 Million cell updates/sec

Title: US-09-835-147a-30_COPY_21_463
Perfect score: 2368
Sequence: 1 APTSTQNKALPENVKYIVL.....NLTMIPAEQLSTPLSHST 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : J. Geneseq_16Dec04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2368	100.0	463	3 AAY70925	Aay70925 Human sol
2	2368	100.0	463	3 AAY70902	Aay70902 Protein e
3	2353	99.4	454	3 AAY70913	Aay70913 Human sol
4	2353	99.4	454	3 AAY70890	Aay70890 Protein e
5	2353	99.4	473	3 AAY70924	Aay70924 Human sol
6	2353	99.4	473	3 AAY70901	Aay70901 Protein e
7	2353	99.4	474	3 AAY70923	Aay70923 Human sol
8	2353	99.4	474	3 AAY70900	Aay70900 Protein e
9	2353	99.4	476	3 AAY70911	Aay70911 Human CD3
10	2353	99.4	476	3 AAY70888	Aay70888 Protein e
11	2353	99.4	478	3 AAY70914	Aay70914 Human sol
12	2353	99.4	478	3 AAY70891	Aay70891 Protein e
13	2350	99.2	464	3 AAY70922	Aay70922 Human sol
14	2350	99.2	464	3 AAY70899	Aay70899 Protein e
15	2348	99.2	439	4 AAB71918	Aab71918 Soluble h
16	2348	99.2	487	3 AAY70921	Aay70921 Human sol
17	2348	99.2	487	3 AAY70898	Aay70898 Protein e
18	2348	99.2	510	2 AA04334	Aaw04334 Human lym
19	2348	99.2	510	2 AA04264	Aaw04264 Human CD3
20	2348	99.2	510	3 AAY70910	Aay70910 Human sol
21	2348	99.2	510	3 AAY70887	Aay70887 Human CD3
22	2348	99.2	510	4 AAB71917	Aab71917 Human sol
23	2348	99.2	510	7 ADJ57262	Adj57262 Human CD3
24	2348	99.2	510	8 ADL24295	Adl24295 Human CD3
25	2348	99.2	510	8 ADQ99453	Adq99453 Human CD3

ALIGNMENTS

RESULT 1

AAY70925

ID AAY70925 standard; protein; 463 AA.

XX AC AAY70925;

XX DT 17-AUG-2000 (first entry)

XX DE Human soluble CD39 fusion protein construct, IggkappaLeolCD39.

XX KW Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; Ig; immunoglobulin kappa.

OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Peptide 1..20

XX FT /label= Leader peptide

XX FT /note= "Derived from human immunoglobulin Ig kappa"

XX FT Cleavage-site 20..21

XX FT /note= "Cleavage site of leader sequence"

XX FT Region 21..24

XX FT /note= "Residues derived from human interleukin 2 (IL2)"

XX FT Protein 25..463

XX FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US022955.

XX PR 16-OCT-1998; 98US-0104585P.

XX PR 06-NOV-1998; 98US-0107466P.

XX PR 13-AUG-1999; 99US-0149010P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX XX

17-AUG-2000	(first entry)	Protein encoded by IgkappaSolCD39 construct.
Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiatic; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; IgkappaSolCD39 construct.		
Homo sapiens.		
Synthetic.		
Key	Location/Qualifiers	
Peptide	1..20	/note= "Igkappa leader sequence"
Cleavage-site	20..21	
Region	21..24	/note= "Derived from IL-2"
Region	25..463	/note= "Soluble portion of CD39"
Region	25..32	/note= "Derived from solCD39"
WO200023094-A2.		
27-APR-2000.		
13-OCT-1999;	99WO-US023641.	
16-OCT-1998;	98US-0104585P.	
06-NOV-1998;	98US-0107456P.	
13-AUG-1999;	99US-0149010P.	
(IMMV) IMMUNEX CORP.		
(CORR) CORNELL RES FOUND INC.		
Maliszewski CR, Gayle RB, Marcus AJ;		
WPI; 2000-339518/29.		
Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.		
Claim 6; Page 116-118; 118pp; English.		
The present sequence is the protein encoded by IgkappaSolCD39 construct. This is used for transient expression of soluble(sol)CD39 in recombinant cells for determining enzymatic activity and platelet inhibitory activity for each protein product. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke		

AA	Sequence 463 AA;	100.0%;	Score 2368;	DB 3;	Length 463;
SQ		Query Match	100.0%;	Pred. No. 7.2e-234;	
		Best Local Similarity	100.0%;		

WPI; 2000-339644/29.

New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiotensin and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.

Claim 6; Page 116-118; 122pp; English.

The present sequence is the fusion protein construct, IckkappaSolCD39. This construct comprises of the leader peptide from human immunoglobulin Ig kappa, linked to the soluble CD39 (solCD39) protein region by few residues derived from human interleukin 2 (hIL2). SolCD39 has apyrase activity and is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiotensin. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 463 AA;

Query Match	100.0%;	Score	2368;	DB	3;	Length	463;
Best Local Similarity	100.0%;	Pred. No.	7.2e-234;				
Matches	443;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

QY	1	APTSTQNKALPENVKYGI	VLDAGSSHTSLVIYK	WPAEKENDTG	VGHVQVEE	CKVKGPGISK	60
DB	21	APTSTQNKALPENVKYGI	VLDAGSSHTSLVIYK	WPAEKENDTG	VGHVQVEE	CKVKGPGISK	80
QY	61	FVQKNEIGIYLTDCMERAREV	IPRSQHQETPVY	LGATAGMRL	LMSESELAD	RVLVDVVE	120
DB	81	FVQKNEIGIYLTDCMERAREV	IPRSQHQETPVY	LGATAGMRL	LMSESELAD	RVLVDVVE	140
QY	121	RLSLNYPDFQCARII	TGQEBGAVGWIT	TINYLKGF	SQKTRFSP	IVPHTNNQETFGALD	180
DB	141	RLSLNYPDFQCARII	TGQEBGAVGWIT	TINYLKGF	SQKTRFSP	IVPHTNNQETFGALD	200
QY	181	LGGA	STQVTFVPQNTTIES	PDNALQFL	RKYGDNVY	THSFCLYCGKDAQWLQKLANDIQVA	240
DB	201	LGGA	STQVTFVPQNTTIES	PDNALQFL	RKYGDNVY	THSFCLYCGKDAQWLQKLANDIQVA	260
QY	241	SNEILLRDCPCFH	PGYKVVNVSDLYK	TPCTKRFEM	TLPPQOF	ETQIGNYYQCHQISILELF	300
DB	261	SNEILLRDCPCFH	PGYKVVNVSDLYK	TPCTKRFEM	TLPPQOF	ETQIGNYYQCHQISILELF	320
QY	301	NTSYCPYSQCAPNG	IFLPLQDGF	GAFAFYFV	WKFLNLTSEK	VSQEKYTEMWKKFCQAP	360
DB	321	NTSYCPYSQCAPNG	IFLPLQDGF	GAFAFYFV	WKFLNLTSEK	VSQEKYTEMWKKFCQAP	380
QY	361	WEEIKTSYAGVKEK	YLSYCFSGTV	YIISLLQ	QYHFTADSWE	HIHPIGKIQSDAGWTIG	420
DB	381	WEEIKTSYAGVKEK	YLSYCFSGTV	YIISLLQ	QYHFTADSWE	HIHPIGKIQSDAGWTIG	440
QY	421	YMLNLNTNMI	PAEQPLSTPL	SHST	443		
DB	441	YMLNLNTNMI	PAEQPLSTPL	SHST	463		

RESULT 2
AAY70902
ID AAY70902 standard; protein; 463 AA.
XX
XX AAY70902;
XX

Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISK 60
DB 21 APTSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISK 80

QY 61 FVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVE 120
DB 81 FVQKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVE 140

QY 121 RSLSNYPDFOGARIITGOEGAGYGWITINYLKGFSGKTRWFSIVPVETNNQETFGALD 180
DB 141 RSLSNYPDFOGARIITGOEGAGYGWITINYLKGFSGKTRWFSIVPVETNNQETFGALD 200

QY 181 LGGASTQVTFVFNQOTIESPDNALQFRLYKGDYNNYTHSFLCYGKQDQALWQKLAKDIQVA 240
DB 201 LGGASTQVTFVFNQOTIESPDNALQFRLYKGDYNNYTHSFLCYGKQDQALWQKLAKDIQVA 260

QY 241 SNEILRDCPFHFGYKVVNVDLYKTPCTKRFEMTLPQOQFEIQIGNYQOCHOSILELF 300
DB 261 SNEILRDCPFHFGYKVVNVDLYKTPCTKRFEMTLPQOQFEIQIGNYQOCHOSILELF 320

QY 301 NTSYCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKYSQEKVTMMKFCQAP 360
DB 321 NTSYCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKYSQEKVTMMKFCQAP 380

QY 361 WEEIKTSYAGVKYLSYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLG 420
DB 381 WEEIKTSYAGVKYLSYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLG 440

QY 421 YMLNLTNMIAPQPLSTPLSHST 443
DB 441 YMLNLTNMIAPQPLSTPLSHST 463

RESULT 3
AA70913
ID AA70913 standard; protein; 454 AA.

XX AA70913;
AC
XX
DT 17-AUG-2000 (first entry)
XX

Human soluble CD39 and IL2 N-terminus comprising fusion construct.

DE Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW anti-anginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
XX Protein 1..15
FT /label= Mature_human_interleukin_2
FT /note= "N-terminal region"
FT 16..454
FT Protein
FT /note= "Human soluble CD39 protein"

XX WO200023459-A1.
XX
XX
PD 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
PR

(IMMV) IMMUNEX CORP.
Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
WPI; 2000-339644/29.
N-PSDB; AAD00206.
New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
Claim 6a; Page 95-97; 122pp; English.

The present sequence is a fusion construct, comprising the N-terminal amino acids of mature human interleukin2 (IL2) and soluble CD39 (solCD39) region, that has apyrase activity. This results in high levels of solCD39 expression and activity in the transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preclampsia, embolism, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

XX Sequence 454 AA;

Query Match 99.4%; Score 2353; DB 3; Length 454;
Best Local Similarity 99.8%; Pred. No. 2.4e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISKPV 62
DB 14 SSTQNKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQVEECRVKPGISKPV 73

QY 63 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 122
DB 74 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 133

QY 123 LSNYPDFOGARIITGOEGAGYGWITINYLKGFSGKTRWFSIVPVETNNQETFGALDLG 182
DB 134 LSNYPDFOGARIITGOEGAGYGWITINYLKGFSGKTRWFSIVPVETNNQETFGALDLG 193

QY 183 GASTQVTFVFNQOTIESPDNALQFRLYKGDYNNYTHSFLCYGKQDQALWQKLAKDIQVASN 242
DB 194 GASTQVTFVFNQOTIESPDNALQFRLYKGDYNNYTHSFLCYGKQDQALWQKLAKDIQVASN 253

QY 243 EILRDCPFHFGYKVVNVDLYKTPCTKRFEMTLPQOQFEIQIGNYQOCHOSILELFNT 302
DB 254 EILRDCPFHFGYKVVNVDLYKTPCTKRFEMTLPQOQFEIQIGNYQOCHOSILELFNT 313

QY 303 SYCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKYSQEKVTMMKFCQAPWE 362
DB 314 SYCPYSQCAFNGIFLPLQDGFAGSAFYVMKFLNLTSEKYSQEKVTMMKFCQAPWE 373

QY 363 EIKTSYAGVKYLSYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLG 422
DB 374 EIKTSYAGVKYLSYCFSGTYILSLLLQGYHFTADSWEHIFIGIKQSDAGWTLG 433

QY 423 LNLNLTNMIAPQPLSTPLSHST 443
DB 434 LNLNLTNMIAPQPLSTPLSHST 454

RESULT 4

AAV70890	Query Match	99.4%;	Score 2353;	DB 3;	Length 454;
ID AAY70890 standard; protein; 454 AA.	Best Local Similarity	99.8%;	Pred No. 2.4e-232;		
XX	Matches 440;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
AC AAY70890;					
XX	17-AUG-2000	(first entry)			
DT					
XX					
DE					
XX	Protein encoded by fusion construct of human soluble CD39 cDNA-1.				
XX	Soluble CD39; ADP-induced platelet activation; platelet aggregation;				
KW	unstable angina; myocardial infarction; stroke; coronary artery disease;				
KW	atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;				
KW	platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;				
KW	cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;				
KW	cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;				
KW	peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;				
KW	PE; pulmonary embolism; transient ischaemic attack; thrombus formation;				
KW	occlusion; reocclusion; stenosis; restenosis; angiogenesis;				
KW	cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;				
KW	coronary ischaemia; vascular occlusion.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
XX					
XX	Key	Location/Qualifiers			
FT	Protein	1..15			
FT		/label= Mature human interleukin_2			
FT		/note= "N-terminal region"			
FT	Protein	16..454			
FT		/note= "Human soluble CD39 protein"			
XX					
XX	WO200023094-A2.				
XX					
XX	27-APR-2000.				
XX					
XX	13-OCT-1999;	99WO-US023641.			
XX					
PR	16-OCT-1998;	98US-0104585P.			
PR	06-NOV-1999;	98US-0107468P.			
PR	13-AUG-1999;	99US-0149010P.			
XX					
XX	(IMV) IMMUNEX CORP.				
PA	(CORR) CORNELL RES. FOUND INC.				
XX					
XX	Maliszewski CR, Gayle RB, Marcus AJ;				
XX					
XX	WPI; 2000-339518/29.				
XX	N-PSDB; AAD00201.				
XX					
XX	Inhibiting platelet activation and recruitment, useful for treating a				
PT	mammal suffering from unstable angina, myocardial infarction, stroke,				
PT	coronary artery disease or injury, comprises administering soluble CD39				
PT	polypeptides.				
XX					
PS	Claim 6; Page 95-97; 118pp; English.				
XX					
CC	The present sequence is the protein encoded by a fusion construct of				
CC	sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from				
CC	the N-terminus of mature human IL2 to the solCD39 coding region results				
CC	in high levels of both expression and activity in the supernatants of				
CC	transfected cells. This is used in the treatment of unstable angina,				
CC	myocardial infarction, stroke, coronary artery disease or injury,				
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,				
CC	platelet-associated ischaemic disorder including lung ischaemia, coronary				
CC	ischaemia and cerebral ischaemia, thrombotic disorder including coronary				
CC	artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,				
CC	peripheral artery thrombosis, venous thrombosis, thrombosis,				
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),				
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing				
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or				
CC	restenosis of blood vessels or stroke				
XX					
SQ	Sequence 454 AA;				

13-OCT-1999; 99WO-US022955.
 16-OCT-1998; 98US-0104585P.
 06-NOV-1998; 98US-0107466P.
 13-AUG-1999; 99US-0149010P.
 (IMMV) IMMUNEX CORP.
 Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 WPI; 2000-339644/29.
 New soluble CD39 polypeptides having apyrase activity, useful for
 inhibiting angiogenesis and treating unstable angina, myocardial
 infarction, stroke, coronary artery disease or injury.
 Claim 6; Page 114-116; 122pp; English.
 The present sequence is the fusion protein construct, pIL2LTrim4. This
 construct comprises of the leader peptide from human interleukin 2 (hIL2)
 and soluble CD39 (solCD39) protein region, having apyrase activity.
 Soluble CD39 is constructed by removing the N- and C-terminal
 transmembrane domains. It retains the capacity to metabolise ATP and ADP
 at relevant concentrations and the ability to block and reverse ADP-
 induced platelet activation and recruitment, including platelet
 aggregation. Soluble CD39 polypeptides are useful for inhibiting
 angiogenesis. It is useful for the treatment of unstable angina, stroke,
 myocardial infarction, coronary artery disease or injury, embolism,
 associated ischaemic disorders including lung, coronary and cerebral
 ischaemia, thrombotic disorders including coronary, peripheral and
 cerebral artery thrombosis, intracardiac and venous thrombosis,
 coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
 transient ischaemic attack. Soluble CD39 is also useful for preventing
 thrombus formation or reformation, occlusion, reocclusion, stenosis or
 restenosis of blood vessels or stroke

Query Match 99.4%; Score 2353; DB 3; Length 473;
 Best Local Similarity 99.8%; Pred. No. 2.6e-232;
 Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 3 TSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVHQQVECRVKGPGISKVF 62
 33 SSTONKALPENKYGIVLDAGSSHTSLYIKWPAEKENDTGVHQQVECRVKGPGISKVF 92
 63 QKNEIGIYLTDCMERARVIPSQHOETPVYLGATAGWRLRMESEELADRVLDVVERS 122
 93 QKNEIGIYLTDCMERARVIPSQHOETPVYLGATAGWRLRMESEELADRVLDVVERS 152
 123 LSNYPDFOGARIITQGBEGAGWITINVLGKFSQKTRWFSIYPYETNNQSTFGALDLG 182
 153 LSNYPDFOGARIITQGBEGAGWITINVLGKFSQKTRWFSIYPYETNNQSTFGALDLG 212
 183 GASTQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 242
 213 GASTQVTFVFPQNTIESPDNALQFRLYKGDYNNVYTHSFLCYGKQALWQKLAKDIQVASN 272
 243 EILRDPCHPGKVVNVDLYKTPCTKRFEMTLFPQFEIQQIGNYQCHQSILELFNT 302
 273 EILRDPCHPGKVVNVDLYKTPCTKRFEMTLFPQFEIQQIGNYQCHQSILELFNT 332
 303 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
 333 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 392
 363 EIKTSVAGKVEKYLSEYCFSGYIILSLLOQGHFTADSWEHFTGKIQGSDAGWTLYGM 422
 393 EIKTSVAGKVEKYLSEYCFSGYIILSLLOQGHFTADSWEHFTGKIQGSDAGWTLYGM 452
 423 LNLTNMIPAEQPLSTPLSHST 443

Db 453 LNLTNMIPAEQPLSTPLSHST 473

RESULT 6
 AAY70901
 ID AAY70901 standard; protein; 473 AA.
 XX
 AC AAY70901;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by Trim 4 construct.
 XX
 DE Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiac;
 KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;
 KW coronary ischaemia; vascular occlusion; pIL2Trim4 variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 26..27
 FT Protein 35..473
 FT /notes "Soluble portion of CD39"
 XX
 PN W0200023094-A2.
 XX
 PD 27-APR-2000.
 XX
 XX 13-OCT-1999; 99WO-US023641.
 XX
 PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX
 PA (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Maliszewski CR, Gayle RB, Marcus AJ;
 XX
 XX WPI; 2000-339518/29.
 XX
 PT Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.
 XX
 XX Example 11; Page 114-116; 118pp; English.
 XX
 CC The present sequence is the protein encoded by Trim4 construct. pIL2Trim4
 CC variant was constructed by removing the human IL2 residues from solCD39
 CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
 CC human IL2 to the solCD39 coding region results in high levels of both
 CC expression and activity in the supernatants of transfected cells. SolCD39
 CC is used in the treatment of unstable angina, myocardial infarction,
 CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
 CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
 CC disorder including lung ischaemia, coronary ischaemia and cerebral
 CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
 CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
 CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
 CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
 CC Soluble CD39 is also useful for preventing thrombus formation or
 CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
 CC vessels or stroke

```
XX SQ Sequence 473 AA;
Query Match 99.4%; Score 2353; DB 3; Length 473;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TSTQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKPGISKVF 62
Db 33 SSTQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKPGISKVF 92
Qy 63 QKVEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 122
Db 93 QKVEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 152
Qy 123 LSNYPDFQOARIITGOEGAYGWITINLLGKFSQKTRWFSIVPVETNNOETFGALDLG 182
Db 153 LSNYPDFQOARIITGOEGAYGWITINLLGKFSQKTRWFSIVPVETNNOETFGALDLG 212
Qy 183 GASTQVTFVPOQTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 242
Db 213 GASTQVTFVPOQTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 272
Qy 243 EILRDPCHFGPGYKKVNVNVDLYKTPCTKRPFMTLPFQOQFIQIGNTYQQCHQSILELFNT 302
Db 273 EILRDPCHFGPGYKKVNVNVDLYKTPCTKRPFMTLPFQOQFIQIGNTYQQCHQSILELFNT 332
Qy 303 SYCYSQCAENGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE 362
Db 333 SYCYSQCAENGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE 392
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 422
Db 393 EIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 452
Qy 423 LNLTNMIPAEQPLSTPLSHST 443
Db 453 LNLTNMIPAEQPLSTPLSHST 473
RESULT 7
AAV70923
ID AAV70923 standard; protein; 474 AA.
XX
AC AAV70923;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, pIL2LTrim3.
XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW anti-angiogenic; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX PH 1..24
XX FT /label= Leader_peptide
XX FT /note= "Derived from human interleukin 2 (hIL2)"
XX FT Cleavage-site 24..25
XX FT /note= "Cleavage site of leader sequence"
XX FT Protein 36..474
XX FT /note= "Human soluble CD39 protein"
XX
PN WO200023459-A1.
XX
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PD 27-APR-2000.
XX
XX PF 13-OCT-1999; 99WO-US022955.
XX
PR 16-OCT-1998; 98US-0104585P.
PR 06-NOV-1998; 98US-0107466P.
PR 13-AUG-1999; 99US-0149010P.
XX
XX PA (IMV ) IMMUNEX CORP.
XX
XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 113-114; 122pp; English.
XX
XX The present sequence is the fusion protein construct, pIL2LTrim3. This
XX construct comprises of the leader peptide from human interleukin 2 (hIL2)
XX and soluble CD39 (solCD39) protein region, having apyrase activity.
XX Soluble CD39 is constructed by removing the N- and C-terminal
XX transmembrane domains. It retains the capacity to metabolise ATP and ADP
XX at relevant concentrations and the ability to block and reverse ADP-
XX induced platelet activation and recruitment, including platelet
XX aggregation. Soluble CD39 polypeptides are useful for inhibiting
XX angiogenesis. It is useful for the treatment of unstable angina, stroke,
XX myocardial infarction, coronary artery disease or injury, embolism,
XX atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-
XX associated ischaemic disorders including lung, coronary and cerebral
XX ischaemia, thrombotic disorders including coronary, peripheral and
XX cerebral artery thrombosis, intracardiac and venous thrombosis,
XX coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and
XX transient ischaemic attack. Soluble CD39 is also useful for preventing
XX thrombus formation or reformation, occlusion, reocclusion, stenosis or
XX restenosis of blood vessels or stroke
XX
XX Sequence 474 AA;
```

```
Query Match 99.4%; Score 2353; DB 3; Length 474;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TSTQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKPGISKVF 62
Db 33 SSTQNKALPENVKYIGVLDAGSSHTSLIYKWPAAEKENDTGVVHQBECRVKPGISKVF 93
Qy 63 QKVEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 122
Db 94 QKVEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 153
Qy 123 LSNYPDFQOARIITGOEGAYGWITINLLGKFSQKTRWFSIVPVETNNOETFGALDLG 182
Db 154 LSNYPDFQOARIITGOEGAYGWITINLLGKFSQKTRWFSIVPVETNNOETFGALDLG 213
Qy 183 GASTQVTFVPOQTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 242
Db 214 GASTQVTFVPOQTIESPDNALQFRLYGKDYNYVTHSFLCYGKDQALWQKLAKDIOVASN 273
Qy 243 EILRDPCHFGPGYKKVNVNVDLYKTPCTKRPFMTLPFQOQFIQIGNTYQQCHQSILELFNT 302
Db 274 EILRDPCHFGPGYKKVNVNVDLYKTPCTKRPFMTLPFQOQFIQIGNTYQQCHQSILELFNT 333
Qy 303 SYCYSQCAENGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE 362
Db 334 SYCYSQCAENGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE 393
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 422
Db 394 EIKTSYAGVKEKYLSEYCFSGTYILSLLOGYHFTADSWEHIFIGIKQSDAGWTILGYM 453
```

QY 423 LNLTNMIPAEQPLSTPLSHST 443
Db 454 LNLTNMIPAEQPLSTPLSHST 474

RESULT 8
AA70900
ID AAY70900 standard; protein; 474 AA.
XX
AC AAY70900;
XX
DT 17-AUG-2000 (first entry)
XX
DE Protein encoded by Trim 3 construct.

Soluble CD39; ADP-induced platelet activation; platelet aggregation;
unstable angina; myocardial infarction; stroke; coronary artery disease;
atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
peripheral artery thrombosis; coagulopathy; deep venous thrombosis;
PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
occlusion; reocclusion; stenosis; restenosis; angiogenesis; antidiabetic;
cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
coronary ischaemia; vascular occlusion; p112Trim3 variant.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT Cleavage-site 24..25
FT Protein 36..474
/note= "Soluble portion of CD39"

XX WO200023094-A2.
XX
XX
XX PD 27-APR-2000.
XX
XX PF 13-OCT-1999; 99WO-US023641.
XX
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX
XX PA (IMKV) IMMUNEX CORP.
XX (CORR) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339518/29.

XX Inhibiting platelet activation and recruitment, useful for treating a
XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.

XX Example 11; Page 113-114; 118pp; English.

XX The present sequence is the protein encoded by Trim3 construct. p112Trim3
XX variant was constructed by removing the human IL2 residues from solCD39
XX fusion construct. Fusion of 12 amino acids from the N-terminus of mature
XX human IL2 to the solCD39 coding region results in high levels of both
XX expression and activity in the supernatants of transfected cells. SolCD39
XX is used in the treatment of unstable angina, myocardial infarction,
XX stroke, coronary artery disease or injury, atherosclerosis, peripheral
XX vascular occlusion, pre-eclampsia, embolism, platelet-associated ischaemic
XX disorder including lung ischaemia, coronary ischaemia and cerebral
XX ischaemia, a thrombotic disorder including coronary artery thrombosis,
XX cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
XX thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
XX thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
XX Soluble CD39 is also useful for preventing thrombus formation or

CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke
XX
SQ Sequence 474 AA;

Query Match 99.4%; Score 2353; DB 3; Length 474;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKV 62
Db :|||||
34 SSTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVEECRVKPGISKV 93
63 QKVNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLRMESEELADRVLDVRS 122
Db :|||||
94 QKVNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGMRLRMESEELADRVLDVRS 153
QY 123 LSNYPDFQGARITITQEGAYGMITINYLKGSOKTRWFSIVPYETNNQETFGALDILG 182
Db :|||||
154 LSNYPDFQGARITITQEGAYGMITINYLKGSOKTRWFSIVPYETNNQETFGALDILG 213
QY 183 GASTQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSLCYGKQALWQKLAKDIQVASN 242
Db :|||||
214 GASTQVTFVPPQNTIESPDNALQFRLYKDYNNVYTHSLCYGKQALWQKLAKDIQVASN 273
QY 243 EILRDPCHPGYKXVNVSDLYKTPCTKRFEMTLPPQFQFQIGIGNYQCHQSILELPT 302
Db :|||||
274 EILRDPCHPGYKXVNVSDLYKTPCTKRFEMTLPPQFQFQIGIGNYQCHQSILELPT 333
QY 303 SYCPYSQCAFNGIFLPLQGDGFAFSAFYFMKELNLTSEKVSQKVTMMKKFCAQPMW 362
Db :|||||
334 SYCPYSQCAFNGIFLPLQGDGFAFSAFYFMKELNLTSEKVSQKVTMMKKFCAQPMW 393
QY 363 BIKTSYAGVKEKYLSEYCFSGTYILSLLLQGHFTADSWEHIFTKIQGSDAGWTLGYM 422
Db :|||||
394 BIKTSYAGVKEKYLSEYCFSGTYILSLLLQGHFTADSWEHIFTKIQGSDAGWTLGYM 453
423 LNLTNMIPAEQPLSTPLSHST 443
454 LNLTNMIPAEQPLSTPLSHST 474

RESULT 9
AA70911
ID AAY70911 standard; protein; 476 AA.
XX
XX AC AAY70911;
XX
XX DT 17-AUG-2000 (first entry)
XX
XX DE Human CD39-L4-1 protein construct.
XX
XX KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;
XX unstable angina; myocardial infarction; stroke; coronary artery disease;
XX atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;
XX platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
XX coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
XX thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
XX antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;
XX cardiant; vasotropic; thrombolytic.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT Region 1..37
FT Cleavage-site 20..21
/note= "Human CD39-L4 protein N-terminal end"
FT FT
FT Cleavage-site 20..21
/note= "Cleavage site of leader sequence"
FT Region 38..476
/note= "Human soluble CD39 protein"
XX
XX WO200023459-A1.

XX PD 27-APR-2000.
 XX PF 13-OCT-1999; 99WO-US022955.
 XX PR 16-OCT-1998; 98US-0104585P.
 XX PR 06-NOV-1998; 98US-0107466P.
 XX PR 13-AUG-1999; 99US-0149010P.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX WPI; 2000-339644/29.
 XX DR
 XX PT New soluble CD39 polypeptides having apyrase activity, useful for
 XX PT inhibiting angiogenesis and treating unstable angina, myocardial
 XX PT infarction, stroke, coronary artery disease or injury.
 XX PS Claim 6; Page 89-91; 122pp; English.
 XX SS
 XX CC The present sequence is a fusion protein construct CD39-L4-1, comprising
 CC CC the human CD39-L4 N-terminal region and soluble CD39 protein. CD39-L4 is
 CC CC a secreted apyrase, belonging to the CD39 family. Soluble CD39 is
 CC CC constructed by removing the N- and C-terminal transmembrane domains. It
 CC CC retains the capacity to metabolise ATP and ADP at relevant concentrations
 CC CC and the ability to block and reverse ADP-induced platelet activation and
 CC CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC CC are useful for inhibiting angiogenesis. It is useful for the treatment of
 CC CC unstable angina, myocardial infarction, stroke, coronary artery disease
 CC CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
 CC CC embolism, platelet-associated ischaemic disorders including lung,
 CC CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
 CC CC peripheral and cerebral artery thrombosis, intracardiac and venous
 CC CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
 CC CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
 CC CC for preventing thrombus formation or reformation, occlusion, reocclusion,
 CC CC stenosis or restenosis of blood vessels or stroke
 XX SS
 XX SQ Sequence 476 AA;
 Query Match 99.4%; Score 2353; DB 3; Length 476;
 Best Local Similarity 99.8%; Pred. No. 2.6e-232;
 Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TSTQNKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKVF 62
 Db :|||||
 QY 36 SSTQNKALPENVKYGIVLDAGSSHTSLYIKWPAEKENDTGTVHQVEECRVKGGISKVF 95
 Db :|||||
 QY 63 QKVNIEIGYLTDCMERAREVTPRSOHTPPYVLGATGWRLLRWESEELADRVLDVVERS 122
 Db :|||||
 QY 96 QKVNIEIGYLTDCMERAREVTPRSOHTPPYVLGATGWRLLRWESEELADRVLDVVERS 155
 Db :|||||
 QY 123 LSNYPDFQGARIIITQBEAGYGMWITINYLKGFQKTRWFSIVPYETNNQETFGALDLG 182
 Db :|||||
 QY 156 LSNYPDFQGARIIITQBEAGYGMWITINYLKGFQKTRWFSIVPYETNNQETFGALDLG 215
 Db :|||||
 QY 183 GASTQVTFVQNTQIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDQVASN 242
 Db :|||||
 QY 216 GASTQVTFVQNTQIESPDNALQFRLYKDYNNVYTHSFLCYGKQDALWQKLAKDQVASN 275
 Db :|||||
 QY 243 EILRDPCHPGYKVVNYSDLVKTCTKRFEMTLPPQFQELQIGNYQQCHQSILELNT 302
 Db :|||||
 QY 276 EILRDPCHPGYKVVNYSDLVKTCTKRFEMTLPPQFQELQIGNYQQCHQSILELNT 335
 Db :|||||
 QY 303 SYCPYSQCAFNGIFLPPQGDGFAFSAFYVNMFLNLTSEKVSQKVBKTEMKKFCAQPWE 362
 Db :|||||
 QY 336 SYCPYSQCAFNGIFLPPQGDGFAFSAFYVNMFLNLTSEKVSQKVBKTEMKKFCAQPWE 395
 Db :|||||
 QY 363 EIKTSYAGVKEKYLEBECPSGNYIISLLIQGHFTADSWEHHTFKTGSDAGHTLGYM 422
 Db :|||||
 QY 396 EIKTSYAGVKEKYLEBECPSGNYIISLLIQGHFTADSWEHHTFKTGSDAGHTLGYM 455
 Db :|||||

QY 423 LNLTNMIPAEQPLSTPLSHST 443
 Db :|||||
 Db 456 LNLTNMIPAEQPLSTPLSHST 476
 RESULT 10
 AAY70888
 ID AAY70888 standard; protein; 476 AA.
 XX AC AAY70888;
 XX DT 17-AUG-2000 (first entry)
 XX DE Protein encoded by CD39-L4-1 construct.
 XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
 KW coronary ischaemia; vascular occlusion.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Region 1..37
 FT /note= "Derived from CD39-L4"
 FT Cleavage-site 20..21
 FT Region 38..476
 FT /note= "Soluble portion of CD39"
 XX PN WC200023094-A2.
 XX PD 27-APR-2000.
 XX PF 13-OCT-1999; 99WO-US023641.
 XX PR 16-OCT-1998; 98US-0104585P.
 PR 06-NOV-1998; 98US-0107466P.
 PR 13-AUG-1999; 99US-0149010P.
 XX (IMMV) IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI; 2000-339518/29.
 XX DR
 XX PT Inhibiting platelet activation and recruitment, useful for treating a
 PT mammal suffering from unstable angina, myocardial infarction, stroke,
 PT coronary artery disease or injury, comprises administering soluble CD39
 PT polypeptides.
 XX Claim 6; Page 89-91; 118pp; English.
 XX PS
 XX CC The present sequence is a fusion construct of human soluble CD39 encoded
 CC CC by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the
 CC CC CD39 family. The fusion construct is used for the expression and activity
 CC CC of soluble CD39 in CHO (chinese hamster ovary) cells. Soluble CD39
 CC CC retains the capacity of wildtype CD39 to metabolise ATP and ADP at
 CC CC physiologically relevant concentrations as well as the ability to block
 CC CC and reverse ADP-induced platelet activation and recruitment including
 CC CC platelet aggregation. This is used in the treatment of unstable angina,
 CC CC myocardial infarction, stroke, coronary artery disease or injury,
 CC CC atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,
 CC CC platelet-associated ischaemic disorder including lung ischaemia, coronary
 CC CC ischaemia and cerebral ischaemia, thrombotic disorder including coronary

```
CC artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis,
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
CC transient ischaemic attack. Soluble CD39 is also useful for preventing
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or
CC restenosis of blood vessels or stroke
XX
SQ Sequence 476 AA;

Query Match          99.4%; Score 2353; DB 3; Length 476;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFV 62
Db :|||||
36 SSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFV 95
Qy 63 QKVNIEGILYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVRS 122
Db :|||||
96 QKVNIEGILYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVRS 155
Qy 123 LSNYPFDFQGARITITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 182
Db :|||||
156 LSNYPFDFQGARITITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 215
Qy 183 GASTQVTFVFPQNTIESPDNALQFRLYKGVNVVTHSFLCYGKDQALWQKLAKDIQVASN 242
Db :|||||
216 GASTQVTFVFPQNTIESPDNALQFRLYKGVNVVTHSFLCYGKDQALWQKLAKDIQVASN 275
Qy 243 EILRDPCHPGYKVKVNVSDLYKTPCTKRFEMTLFPQGFQEGTGNVQCHQSILELNT 302
Db :|||||
276 EILRDPCHPGYKVKVNVSDLYKTPCTKRFEMTLFPQGFQEGTGNVQCHQSILELNT 335
Qy 303 SYCPYSQCAFNGIFLPLPQGFQAFSAFYFMKFLNLTSEKVSQEKVTMMKKFCAQDWE 362
Db :|||||
336 SYCPYSQCAFNGIFLPLPQGFQAFSAFYFMKFLNLTSEKVSQEKVTMMKKFCAQDWE 395
Qy 363 EIKTSYAGVKEKYLSEYCFSTGYILSLLLQGHFTADSWEHIFIGIKQSDAGWTILGYM 422
Db :|||||
396 EIKTSYAGVKEKYLSEYCFSTGYILSLLLQGHFTADSWEHIFIGIKQSDAGWTILGYM 455
Qy 423 LNLTNMTPAEQPLSTPLSHST 443
Db :|||||
456 LNLTNMTPAEQPLSTPLSHST 476

RESULT 11
ID AAY70914 standard; protein; 478 AA.
AC
XX
XX AAY70914;
XX
DT 17-AUG-2000 (first entry)
DE
DE Human soluble CD39 fusion protein construct, pIL2LsolCD39.
XX
XX Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW anti-angiogenic; cerebroprotective; antiarteriosclerotic; anticoagulant;
KW cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1.24
FT Peptide
FT /label= Leader peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT Protein
FT 25.36
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FT /label= Mature human interleukin 2
FT /note= "Derived from N-terminal end of human IL2"
FT Region 37..39
FT Protein /note= "Linker"
FT 40..478
FT /note= "Human soluble CD39 protein"
XX
XX W0200023459-A1.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US022955.
XX
XX 16-OCT-1998; 98US-0104585P.
XX 06-NOV-1998; 98US-0107466P.
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX N-PSDB; AAD00207.
XX
XX New soluble CD39 polypeptides having apyrase activity, useful for
XX inhibiting angiogenesis and treating unstable angina, myocardial
XX infarction, stroke, coronary artery disease or injury.
XX
XX Disclosure; Page 99-101; 122pp; English.
XX
XX The present sequence is a fusion construct pIL2LsolCD39, comprising the
XX leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
XX mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,
XX having apyrase activity. This produces high levels of solCD39 expression
XX and activity in the transfected cells. Soluble CD39 is constructed by
XX removing the N- and C-terminal transmembrane domains. It retains the
XX capacity to metabolise ATP and ADP at relevant concentrations and the
XX ability to block and reverse ADP-induced platelet activation and
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides
XX are useful for inhibiting angiogenesis. It is useful for the treatment of
XX unstable angina, myocardial infarction, stroke, coronary artery disease
XX or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,
XX embolism, platelet-associated ischaemic disorders including lung,
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,
XX peripheral and cerebral artery thrombosis, intracardiac and venous
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
XX for preventing thrombus formation or reformation, occlusion, reocclusion,
XX stenosis or restenosis of blood vessels or stroke
XX
XX SQ Sequence 478 AA;

Query Match          99.4%; Score 2353; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFV 62
Db :|||||
38 SSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHQVECRVKGPGISKFV 97
Qy 63 QKVNIEGILYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVRS 122
Db :|||||
98 QKVNIEGILYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESELADRLVDVVRS 157
Qy 123 LSNYPFDFQGARITITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 182
Db :|||||
158 LSNYPFDFQGARITITGOEGAYGWITINYLKGFSQKTRWFSIVPYETNNQETFGALDLG 217
Qy 183 GASTQVTFVFPQNTIESPDNALQFRLYKGVNVVTHSFLCYGKDQALWQKLAKDIQVASN 242
Db :|||||
218 GASTQVTFVFPQNTIESPDNALQFRLYKGVNVVTHSFLCYGKDQALWQKLAKDIQVASN 277
Qy 243 EILRDPCHPGYKVKVNVSDLYKTPCTKRFEMTLFPQGFQEGTGNVQCHQSILELNT 302
```

```
Db 278 EILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPQQFEIQGNYQQHQSIILEFNT 337
Qy 303 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
Db 338 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 422
Db 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 457
Qy 423 LNLTNMIPAEQPLSTPLSHST 443
Db 458 LNLTNMIPAEQPLSTPLSHST 478

RESULT 12
AA70891
ID AAY70891 standard; protein; 478 AA.
XX
AC AAY70891;
XX
DT 17-AUG-2000 (first entry)
XX
DE Protein encoded by pIL2Lsol CD39.
XX
KW Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; stroke; coronary artery disease;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombotic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antidiagonal; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
KW coronary ischaemia; vascular occlusion.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Location/Qualifiers
FT Peptide 1..24
FT Protein /note= "huIL2 leader sequence"
FT Protein 25..36
FT Region 37..39
FT Protein /note= "Linker"
FT Protein 40..478
FT Protein /note= "SolCD39 protein"
XX
WO200023094-A2.
XX
27-APR-2000.
XX
13-OCT-1999; 99WO-US023641.
XX
16-OCT-1998; 98US-0104585P.
XX
06-NOV-1998; 98US-0107466P.
XX
13-AUG-1999; 99US-0149010P.
XX
(IMMV ) IMMUNEX CORP.
XX
(CORR ) CORNELL RES FOUND INC.
XX
Maliszewski CR, Gayle RB, Marcus AJ;
XX
WPI; 2000-339518/29.
XX
N-PSDB; AAD00202.
XX
Inhibiting platelet activation and recruitment, useful for treating a
XX
mammal suffering from unstable angina, myocardial infarction, stroke;
XX
coronary artery disease or injury, comprises administering soluble CD39
XX
polypeptides.
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XX Disclosure; Page 99-101; 118pp; English.
XX
CC The present sequence is protein encoded by the coding region of
CC pIL2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase
CC activity. Fusion of 12 amino acids from the N-terminus of mature human
CC IL2 to the solCD39 coding region results in high levels of both
CC expression and activity in the supernatants of transfected cells. This is
CC used in the treatment of unstable angina, myocardial infarction, stroke,
CC coronary artery disease or injury, atherosclerosis, peripheral vascular
CC occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder
CC including lung ischaemia, coronary ischaemia and cerebral ischaemia, a
CC thrombotic disorder including coronary artery thrombosis, cerebral artery
CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT),
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
CC useful for preventing thrombus formation or reformation, occlusion,
CC reocclusion, stenosis or restenosis of blood vessels or stroke
XX
SQ Sequence 478 AA;
XX
Query Match 99.4%; Score 2353; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 2.6e-232;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFV 62
Db 38 SSTQNKALPENVKYGVILVDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKGGISKFV 97
Qy 63 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS 122
Db 98 QKVNIEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMELLRMESEELADRVLDVVERS 157
Qy 123 LSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 182
Db 158 LSNYPDFQGARITGOEGAYGWITINYLKGFQSKTRWFSIVPYETNNQETFGALDLG 217
Qy 183 GASTQVTFVQNGTIESPDNALQFRLYKDYVYTHSFLCYGKDQALWQKLAKDIOVASN 242
Db 218 GASTQVTFVQNGTIESPDNALQFRLYKDYVYTHSFLCYGKDQALWQKLAKDIOVASN 277
Qy 243 EILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPQQFEIQGNYQQHQSIILEFNT 302
Db 278 EILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPQQFEIQGNYQQHQSIILEFNT 337
Qy 303 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
Db 338 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 422
Db 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFIGIKQSDAGWTILGYM 457
Qy 423 LNLTNMIPAEQPLSTPLSHST 443
Db 458 LNLTNMIPAEQPLSTPLSHST 478

RESULT 13
AA70922
ID AAY70922 standard; protein; 464 AA.
XX
AC AAY70922;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human soluble CD39 fusion protein construct, pIL2Ltrim1.
XX
KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;
```

KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;
KW antidiagonal; cerebroprotective; antiarteriosclerotic; anticoagulant;
XX cardiac; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
OS Homo sapiens.
XX Synthetic.
FH Key
FT Peptide
FT 1..24
FT /label= Leader peptide
FT /note= "Derived from human interleukin 2 (hIL2)"
FT Cleavage-site
FT 24..25
FT /note= "Cleavage site of leader sequence"
FT Protein
FT 26..464
FT /note= "Human soluble CD39 protein"
XX WO20023459-A1.
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US022955.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMMUNEX CORP.
XX PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
XX WPI; 2000-339644/29.
XX DR
XX New soluble CD39 polypeptides having apyrase activity, useful for
PT inhibiting angiogenesis and treating unstable angina, myocardial
PT infarction, stroke, coronary artery disease or injury.
XX
XX Claim 6; Page 111-112; 122pp; English.
XX
XX The present sequence is the fusion protein construct, pIL2LTrim1. This
CC construct comprises of the leader peptide from human interleukin 2 (hIL2)
CC and soluble CD39 (solCD39) protein region, having apyrase activity. The
CC two regions are joined by an intervening Ala residue. Soluble CD39 is
CC constructed by removing the N- and C-terminal transmembrane domains. It
CC retains the capacity to metabolise ATP and ADP at relevant concentrations
CC and the ability to block and reverse ADP-induced platelet activation and
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
CC are useful for inhibiting angiogenesis. It is useful for the treatment of
CC unstable angina, stroke, myocardial infarction, coronary artery disease
CC or injury, embolism, atherosclerosis, peripheral vascular occlusion,
CC preclampsia, platelet-associated ischaemic disorders including lung,
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,
CC peripheral and cerebral artery thrombosis, intracardiac and venous
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful
CC for preventing thrombus formation or reformation, occlusion, reocclusion,
CC stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 464 AA;
Query Match 99.2%; Score 2350; DB 3; Length 464;
Best Local Similarity 99.5%; Pred. No. 5.1e-232;
Matches 439; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 TSTQKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHGVHVECRVKPGISKFV 62
DB ::
DB 24 SATQKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGTVHGVHVECRVKPGISKFV 83
QY 63 OKVNEIGLYLDCMERAREVIPSQHOETPVYLGATGMRLLRMESESLADRVLDVRS 122
DB 84 OKVNEIGLYLDCMERAREVIPSQHOETPVYLGATGMRLLRMESESLADRVLDVRS 143
QY 123 LSNYPDFQARIITGQEGAYGWTITNVLGKFSQKTRWFSIVPYETNNQTFGALDGLG 182

Db 144 LSNYPDFQARIITGQEGAYGWTITNVLGKFSQKTRWFSIVPYETNNQTFGALDGLG 203
QY 183 GASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 242
Db 204 GASTQVTFVPQNTIESPDNALQFRLYGKDYNNVYTHSFLCYGKDQALWQKLAKDIQVASN 263
QY 243 EILRDPCHPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQTGNYQCQHSIILEFNT 302
Db 264 EILRDPCHPGYKVVVNSDLYKTPCTKRFEMTLPFQOFEIQTGNYQCQHSIILEFNT 323
QY 303 SYCPYSQCAFNGIFLPPLOQDGFASFYFVWKFNLNTSEKVSQSKVTMMKKFCAQWE 362
Db 324 SYCPYSQCAFNGIFLPPLOQDGFASFYFVWKFNLNTSEKVSQSKVTMMKKFCAQWE 383
QY 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFGIKQSGDAGWTLGYM 422
Db 384 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHFGIKQSGDAGWTLGYM 443
QY 423 LNLTNMIPAEQPLSTPLSHST 443
Db 444 LNLTNMIPAEQPLSTPLSHST 464
RESULT 14
AAAY70899
ID AAAY70899 standard; protein; 464 AA.
XX AC AAAY70899;
XX DT 17-AUG-2000 (first entry)
XX DE Protein encoded by Trim 1 construct.
XX KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;
KW unstable angina; myocardial infarction; stroke; coronary artery disease;
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiac;
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
XX coronary ischaemia; vascular occlusion; pIL2Trim1 variant.
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Cleavage-site 24..25
FT Protein 26..464
FT /note= "Soluble portion of CD39"
XX WO20023094-A2.
XX PD 27-APR-2000.
XX PF 13-OCT-1999; 99WO-US023641.
XX PR 16-OCT-1998; 98US-0104585P.
XX PR 06-NOV-1998; 98US-0107466P.
XX PR 13-AUG-1999; 99US-0149010P.
XX PA (IMMUNEX CORP.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Maliszewski CR, Gayle RB, Marcus AJ;
XX WPI; 2000-339518/29.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
PT mammal suffering from unstable angina, myocardial infarction, stroke,
PT coronary artery disease or injury, comprises administering soluble CD39

PT polypeptides.

XX Example 11; Page 111-112; 118pp; English.

XX The present sequence is the protein encoded by Trim1 construct. pIL2Trim1
CC variant was constructed by removing the human IL2 residues from solCD39
CC fusion construct. Fusion of 12 amino acids from the N-terminus of mature
CC human IL2 to the solCD39 coding region results in high levels of both
CC expression and activity in the supernatants of transfected cells. SolCD39
CC is used in the treatment of unstable angina, myocardial infarction,
CC stroke, coronary artery disease or injury, atherosclerosis, peripheral
CC vascular occlusion, preclampsia, embolism, platelet-associated ischaemic
CC disorder including lung ischaemia, coronary ischaemia and cerebral
CC ischaemia, a thrombotic disorder including coronary artery thrombosis,
CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery
CC thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous
CC thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.
CC Soluble CD39 is also useful for preventing thrombus formation or
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood
CC vessels or stroke

XX Sequence 464 AA;

Query Match 99.2%; Score 2350; DB 3; Length 464;

Best Local Similarity 99.5%; Pred. No. 5.1e-232;

Matches 439; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TSTQKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQVECRVKGPGISKVF 62
Db ::::|||||
Qy 24 SATQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQVECRVKGPGISKVF 83
Db ::::|||||
Qy 63 QKWEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVERSL 122
Db 84 QKWEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVERSL 143
Qy 123 LSNTPDFQGARIIITQEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG 182
Db 144 LSNTPDFQGARIIITQEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLG 203
Qy 183 GASQVTPVQNOTIESPDNALQRLYCKDYNVYTHSLFCYCKDQALWOKLAKDIOVASN 242
Db 204 GASQVTPVQNOTIESPDNALQRLYCKDYNVYTHSLFCYCKDQALWOKLAKDIOVASN 263
Qy 243 EILRDPCHPGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTNT 302
Db 264 EILRDPCHPGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTNT 323
Qy 303 SYCPSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
Db 324 SYCPSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 383
Qy 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHYFTADSWEHIFIGIKIQGSDAGWTLGYM 422
Db 384 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHYFTADSWEHIFIGIKIQGSDAGWTLGYM 443
Qy 423 LNLTMIPAEQPLSTPLSHST 443
Db 444 LNLTMIPAEQPLSTPLSHST 464

RESULT 15

AAB71918

ID AAB71918 standard; protein; 439 AA.

XX AAB71918;

AC AAB71918;

XX 09-MAY-2001 (first entry)

XX Soluble human CD39 polypeptide.

XX Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;

KW stroke; thrombotic disorder; ischaemic disorder.

XX

XX

OS Homo sapiens.

XX WO200111949-A1.

XX 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US022060.

XX 13-AUG-1999; 99US-00374586.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Pinsky DJ;

XX WPI; 2001-202805/20.

XX Treating stroke in a subject susceptible to intracranial hemorrhaging and
XX an ischemic disorder, involves administering a CD39 polypeptide which
XX inhibits ADP-mediated platelet aggregation or leukocyte accumulation.

XX Claim 3; Page 14; 118pp; English.

XX The present sequence is the active fragment of human CD39. CD39 or its
XX active fragment may be administered to treat or prevent stroke in a
XX subject susceptible to intracranial haemorrhaging or an ischaemic
XX disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
XX or leukocyte accumulation and/or ATP by increasing ADP catabolism to the
XX subject. CD39 or its active fragment is useful for treating or preventing
XX stroke, thrombotic disorders and ischaemic disorders such as peripheral
XX vascular disorder, pulmonary embolus, venous thrombosis, myocardial
XX infarction, transient ischaemic attack, unstable angina, reversible
XX ischaemic neurological deficit and sickle cell anaemia. It is also useful
XX for treating or preventing a stroke disorder in a subject undergoing
XX heart surgery, lung surgery, spinal surgery, brain surgery, vascular
XX surgery, abdominal surgery, or organ transplantation surgery

XX Sequence 439 AA;

Query Match 99.2%; Score 2348; DB 4; Length 439;

Best Local Similarity 100.0%; Pred. No. 7.5e-232;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVMHQVECRVKGPGISKVFQK 60

Qy 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVERSL 124

Db 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLDVVERSL 120

Qy 125 NYPDFQGARIIITQEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 184

Db 121 NYPDFQGARIIITQEGAGYMTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 180

Qy 185 STQVTFVQNOTIESPDNALQRLYCKDYNVYTHSLFCYCKDQALWOKLAKDIOVASNEI 244

Db 181 STQVTFVQNOTIESPDNALQRLYCKDYNVYTHSLFCYCKDQALWOKLAKDIOVASNEI 240

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Db 241 LRDPCHPGYKKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQQCHQSILELFTNTSY 300

Qy 305 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEI 364

Db 301 CPYSQCAFNGIFLPPLOQDFGAFSAFYVMKFLNLTSEKVSQEKVTMMKKFCAQPWEI 360

Qy 365 KTSYAGVKEKYLSEYCFSGTYILSLLOQGHYFTADSWEHIFIGIKIQGSDAGWTLGYMLN 424

Db 361 KTSYAGVKEKYLSEYCFSGTYILSLLOQGHYFTADSWEHIFIGIKIQGSDAGWTLGYMLN 420

Qy 425 LTNMIPAEQPLSTPLSHST 443

Db 421 LTNMIPAEQPLSTPLSHST 439

Search completed: March 7, 2005, 13:13:13
Job time : 74.4797 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 13:23:03 ; Search time 51.9709 Seconds
(without alignments)
2804.781 Million cell updates/sec

Title: US-09-835-147A-30_COPY_21_463

Perfect score: 2368
Sequence: 1 APTSTQNKALPENKYGIVL.....NLTNMIPABQPLSTPLSHST 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2368	100.0	463	9 US-09-835-147-30	Sequence 30, Appl
2	2353	99.4	454	9 US-09-835-147-6	Sequence 6, Appli
3	2353	99.4	473	9 US-09-835-147-29	Sequence 29, Appl
4	2353	99.4	474	9 US-09-835-147-28	Sequence 28, Appl
5	2353	99.4	476	9 US-09-835-147-3	Sequence 3, Appli
6	2353	99.4	478	9 US-09-835-147-8	Sequence 8, Appli
7	2350	99.2	464	9 US-09-835-147-27	Sequence 27, Appl
8	2348	99.2	439	9 US-09-374-586-2	Sequence 2, Appli
9	2348	99.2	487	9 US-09-835-147-26	Sequence 26, Appl
10	2348	99.2	502	13 US-10-092-063-38	Sequence 38, Appl
11	2348	99.2	510	9 US-09-835-147-2	Sequence 2, Appli
12	2348	99.2	510	9 US-09-374-586-1	Sequence 1, Appli
13	2348	99.2	510	10 US-09-781-796B-1	Sequence 1, Appli

14	2348	99.2	510	16	US-10-646-308-30	Sequence 30, Appl
15	2294	96.9	476	9	US-09-835-147-4	Sequence 4, Appli
16	1009	42.6	495	9	US-09-823-356-4	Sequence 4, Appli
17	910.5	38.5	529	9	US-09-923-304-4	Sequence 4, Appli
18	906.5	38.3	458	13	US-10-052-586-496	Sequence 496, App
19	906.5	38.3	458	14	US-10-174-590-496	Sequence 496, App
20	906.5	38.3	458	14	US-10-176-758-496	Sequence 496, App
21	906.5	38.3	458	14	US-10-175-737-496	Sequence 496, App
22	906.5	38.3	458	14	US-10-174-581-496	Sequence 496, App
23	906.5	38.3	458	14	US-10-176-483-496	Sequence 496, App
24	906.5	38.3	458	14	US-10-176-749-496	Sequence 496, App
25	906.5	38.3	458	14	US-10-176-914-496	Sequence 496, App
26	906.5	38.3	458	14	US-10-176-915-496	Sequence 496, App
27	906.5	38.3	458	14	US-10-173-706-496	Sequence 496, App
28	906.5	38.3	458	14	US-10-175-738-496	Sequence 496, App
29	906.5	38.3	458	14	US-10-175-752-496	Sequence 496, App
30	906.5	38.3	458	14	US-10-176-482-496	Sequence 496, App
31	906.5	38.3	458	14	US-10-176-757-496	Sequence 496, App
32	906.5	38.3	458	14	US-10-176-913-496	Sequence 496, App
33	906.5	38.3	458	14	US-10-180-552-496	Sequence 496, App
34	906.5	38.3	458	14	US-10-180-557-496	Sequence 496, App
35	906.5	38.3	458	14	US-10-173-700-496	Sequence 496, App
36	906.5	38.3	458	14	US-10-174-572-496	Sequence 496, App
37	906.5	38.3	458	14	US-10-174-579-496	Sequence 496, App
38	906.5	38.3	458	14	US-10-174-582-496	Sequence 496, App
39	906.5	38.3	458	14	US-10-175-588-496	Sequence 496, App
40	906.5	38.3	458	14	US-10-175-739-496	Sequence 496, App
41	906.5	38.3	458	14	US-10-175-740-496	Sequence 496, App
42	906.5	38.3	458	14	US-10-175-743-496	Sequence 496, App
43	906.5	38.3	458	14	US-10-176-488-496	Sequence 496, App
44	906.5	38.3	458	14	US-10-176-492-496	Sequence 496, App
45	906.5	38.3	458	14	US-10-176-747-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match 100.0%; Score 2368; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.9e-211;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVEECRVKGGISK 60
DB 21 APTSTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVEECRVKGGISK 80
QY 61 FVQKNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVE 120
DB 81 FVQKNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVE 140
QY 121 RLSNYPDFQOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALD 180
DB 141 RLSNYPDFQOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALD 200
QY 181 LGGASTQVTFVQPNQTIIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVA 240
DB 201 LGGASTQVTFVQPNQTIIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVA 260
QY 241 SNEILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIOGIGNYQQCHQSILELF 300
DB 261 SNEILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIOGIGNYQQCHQSILELF 320
QY 301 NTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMKKFCAOP 360
DB 321 NTSYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMKKFCAOP 380
QY 361 WBEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTIG 420
DB 381 WBEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTIG 440
QY 421 YMLNLTNMPAEQPLSTPLSHST 443
DB 441 YMLNLTNMPAEQPLSTPLSHST 463

RESULT 2

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 99.4%; Score 2353; DB 9; Length 454;
Best Local Similarity 99.8%; Pred. No. 4.7e-210;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 TSTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVEECRVKGGISK 62
DB 14 SSTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVEECRVKGGISK 73

QY 63 QKVNIEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 122
DB 74 QKVNIEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 133
QY 123 LSNYPDFQOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALD 182
DB 134 LSNYPDFQOGARIITGOEGAYGWITINYLKGFQKTRWFSIVPYETNNQETFGALD 193
QY 183 GASTQVTFVQPNQTIIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASN 242
DB 194 GASTQVTFVQPNQTIIESPDNALQFRLYKGDYNNVYTHSFLCYGKQDQALWQKLAKDIQVASN 253
QY 243 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIOGIGNYQQCHQSILELF 302
DB 254 EILRDPCHFGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIOGIGNYQQCHQSILELF 313
QY 303 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMKKFCAOPWE 362
DB 314 SYCPYSQCAFNGIFLPPLOQDGFAGSAFYFVWKFNLNTSEKVSQEKVTEMKKFCAOPWE 373
QY 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTIG 422
DB 374 EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHFIKIQGSDAGWTIG 433
QY 423 LNLNLTNMPAEQPLSTPLSHST 443
DB 434 LNLNLTNMPAEQPLSTPLSHST 454

RESULT 3

US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-29

Query Match 99.4%; Score 2353; DB 9; Length 473;
Best Local Similarity 99.8%; Pred. No. 5e-210;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 33 SSTQNKALPENVKYIGVLDAGSSHTSLIYIKWPAEKENDTGVVHVEECRVKGGISK 92
QY 63 QKVNIEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 122
DB 93 QKVNIEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERS 152

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DB 153 LSNYPDFQAGARIITQOEBGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDGLG 212
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QY 243 EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFT 302
DB 273 EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFT 332
QY 303 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWE 362
DB 333 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWE 392
QY 363 EIKTSYAGVKEKYLSEYCSGTYILSLLOQGHFTADSWEHIFPIKIOGSDAGWTLGYM 422
DB 393 EIKTSYAGVKEKYLSEYCSGTYILSLLOQGHFTADSWEHIFPIKIOGSDAGWTLGYM 452
QY 423 LNLNMPAEQPLSTPLSHST 443
DB 453 LNLNMPAEQPLSTPLSHST 473

RESULT 4

US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-28

Query Match 99.4%; Score 2353; DB 9; Length 474;
Best Local Similarity 99.8%; Pred. No. 5e-210;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 34 SSTONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 93
QY 63 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERS 122
DB 94 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERS 153
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DB 154 LSNYPDFQAGARIITQOEBGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDGLG 213

QY 183 GASTQVTFVPQNTTIESPNALQFRLYGKDYNNVYTHSFCLYCKDQALWOKLAKDIOVASN 242
DB 214 GASTQVTFVPQNTTIESPNALQFRLYGKDYNNVYTHSFCLYCKDQALWOKLAKDIOVASN 273
QY 243 EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFT 302
DB 274 EILRDPCHFPGYKVVVNSDLYKTPCTKRFEMTLPPQOFEIOGIGNYQOCHOSILELFT 333
QY 303 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWE 362
DB 334 SYCPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTSEKVSQEKVTEMKFKCAQPWE 393
QY 363 EIKTSYAGVKEKYLSEYCSGTYILSLLOQGHFTADSWEHIFPIKIOGSDAGWTLGYM 422
DB 394 EIKTSYAGVKEKYLSEYCSGTYILSLLOQGHFTADSWEHIFPIKIOGSDAGWTLGYM 453
QY 423 LNLNMPAEQPLSTPLSHST 443
DB 454 LNLNMPAEQPLSTPLSHST 474

RESULT 5

US-09-835-147-3
; Sequence 3, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-3

Query Match 99.4%; Score 2353; DB 9; Length 476;
Best Local Similarity 99.8%; Pred. No. 5e-210;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TSTONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 62
DB 36 SSTONKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVQVEECRVKPGISKVF 95
QY 63 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERS 122
DB 96 QKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRLVDVVERS 155
QY 123 LSNYPDFQAGARIITQOEBGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDGLG 182
DB 156 LSNYPDFQAGARIITQOEBGAYGWITINYLKGFQSKTRWFSIVPVETNNQETFGALDGLG 215
QY 183 GASTQVTFVPQNTTIESPNALQFRLYGKDYNNVYTHSFCLYCKDQALWOKLAKDIOVASN 242
DB 216 GASTQVTFVPQNTTIESPNALQFRLYGKDYNNVYTHSFCLYCKDQALWOKLAKDIOVASN 275

QY 243 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 302
DB 276 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 335
QY 303 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
DB 336 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 395
QY 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHFTADSWEHIFIGKIQGSDAGWTLGYM 422
DB 396 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHFTADSWEHIFIGKIQGSDAGWTLGYM 455
QY 423 LNLTNMIPAEQPLSTPLSHST 443
DB 456 LNLTNMIPAEQPLSTPLSHST 476

RESULT 6

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-8

Query Match 99.4%; Score 2353; DB 9; Length 478;
Best Local Similarity 99.8%; Pred. No. 5e-210;
Matches 440; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 TSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBVECRVKGPGISKVF 62
DB 38 SSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBVECRVKGPGISKVF 97
QY 63 OKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWMLLWSEELADRLVDVVERS 122
DB 98 OKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWMLLWSEELADRLVDVVERS 157
QY 123 LSNYPDFQAGRIITGQEGAYGWTITNYLLKFSQKTRWFSIVPVYETNNQETFGALDLG 182
DB 158 LSNYPDFQAGRIITGQEGAYGWTITNYLLKFSQKTRWFSIVPVYETNNQETFGALDLG 217
QY 183 GASTQVTFVQNOTIESPDNALQFRLYGKDYNNVTHSFCLCYGKDQALWOKLAKDIQVASN 242
DB 218 GASTQVTFVQNOTIESPDNALQFRLYGKDYNNVTHSFCLCYGKDQALWOKLAKDIQVASN 277
QY 243 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 302
DB 278 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 337

QY 303 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
DB 338 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 397
QY 363 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHFTADSWEHIFIGKIQGSDAGWTLGYM 422
DB 398 EIKTSYAGVKEKYLSEYCFSGTYILSLLOQGHFTADSWEHIFIGKIQGSDAGWTLGYM 457
QY 423 LNLTNMIPAEQPLSTPLSHST 443
DB 458 LNLTNMIPAEQPLSTPLSHST 478

RESULT 7

US-09-835-147-27
; Sequence 27, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: Construct of human CD39
US-09-835-147-27

Query Match 99.2%; Score 2350; DB 9; Length 464;
Best Local Similarity 99.5%; Pred. No. 9.2e-210;
Matches 439; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 TSTONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBVECRVKGPGISKVF 62
DB 24 SATONKALPENVKYIGVLDAGSSHTSLYIKWPAEKENDTGVVHQBVECRVKGPGISKVF 83
QY 63 OKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWMLLWSEELADRLVDVVERS 122
DB 84 OKNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGWMLLWSEELADRLVDVVERS 143
QY 123 LSNYPDFQAGRIITGQEGAYGWTITNYLLKFSQKTRWFSIVPVYETNNQETFGALDLG 182
DB 144 LSNYPDFQAGRIITGQEGAYGWTITNYLLKFSQKTRWFSIVPVYETNNQETFGALDLG 203
QY 183 GASTQVTFVQNOTIESPDNALQFRLYGKDYNNVTHSFCLCYGKDQALWOKLAKDIQVASN 242
DB 204 GASTQVTFVQNOTIESPDNALQFRLYGKDYNNVTHSFCLCYGKDQALWOKLAKDIQVASN 263
QY 243 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 302
DB 264 EILRDPCHFGYKVVNSDLVKTCTKRFEMTLFQOFEIOGIGNYQOCHQSILELFT 323
QY 303 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 362
DB 324 SYCPYSQCAFNGIFLPLQDGFAGSAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWE 383

QY 363 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYM 422
Db 384 EIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYM 443
QY 423 LNTNMIPAEQPLSTPLSHST 443
Db 444 LNTNMIPAEQPLSTPLSHST 464

RESULT 8

US-09-374-586-2
; Sequence 2, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match 99.2%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.3e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWVHVQVEBCRVKPGISKFVOK 64
Db 1 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWVHVQVEBCRVKPGISKFVOK 60
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 124
Db 61 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 120
QY 125 NYPPDFQAGARIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGA 184
Db 121 NYPPDFQAGARIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGA 180
QY 185 STQVTFVQNTIESPDNALQFLYKDYNVYTHSFLCYGKQOALWQKLAKDIOVASNEI 244
Db 181 STQVTFVQNTIESPDNALQFLYKDYNVYTHSFLCYGKQOALWQKLAKDIOVASNEI 240
QY 245 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 304
Db 241 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 300
QY 305 CPYSQAFNGIFLPLQDGFAGSAFYFVWKFNLNLTSEKVSQEKVTMMKFCQAPWBEI 364
Db 301 CPYSQAFNGIFLPLQDGFAGSAFYFVWKFNLNLTSEKVSQEKVTMMKFCQAPWBEI 360
QY 365 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYMLN 424
Db 361 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYMLN 420
QY 425 LTNMIPAEQPLSTPLSHST 443
Db 421 LTNMIPAEQPLSTPLSHST 439

RESULT 9

US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 99.2%; Score 2348; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.5e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWVHVQVEBCRVKPGISKFVOK 64
Db 49 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWVHVQVEBCRVKPGISKFVOK 108
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 124
Db 109 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRVLDVVERSL 168
QY 125 NYPPDFQAGARIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGA 184
Db 169 NYPPDFQAGARIITGQEGAYGWITINYLIGKFSQKTRWFSIVPYETNNQETFGALDLGA 228
QY 185 STQVTFVQNTIESPDNALQFLYKDYNVYTHSFLCYGKQOALWQKLAKDIOVASNEI 244
Db 229 STQVTFVQNTIESPDNALQFLYKDYNVYTHSFLCYGKQOALWQKLAKDIOVASNEI 288
QY 245 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 304
Db 289 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 348
QY 305 CPYSQAFNGIFLPLQDGFAGSAFYFVWKFNLNLTSEKVSQEKVTMMKFCQAPWBEI 364
Db 349 CPYSQAFNGIFLPLQDGFAGSAFYFVWKFNLNLTSEKVSQEKVTMMKFCQAPWBEI 408
QY 365 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYMLN 424
Db 409 KTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIHFQIKQSGDAGWTIGYMLN 468
QY 425 LTNMIPAEQPLSTPLSHST 443
Db 469 LTNMIPAEQPLSTPLSHST 487

RESULT 10

US-10-092-063-38
; Sequence 38, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265

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; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 38
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-38

Query Match          99.2%; Score 2348; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TONKALPENVKYGVILVLDAGSSHTSLIYKPAEKENDTGTVHVEECRVKGPISKFVOK 64
DB 38 TONKALPENVKYGVILVLDAGSSHTSLIYKPAEKENDTGTVHVEECRVKGPISKFVOK 97

QY 65 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 124
DB 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157

QY 125 NYPDFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 184
DB 158 NYPDFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217

QY 185 STQVTFVFPNQITESPNDALQRLYKGDYVNVVTHSFLCYGKDQALWQKLAKDIOVASNEI 244
DB 218 STQVTFVFPNQITESPNDALQRLYKGDYVNVVTHSFLCYGKDQALWQKLAKDIOVASNEI 277

QY 245 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 304
DB 278 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 337

QY 305 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
DB 338 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397

QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFGKIQSDAGWTLYMLN 424
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFGKIQSDAGWTLYMLN 457

QY 425 LTNMIPAEQPLSTPLSHST 443
DB 458 LTNMIPAEQPLSTPLSHST 476

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RESULT 11
US-09-835-147-2
; Sequence 2, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpe, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16

```

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; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-147-2

Query Match          99.2%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TONKALPENVKYGVILVLDAGSSHTSLIYKPAEKENDTGTVHVEECRVKGPISKFVOK 64
DB 38 TONKALPENVKYGVILVLDAGSSHTSLIYKPAEKENDTGTVHVEECRVKGPISKFVOK 97

QY 65 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 124
DB 98 VNEIGIYLTDCMERAREVIPSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157

QY 125 NYPDFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 184
DB 158 NYPDFQGARITGQEGAYGWITINLLGKFSQKTRWFSIVPYETNNQETFGALDLGA 217

QY 185 STQVTFVFPNQITESPNDALQRLYKGDYVNVVTHSFLCYGKDQALWQKLAKDIOVASNEI 244
DB 218 STQVTFVFPNQITESPNDALQRLYKGDYVNVVTHSFLCYGKDQALWQKLAKDIOVASNEI 277

QY 245 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 304
DB 278 LRDPCHPGYKVKVNVSDLYKTPCTKRPEMTLPFOQFEIQGIGNYQOCHQSILELFTSY 337

QY 305 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
DB 338 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397

QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFGKIQSDAGWTLYMLN 424
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLQGYHFTADSWEHIFGKIQSDAGWTLYMLN 457

QY 425 LTNMIPAEQPLSTPLSHST 443
DB 458 LTNMIPAEQPLSTPLSHST 476

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RESULT 12
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match          99.2%; Score 2348; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 64
DB 38 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 124
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 125 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 184
DB 158 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 185 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 244
DB 218 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 245 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 304
DB 278 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 337
QY 305 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
DB 338 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQSDAGWTGLGYMLN 424
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQSDAGWTGLGYMLN 457
QY 425 LTNMIPAEQPLSTPLSHST 443
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 13
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNI, Jean
; APPLICANT: ROBSON, Simon
; APPLICANT: BACH, Fritz H.
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 99.2%; Score 2348; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 64
DB 38 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 124

DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 125 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 184
DB 158 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 185 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 244
DB 218 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 245 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 304
DB 278 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 337
QY 305 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 364
DB 338 CPYSQCAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI 397
QY 365 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQSDAGWTGLGYMLN 424
DB 398 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFGKIQSDAGWTGLGYMLN 457
QY 425 LTNMIPAEQPLSTPLSHST 443
DB 458 LTNMIPAEQPLSTPLSHST 476

RESULT 14
US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 99.2%; Score 2348; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e-209;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 64
DB 38 TQNKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGWHQVBECECRVKGPGISKFKVOK 97
QY 65 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 124
DB 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLS 157
QY 125 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 184
DB 158 NYPFDFQAGARIITGOBEGAYGMITINYLKGFSSQKTRWFSIVPYETNNQETFGALDLGGA 217
QY 185 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 244
DB 218 STQVTFVFPQNTIESPDNALQFRLYKGDYNNVTHSFLCYGKQDQALWQKLAKDIOVASNEI 277
QY 245 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 304
DB 278 LRDPCFHPGKVKVNVSDLYKTPCTKRFEMTLPPQOFEIQGIGNYQOCHQSILELFTNSY 337

